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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 21:57:09 ; Search time 700 Seconds
(without alignments)
10736.472 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtcgactctggcctcactg.....agaacccaanaaagaacc 4228Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	4228	100.0	4228	3	US-09-479-855-3
3	268	6.3	2148	3	US-09-227-421-1
4	268	6.3	2148	3	US-09-479-855-1
5	55	1.3	2408	2	US-08-486-013-69
6	55	1.3	2408	2	US-08-482-279-69
7	55	1.3	2408	2	US-08-342-268-69
8	55	1.3	2408	3	US-09-397-386-69
9	55	1.3	2408	3	US-09-015-968-69
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27	25	0.6	48	2	US-07-931-473B-37	Sequence 37, Appl
28	25	0.6	48	2	US-08-199-507B-55	Sequence 55, Appl
29	25	0.6	48	2	US-07-714-131C-37	Sequence 37, Appl
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54	25	0.6	48	3	US-10-037-986-37	Sequence 37, Appl
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59	25	0.6	63	3	US-09-816-089A-3	Sequence 3, Appl
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87	24	0.6	49	3	US-09-302-620B-75	Sequence 75, Appl
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99 24 0.6 53 3 US-08-465-679-56 Sequence 56, Appl1
100 24 0.6 54 2 US-08-446-919A-7 Sequence 7, Appl1

ALIGNMENTS

RESULT 1

US-09-227-421-3
; Sequence 3, Application US/09227421
; Patent No. 6559357
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
; TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
; FILE REFERENCE: 023070-090700PC
; CURRENT APPLICATION NUMBER: US/09/227,421
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4228
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)-(4228)
; OTHER INFORMATION: ANT promoter
US-09-227-421-3

Query Match 100.0%; Score 4228; DB 3; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4141 TTTAGCTTACTTCTGAGAGATTATTAAGAAAGAGTGAAGATACATTATAGAAAG 4200
Db 4141 TTTAGCTTACTTCTGAGAGATTATTAAGAAAGAGTGAAGATACATTATAGAAAG 4200
Qy 4201 AGGAAGCAAGAACCAAAAAAGAAACC 4228
Db 4201 AGGAAGCAAGAACCAAAAAAGAAACC 4228

RESULT 2

US-09-479-855-3
; Sequence 3, Application US/09479855
; Patent No. 6639128
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
; FILE REFERENCE: 023070-090720US
; CURRENT APPLICATION NUMBER: US/09/479,855
; CURRENT FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4228
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: ANT gene 5' promoter
US-09-479-855-3

Query Match 100.0%; Score 4228; DB 3; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACCTTAAGGCTCACTGGCTTAATACGACTCATATAGGAGAGTCGAGATCCCTTA 60
Db 1 GTGACCTTAAGGCTCACTGGCTTAATACGACTCATATAGGAGAGTCGAGATCCCTTA 60
Qy 61 GTTAGAAAAAACTTTCTTTGTACGTGTGTGTGTGTTTAACTCAATTAATACATGTC 120
Db 61 GTTAGAAAAAACTTTCTTTGTACGTGTGTGTGTGTTTAACTCAATTAATACATGTC 120
Qy 121 ACATGTGATTCACATATATATATTAATGAATTTGAATTTATCATATTAATGAATTCAT 180
Db 121 ACATGTGATTCACATATATATATTAATGAATTTGAATTTATCATATTAATGAATTCAT 180
Qy 181 TATATATATATACCTGACATTAACCAACCAATGTTTCTGCTTTATGATATGTTCTATAT 240
Db 181 TATATATATATACCTGACATTAACCAACCAATGTTTCTGCTTTATGATATGTTCTATAT 240

Db 181 TATATATATATACCTGACATTAACCAACCAATGTTTCTGCTTTATGATATGTTCTATAT 240
Qy 241 GTTGACCTGATTAAT 300
Db 241 GTTGACCTGATTAAT 300
Qy 301 AAAAGTGAACCAAAAGCATTCATGTTTGTGTTTACTTTGTTTGTGTTTAAACGATTAAT 360
Db 301 AAAAGTGAACCAAAAGCATTCATGTTTGTGTTTACTTTGTTTGTGTTTAAACGATTAAT 360
Qy 361 ATGATTAATGAAGATTAATCTTTACTAATTAATTAATTAATTTGGAAAAACAATTTAA 420
Db 361 ATGATTAATGAAGATTAATCTTTACTAATTAATTAATTAATTTGGAAAAACAATTTAA 420
Qy 421 ATATGTGATGCTTCAGTGCCTCACTGTTCAGAAATTAATCTGATTAATCTACTTGAA 480
Db 421 ATATGTGATGCTTCAGTGCCTCACTGTTCAGAAATTAATCTGATTAATCTACTTGAA 480
Qy 481 CTAGAAAGTTGATATACATTAACAAGTGAATATTTTAAAGACCGTACATTAACAATGAT 540
Db 481 CTAGAAAGTTGATATACATTAACAAGTGAATATTTTAAAGACCGTACATTAACAATGAT 540
Qy 541 CGATCAATTAACAATTAATTAATGAGACTAGATCAATCAAGATGAGATGACTAGACATA 600
Db 541 CGATCAATTAACAATTAATTAATGAGACTAGATCAATCAAGATGAGATGACTAGACATA 600
Qy 601 TACACAGCTTAGAATTTGTACAAAGAGTGAAGAAATAGTTCTATATCAATTTAAAAAGA 660
Db 601 TACACAGCTTAGAATTTGTACAAAGAGTGAAGAAATAGTTCTATATCAATTTAAAAAGA 660
Qy 661 TATGATTTCACTTACGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
Db 661 TATGATTTCACTTACGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
Qy 721 TGTGTTTGTGTTTACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
Db 721 TGTGTTTGTGTTTACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
Qy 781 AACTGTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
Db 781 AACTGTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
Qy 841 TACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 841 TACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Qy 901 TATGTTAAGCTTACAAATTTTCTTTAGATTAATTAATTAATTAATTAATTAATTAAT 960
Db 901 TATGTTAAGCTTACAAATTTTCTTTAGATTAATTAATTAATTAATTAATTAATTAATTA 960
Qy 961 CCTTGACGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
Db 961 CCTTGACGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
Qy 1021 TCTGTCCTTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
Db 1021 TCTGTCCTTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
Qy 1081 GAGATCCCATCTAGCGCTTCAAGTTCGCTTCCTGCACTTTGGCGGTGTTGACT 1140
Db 1081 GAGATCCCATCTAGCGCTTCAAGTTCGCTTCCTGCACTTTGGCGGTGTTGACT 1140
Qy 1141 TTTTTCCTAATGCTGTTGTTTGACTTAATTTTCTCAAGTGAAGATTAATCAAGAAACT 1200
Db 1141 TTTTTCCTAATGCTGTTGTTTGACTTAATTTTCTCAAGTGAAGATTAATCAAGAAACT 1200
Qy 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATATATGCTGAAGAAACATTAATGAC 1260
Db 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATATATGCTGAAGAAACATTAATGAC 1260
Qy 1261 ACTAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
Db 1261 ACTAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320

QY	1321	AATCAAAGGAAGAGAGAGGAGCCTCTTCGTCGTATGATTTCCCTCTTAAACACTGCT	1380
DB	1321	AATCAAGGAAGAGAGAGGAGCCTCTTCGTCGTATGATTTCCCTCTTAAACACTGCT	1380
QY	1381	CCCATATCTCTTTTAACTTCCAACAAAATCATGACAGGAAAATCTGCTCGTATC	1440
DB	1381	CCCATATCTCTTTTAACTTCCAACAAAATCATGACAGGAAAATCTGCTCGTATC	1440
QY	1441	ACTTTCATGCAAAATTAAACTPAAATTTTGGTATTTTTTGCAAGTCTGCTGTTTTAAG	1500
DB	1441	ACTTTCATGCAAAATTAAACTPAAATTTTGGTATTTTTTGCAAGTCTGCTGTTTTAAG	1500
QY	1501	TGCAATATTTGGTATACATATATGATGATATACATCCAGAGTATCAATAATGAT	1560
DB	1501	TGCAATATTTGGTATACATATATGATGATATACATCCAGAGTATCAATAATGAT	1560
QY	1561	CTCCTTCTGCTTATCAATPAAATTACACACAATTAGCTATCAAGCTAATPAAATTACACA	1620
DB	1561	CTCCTTCTGCTTATCAATPAAATTACACACAATTAGCTATCAAGCTAATPAAATTACACA	1620
QY	1621	CATTCTCTTATCAATTTTATATGATPAAATAAACAACGACTATATGCTACAGAGTT	1680
DB	1621	CATTCTCTTATCAATTTTATATGATPAAATAAACAACGACTATATGCTACAGAGTT	1680
QY	1681	GGAATTAAGGCAATATATGCTCTTATGCGAAGAAATTTTTTGGTATATGATPAAACTGCTG	1740
DB	1681	GGAATTAAGGCAATATATGCTCTTATGCGAAGAAATTTTTTGGTATATGATPAAACTGCTG	1740
QY	1741	GGAATAAATAATCCAGCTATATATGCTCAATTTAAAGGATATGATTTAAATGCTTTAATCA	1800
DB	1741	GGAATAAATAATCCAGCTATATATGCTCAATTTAAAGGATATGATTTAAATGCTTTAATCA	1800
QY	1801	TTAATAATTAAGGTTTTTGGCTTTTAAAGGTTACACCGCTTAATTCATCATTAAGAGAT	1860
DB	1801	TTAATAATTAAGGTTTTTGGCTTTTAAAGGTTACACCGCTTAATTCATCATTAAGAGAT	1860
QY	1861	ATTATCTTGTATCGAATTTCCAAAATACTTTTTTTAAACATATAGAAAATTTTTCAGACTTT	1920
DB	1861	ATTATCTTGTATCGAATTTCCAAAATACTTTTTTTAAACATATAGAAAATTTTTCAGACTTT	1920
QY	1921	TTAATAATTAAGGTTACATTTATTTGGGTTCAATPAAATATGTTTCCACGTAAGTTGGAGGT	1980
DB	1921	TTAATAATTAAGGTTACATTTATTTGGGTTCAATPAAATATGTTTCCACGTAAGTTGGAGGT	1980
QY	1981	TTAACCAATGAAATGTTTTTGAATTTAAAAAACATATAATTTTCTAGTAATTTACACATT	2040
DB	1981	TTAACCAATGAAATGTTTTTGAATTTAAAAAACATATAATTTTCTAGTAATTTACACATT	2040
QY	2041	TTTAAACGTCATCCAGATTTGATATAGTGAACAAATCTGAAAACAATTTTTTTTTTCTTG	2100
DB	2041	TTTAAACGTCATCCAGATTTGATATAGTGAACAAATCTGAAAACAATTTTTTTTTTCTTG	2100
QY	2101	AATCTGTATTAATTTCTCTGCTGCGACATCTTTCGAGGATTTGACCAACGACTPACATA	2160
DB	2101	AATCTGTATTAATTTCTCTGCTGCGACATCTTTCGAGGATTTGACCAACGACTPACATA	2160
QY	2161	TTGAAGAAGAAATATCCACAGAGGATGATAGGTTAGATCCCACTCAAAATCTTTTGT	2220
DB	2161	TTGAAGAAGAAATATCCACAGAGGATGATAGGTTAGATCCCACTCAAAATCTTTTGT	2220
QY	2221	CTTTGTATTTATGAAAAACAATATTTATCAGGAAAAAAACGTTTCTTCTATGTTGTA	2280
DB	2221	CTTTGTATTTATGAAAAACAATATTTATCAGGAAAAAAACGTTTCTTCTATGTTGTA	2280
QY	2281	TAAATATTAAGATATATCAAAATTTAATCTAGTATGATTTATACATCTTCAAACTT	2340
DB	2281	TAAATATTAAGATATATCAAAATTTAATCTAGTATGATTTATACATCTTCAAACTT	2340
QY	2341	ACCATCTTCAACATTAATATTTGATCAATTTTATTTTTTAACTPAACTATCTTCACTA	2400
DB	2341	ACCATCTTCAACATTAATATTTGATCAATTTTATTTTTTAACTPAACTATCTTCACTA	2400

QY	2401	AAAAAATGCAAAAGAGATATATATTTAAGTCAAAAGTAATTAAGAATGAGTGGGTAT	2460
Db	2401	AAAAAATGCAAAAGAGATATATTTAAGTCAAAAGTAATTAAGAATGAGTGGGTAT	2460
QY	2461	TCTTCAGCAAAACGGCGCGTGAAGAGTGTCTTATCTCAATTACAGCTGGGTTGTGCAG	2520
Db	2461	TCTTCAGCAAAACGGCGCGTGAAGAGTGTCTTATCTCAATTACAGCTGGGTTGTGCAG	2520
QY	2521	ACATCATAGGGCGTACGATATATTTGAGCTTTACTGTACGTAAAGCTTTAAATATCTAGT	2580
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QY	2581	TAGTTCCTACCTGTACAAACAAACAAATCCAAATTCGTAACATATATACAAATCTACTA	2640
Db	2581	TAGTTCCTACCTGTACAAACAAACAAATCCAAATTCGTAACATATATACAAATCTACTA	2640
QY	2641	GTACTAGATTAAGCTAAGTATACATACGCTTTTGGCAAAATTCGTAACATATCTACTA	2700
Db	2641	GTACTAGATTAAGCTAAGTATACATACGCTTTTGGCAAAATTCGTAACATATCTACTA	2700
QY	2701	CAAACTTGAAATGTTTGTTTGTAATTTATCTTAAACCAAAAGTTTGAATGTGCATTGGG	2760
Db	2701	CAAACTTGAAATGTTTGTTTGTAATTTATCTTAAACCAAAAGTTTGAATGTGCATTGGG	2760
QY	2761	AGCTACACTAGTCCCTTTTTCGCCAAATATCTCTTACATGACCGGTTTAAAGT	2820
Db	2761	AGCTACACTAGTCCCTTTTTCGCCAAATATCTCTTACATGACCGGTTTAAAGT	2820
QY	2821	ATTTTAAACCAAAATTTTAAATTTTGTCGTGAAGGTACAAACATGTCATATATAGAGA	2880
Db	2821	ATTTTAAACCAAAATTTTAAATTTTGTCGTGAAGGTACAAACATGTCATATATAGAGA	2880
QY	2881	CAGCATCGTTTATCAAAATAATGTGCATGTATTGGAAATCAATATATTAATACGAATTA	2940
Db	2881	CAGCATCGTTTATCAAAATAATGTGCATGTATTGGAAATCAATATATTAATACGAATTA	2940
QY	2941	GCGACTCACTTGTTTAAATAGTTTGAAGATATGAATTAATAAATGAATTCAAAGATA	3000
Db	2941	GCGACTCACTTGTTTAAATAGTTTGAAGATATGAATTAATAAATGAATTCAAAGATA	3000
QY	3001	CAGAGCTATATATGTCGGGTCAATTAGACCGGTGACCAAAAGTTTCGTGTAATTTCTAC	3060
Db	3001	CAGAGCTATATATGTCGGGTCAATTAGACCGGTGACCAAAAGTTTCGTGTAATTTCTAC	3060
QY	3061	GGTGGGTCAATAGAAATTTTGGACTTTTCTCACCCCTTTATGAACTTCGTATATAGTTT	3120
Db	3061	GGTGGGTCAATAGAAATTTTGGACTTTTCTCACCCCTTTATGAACTTCGTATATAGTTT	3120
QY	3121	TGTGGATTAATATTTGTATTCGTATATTTTTTGTTCATATATGATATAGTAATTCGA	3180
Db	3121	TGTGGATTAATATTTGTATTCGTATATTTTTTGTTCATATATGATATAGTAATTCGA	3180
QY	3181	CGATTAAGAAAGCTTTTATTTAATTTGAATTTAAACCTTTGTTTGGAAATGACT	3240
Db	3181	CGATTAAGAAAGCTTTTATTTAATTTGAATTTAAACCTTTGTTTGGAAATGACT	3240
QY	3241	CATACACAAGGTAAAGTTGATAGGTATCCAAATTCAGAAATGTTTCGAGAGCGCTC	3300
Db	3241	CATACACAAGGTAAAGTTGATAGGTATCCAAATTCAGAAATGTTTCGAGAGCGCTC	3300
QY	3301	GAGTGTCTTACACCATCTGTACCAACTCGTATGAGGTTTATATATAGGTTTTTCTTCTT	3360
Db	3301	GAGTGTCTTACACCATCTGTACCAACTCGTATGAGGTTTATATATAGGTTTTTCTTCTT	3360
QY	3361	TTTCCAAATGCTTTATTAATGAACAACCTTAATTTCTTTTAAATATAGGTTAAGAT	3420
Db	3361	TTTCCAAATGCTTTATTAATGAACAACCTTAATTTCTTTTAAATATAGGTTAAGAT	3420
QY	3421	CTTGAATTTTCGTGATTTTAAACCAAGGTTTCAATTCCTCTTACACAAAATTAATTA	3480
Db	3421	CTTGAATTTTCGTGATTTTAAACCAAGGTTTCAATTCCTCTTACACAAAATTAATTA	3480
QY	3481	AAAAGTTTCAATTAATTAAGAAATCTAATTTTGTGATCAAGAGTTTATATATAGCT	3540

Db	3481	AAAAAGTTTCAATATTAATAAGAACTCTAAATTTTGTAGTTCAAGAGTTTAATGATAGCT	3540
Qy	3541	GAAGAATTATGAATGATTCGAAGTTTGGCAACAGATGGTCGATGATGACATTAACAAAA	3600
Db	3541	GAAGAATTATGAATGATTCGAAGTTTGGCAACAGATGGTCGATGATGACATTAACAAAA	3600
Qy	3601	CATGCATCAAAATTAATATTTGCTGCTTAGACGAAGAAAACGATTGAAATTAACACAAACAT	3660
Db	3601	CATGCATCAAAATTAATATTTGCTGCTTAGACGAAGAAAACGATTGAAATTAACACAAACAT	3660
Qy	3661	CGTTAACCACTTAAATAATCTTAGAATAATTTGTAGTATATTTCTGTAAAGAGAGG	3720
Db	3661	CGTTAACCACTTAAATAATCTTAGAATAATTTGTAGTATATTTCTGTAAAGAGAGG	3720
Qy	3721	TATCATATCTTACAAAAAAATCTCATTTCAGATTAATAATATGTTGTCGAATCGTTACCA	3780
Db	3721	TATCATATCTTACAAAAAAATCTCATTTCAGATTAATAATATGTTGTCGAATCGTTACCA	3780
Qy	3781	AGTATGTTTTGCTGCTCATGAGTTGATATGTAACCTGCTCTTGAAGCAATATAGTTCTAAG	3840
Db	3781	AGTATGTTTTGCTGCTCATGAGTTGATATGTAACCTGCTCTTGAAGCAATATAGTTCTAAG	3840
Qy	3841	TTTTAAATGTTTTCAAAAGCTTTACAAAATTAATAATAATAAGAGTGAATTTGTAGGG	3900
Db	3841	TTTTAAATGTTTTCAAAAGCTTTACAAAATTAATAATAATAAGAGTGAATTTGTAGGG	3900
Qy	3901	CTAAAGGGAATAATTAATAATAATAATAAGAAACGCTCTTTCATATAGAACAC	3960
Db	3901	CTAAAGGGAATAATTAATAATAATAATAATAAGAAACGCTCTTTCATATAGAACAC	3960
Qy	3961	AGATCCCAACGGAATTCAAACAGCAAAATTTGCTTGGCTCTCTCTCTATTAATAATATC	4020
Db	3961	AGATCCCAACGGAATTCAAACAGCAAAATTTGCTTGGCTCTCTCTCTATTAATAATATC	4020
Qy	4021	CTCTCAAAAAACCTCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTGTTCTTACCGCAA	4080
Db	4021	CTCTCAAAAAACCTCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTGTTCTTACCGCAA	4080
Qy	4081	CAAAAGAAAAACCAAAAGTTTGAGAAAAATGGTGTGTTGCTGTGTGAACCAATGATGGGT	4140
Db	4081	CAAAAGAAAAACCAAAAGTTTGAGAAAAATGGTGTGTTGCTGTGTGAACCAATGATGGGT	4140
Qy	4141	TTTAGCTTACTACTTCGAGAGATTATAGAAAAGAAAGTAGAGATACATTATAGAAAAG	4200
Db	4141	TTTAGCTTACTACTTCGAGAGATTATAGAAAAGAAAGTAGAGATACATTATAGAAAAG	4200
Qy	4201	AGAGAGACGAACCAAAAAAAAGAAACC 4228	
Db	4201	AGAGAGACGAACCAAAAAAAAGAAACC 4228	

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1 RESULT 3
2 US-09-227-421-1
3 Sequence 1, Application US/09227421
4 Patent No. 6559357
5 GENERAL INFORMATION:
6 APPLICANT: Fischer, Robert L.
7 APPLICANT: Mizukami, Yukiko
8 APPLICANT: The Regents of the University of California
9 TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
10 TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
11 FILE REFERENCE: 023070-050700PC
12 CURRENT APPLICATION NUMBER: US/09/227,421
13 CURRENT FILING DATE: 1999-01-08
14 PRIOR APPLICATION NUMBER: US 09/227,421
15 PRIOR FILING DATE: 1999-01-08
16 NUMBER OF SEQ ID NOS: 8
17 SOFTWARE: PatentIn Ver. 2.1
18 SEQ ID NO 1
19 LENGTH: 2148
20 TYPE: DNA
21 ORGANISM: Arabidopsis thaliana

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (269)..(1936)
; OTHER INFORMATION: AINTEGUMENTA (ANT)
; NAME/KEY: misc feature
; LOCATION: (1109)..(1339)
; OTHER INFORMATION: encodes first AP2 domain
; NAME/KEY: misc feature
; LOCATION: (1340)..(1414)
; OTHER INFORMATION: encodes linker region
; NAME/KEY: misc feature
; LOCATION: (1415)..(1621)
; OTHER INFORMATION: encodes second AP2 domain
US-09-227-421-1

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Query Match	6.3%: Score 268; DB 3; Length 2148;
Best Local Similarity	100.0%; Pred. No. 5.3e-96;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 3961 AGATCCCAACGATTTCAAACAGCAAAATTTGCTTTGCTCTCTCTCTATTAATATATC	4020
DB 1 AGATCCCAACGATTTCAAACAGCAAAATTTGCTTTGCTCTCTCTCTATTAATATATC	60
QY 4021 CTCCTAAAAACCTCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTTCTCTACCGCA	4086
DB 61 CTCCTAAAAACCTCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTTCTCTACCGCA	120
QY 4081 CAAAGAAAAAACAAAGTTTGAAGAAATGGTGTTGCTGTGTGAACCAATGATTTGGGT	4148
DB 121 CAAAGAAAAAACAAAGTTTGAAGAAATGGTGTTGCTGTGTGAACCAATGATTTGGGT	180
QY 4141 TTTAGCTTACTACTTCGAGAGATTATAGAAGAAAGTGAAGATACATTATAGAAAGA	4200
DB 181 TTTAGCTTACTACTTCGAGAGATTATAGAAGAAAGTGAAGATACATTATAGAAAGA	240
QY 4201 AGAGAGCAAGAAACCAAAAAAGAAACC 4228	
DB 241 AGAGAGCAAGAAACCAAAAAAGAAACC 268	
RESULT 4	
US-09-479-855-1	
Sequence 1, Application US/09479855	
Patent No. 6639128	
GENERAL INFORMATION:	
APPLICANT: Fischer, Robert L.	
APPLICANT: Mizukami, Yukiko	
TITLE OF INVENTION: The Regents of the University of California	
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility	
FILE REFERENCE: 023070-090720US	
CURRENT APPLICATION NUMBER: US/09/479, 855	
CURRENT FILING DATE: 2000-01-07	
NUMBER OF SEQ ID NOS: 8	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 1	
LENGTH: 2148	
TYPE: DNA	
ORGANISM: Arabidopsis thaliana	
FEATURE:	
OTHER INFORMATION: AINTEGUMENTA (ANT) cDNA	
NAME/KEY: CDS	
LOCATION: (269)..(1916)	
OTHER INFORMATION: AINTEGUMENTA (ANT)	
US-09-479-855-1	
Query Match	6.3%: Score 268; DB 3; Length 2148;
Best Local Similarity	100.0%; Pred. No. 5.3e-96;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 3961 AGATCCCAACGATTTCAAACAGCAAAATTTGCTTTGCTCTCTCTATTAATATATC	4020
DB 1 AGATCCCAACGATTTCAAACAGCAAAATTTGCTTTGCTCTCTCTATTAATATATC	60

Qy 4021 CTCTCAAAAACCTCTCTATATCTCTAAAGCCCTCTCTGTTTCTTACCGCA 4080
|
Db 61 CTCTCAAAAACCTCTCTATATCTCTAAAGCCCTCTCTGTTTCTTACCGCA 120
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Qy 4081 CAAAGAAAAAACAAGTTTGAGAAAAATGCTGTCTGTGTAAACCAATGATTGGGT 4140
|
Db 121 CAAAGAAAAAACAAGTTTGAGAAAAATGCTGTCTGTGTAAACCAATGATTGGGT 180
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Qy 4141 TTTAGTTACTACTTCGAGAGATTATAGAAAAAGAGTAGAATACATTATAGAAAGA 4200
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Db 181 TTTAGTTACTACTTCGAGAGATTATAGAAAAAGAGTAGAATACATTATAGAAAGA 240
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Qy 4201 AGAGAGCAAGAAACCAAAAAAGAAACC 4228
|
Db 241 AGAGAGCAAGAAACCAAAAAAGAAACC 268
|
RESULT 5
US-08-486-013-69
Sequence 69, Application US/08486013
Patent No. 5731149
GENERAL INFORMATION:
APPLICANT: Selseled, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
NUMBER OF INVENTION: of Their Use
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,013
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-486-013-69
Query Match 1.3%; Score 55; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GTGACTCTAGGCGCTCACTGAGCTCAATATGAGCTGAGGAGCTCGAGGATC 55
|||||

Db 666 GTGACTCTAGGCGCTCACTGAGCTCAATATGAGCTGAGGAGCTCGAGGATC 720
|
RESULT 6
US-08-482-279-69
Sequence 69, Application US/08482279
Patent No. 5840498
GENERAL INFORMATION:
APPLICANT: Selseled, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
NUMBER OF INVENTION: of Their Use
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,279
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-482-279-69
Query Match 1.3%; Score 55; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GTGACTCTAGGCGCTCACTGAGCTCAATATGAGCTGAGGAGCTCGAGGATC 55
|||||
Db 666 GTGACTCTAGGCGCTCACTGAGCTCAATATGAGCTGAGGAGCTCGAGGATC 720
|
RESULT 7
US-08-342-268-69
Sequence 69, Application US/08342268
Patent No. 5844072
GENERAL INFORMATION:
APPLICANT: Selseled, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
NUMBER OF INVENTION: of Their Use
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,268
FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-342-268-69

Query Match 1.3%; Score 55; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCACTTAGGCTCAGCTGAGCTAATAGCACTCACTATTAGGAGCTCGAGATC 55
DB 666 GTGCACTTAGGCTCAGCTGAGCTAATAGCACTCACTATTAGGAGCTCGAGATC 720

RESULT 8
US-09-015-968-69
Sequence 69, Application US/09015968
Patent No. 6057425
GENERAL INFORMATION:
APPLICANT: Seistead, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-015-968-69

Query Match 1.3%; Score 55; DB 3; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCACTTAGGCTCAGCTGAGCTAATAGCACTCACTATTAGGAGCTCGAGATC 55
DB 666 GTGCACTTAGGCTCAGCTGAGCTAATAGCACTCACTATTAGGAGCTCGAGATC 720

RESULT 9
US-09-397-386-69
Sequence 69, Application US/09397386
Patent No. 6300470
GENERAL INFORMATION:
APPLICANT: Seistead, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,386
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-397-386-69

Query Match 1.3%; Score 55; DB 3; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 666 GTGACTTATGGCTCTACTGGCTTATACGACTCACTATATAGGAGCTCGAGATC 55
1 GTGACTTATGGCTCTACTGGCTTATACGACTCACTATATAGGAGCTCGAGATC 55
666 GTGACTTATGGCTCTACTGGCTTATACGACTCACTATATAGGAGCTCGAGATC 720

RESULT 10
US-08-459-448A-26/C
Sequence 26, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Kozel, Michael G.
APPLICANT: Deest, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launig, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Sutcliffe, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336art's Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8582
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-448A-26

Query Match 0.8%; Score 32; DB 2; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 TTGGCTTATAGCACTCACTATATAGGAGCTCGA 50
4162 TTGGCTTATAGCACTCACTATATAGGAGCTCGA 4131

RESULT 11
US-08-459-595A-26/C
Sequence 26, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launib, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451

FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-595A-26
Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 TGGCTTAATACGACTCACTATAGGAGCTCGA 50
DB 4162 TGGCTTAATACGACTCACTATAGGAGCTCGA 4131
RESULT 12
US-08-459-504B-26/C
Sequence 26, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launib, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mel98, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
FAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:

NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
US-08-459-504B-26
Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cv 19 TGGCTATACGACTGACTATAGGAGCTCGA 50
Db 4162 TGGCTATACGACTGACTATAGGAGCTCGA 4131
RESULT 13
US-08-459-444-26/C
Sequence 26, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-JUN-1995
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mel98, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/PL/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
FAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE: NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE: NAME/KEY: exon
LOCATION: 1481..2366
FEATURE: NAME/KEY: intron
LOCATION: 2367..2451
FEATURE: NAME/KEY: exon
LOCATION: 2452..2602
FEATURE: NAME/KEY: intron
LOCATION: 2603..2690
FEATURE: NAME/KEY: exon
LOCATION: 2691..2804
FEATURE: NAME/KEY: intron
LOCATION: 2805..2906
FEATURE: NAME/KEY: exon
LOCATION: 2907..3075
FEATURE: NAME/KEY: intron
LOCATION: 3076..3177
FEATURE: NAME/KEY: exon
LOCATION: 3178..3304
FEATURE: NAME/KEY: intron
LOCATION: 3305..3398
FEATURE: NAME/KEY: exon
LOCATION: 3399..3498
FEATURE: NAME/KEY: intron
LOCATION: 3499..3713
FEATURE: NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-08-459-444-26
Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 TGGCTTAATGACGACTCATATAGGAGCTCGA 50
DB 4162 TGGCTTAATGACGACTCATATAGGAGCTCGA 4131
RESULT 14
US-09-547-422-26/c
Sequence 26, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Deeal, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE: NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE: NAME/KEY: exon
LOCATION: 1481..2366
FEATURE: NAME/KEY: intron
LOCATION: 2367..2451
FEATURE: NAME/KEY: exon
LOCATION: 2452..2602
FEATURE: NAME/KEY: intron
LOCATION: 2603..2690
FEATURE: NAME/KEY: exon
LOCATION: 2691..2804
FEATURE: NAME/KEY: intron
LOCATION: 2805..2906
FEATURE: NAME/KEY: exon
LOCATION: 2907..3075
FEATURE: NAME/KEY: intron
LOCATION: 3076..3177
FEATURE: NAME/KEY: exon
LOCATION: 3178..3304

NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-547-422-26

Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGCTAATAGACTCACTATAGGAGCTCGA 50
DB 4162 TGGCTAATAGACTCACTATAGGAGCTCGA 4131

RESULT 15
US-09-988-462-26/C
Sequence 26, Application US/09988462
Patent No. 6720488
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. 6720488-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Melis, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"

FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-988-462-26

Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGCTAATAGACTCACTATAGGAGCTCGA 50
DB 4162 TGGCTAATAGACTCACTATAGGAGCTCGA 4131

RESULT 16
US-07-951-715A-26/C
Sequence 26, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.

APPLICANT: Evoia, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Meriin, Ellis J.
APPLICANT: Launig, Karen L.
APPLICANT: Rothelein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sprull, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1416..1425
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2449
FEATURE:
NAME/KEY: exon
LOCATION: 2450..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2688
FEATURE:
NAME/KEY: exon
LOCATION: 2689..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3074

FEATURE:
NAME/KEY: intron
LOCATION: 3075..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3305
FEATURE:
NAME/KEY: intron
LOCATION: 3306..3397
FEATURE:
NAME/KEY: exon
LOCATION: 3398..3497
FEATURE:
NAME/KEY: intron
LOCATION: 3498..3712
FEATURE:
NAME/KEY: exon
LOCATION: 3713..3811
US-07-951-715A-26

Query Match 0.7%; Score 31; DB 2; Length 4165;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 GGCTAATAGCACTCACTAATAGGAGCTCGA 50
Db 4165 GGCTAATAGCACTCACTAATAGGAGCTCGA 4135

RESULT 17
US-09-308-090-1
Sequence 1, Application US/09308090
Patent No. 6395963
GENERAL INFORMATION:
APPLICANT: OHL, Stephan
APPLICANT: Van Der Lee, Frederique
APPLICANT: Goddijn, Oscar
APPLICANT: Klap, Joke
APPLICANT: Sijmons, Peter
TITLE OF INVENTION: Nematode-Inducible Regulatory DNA Sequences
FILE REFERENCE: MOG 57680
CURRENT APPLICATION NUMBER: US/09/308,090
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/EP97/06472
EARLIER FILING DATE: 1997-11-18
EARLIER APPLICATION NUMBER: EP 96203213.2
EARLIER FILING DATE: 1996-11-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 3484
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (3482)..(3484)
US-09-308-090-1

Query Match 0.7%; Score 28; DB 3; Length 3484;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGCACTCACTAATAGGAGCTCGA 50
Db 698 CTAATAGCACTCACTAATAGGAGCTCGA 725

RESULT 18
US-09-380-090A-1
Sequence 1, Application US/09380090A
Patent No. 6555529
GENERAL INFORMATION:
APPLICANT: OHL, Stephan Andreas

;; SIMONS, Peter Christiaan
;; KLEIN-VAN DER LEE, Frederique
;; Marianne
;; GODDUN, Oscar
;; Klap, Joke
;; TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
;; SEQUENCES
;;
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hale and Dorr LLP
;; STREET: 60 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: United States
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/380,090A
;; FILING DATE: 17-May-1999
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/EP97/06472
;; FILING DATE: 18-NOV-1997
;; APPLICATION NUMBER: EP 96203213.2
;; FILING DATE: 18-NOV-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Superko, Colleen
;; REGISTRATION NUMBER: 39,850
;; REFERENCE/DOCKET NUMBER: SYN-010
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 526-6000
;; TELEFAX: (617) 526-5000
;;
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3484 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Arabidopsis thaliana
;; STRAIN: C24
;;
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3481..3484
;; OTHER INFORMATION: /codon_start= 3482
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
;;
;; US-09-380-090A-1
;;
Query Match 0.7%; Score 28; DB 3; Length 3484;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAGCTCGA 50
Db 698 CTAATAGACTCACTATAGGAGCTCGA 725

RESULT 19
PCT-US96-11473A-23
Sequence 23; Application PC/TUS9611473A
GENERAL INFORMATION:
APPLICANT: LARRY GOLD
APPLICANT: MICHAEL LOCHRIE
APPLICANT: HANG CHEN
APPLICANT: CRAIG TUERK
TITLE OF INVENTION: INTRACELLULAR ACTION OF

;; TITLE OF INVENTION: NUCLEIC ACID LIGANDS
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Swanson and Bratschum, L.L.C.
;; STREET: 8400 East Prentice Avenue, Suite #200
;; CITY: Englewood
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
;; OPERATING SYSTEM: IBM compatible
;; SOFTWARE: Wordperfect 6.0
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/11473A
;; FILING DATE:
;; CLASSIFICATION:
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/521,515
;; FILING DATE: 30-AUGUST-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/000,872
;; FILING DATE: 11-JULY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barry J. Swanson
;; REGISTRATION NUMBER: 33,215
;; REFERENCE/DOCKET NUMBER: NEX45/PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 793-3333
;; TELEFAX: (303) 793-3433
;;
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 239 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: RNA
;;
;; PCT-US96-11473A-23
;;
Query Match 0.6%; Score 26; DB 6; Length 239;
Best Local Similarity 76.9%; Pred. No. 1.6;
Matches 20; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAGCTC 48
Db 94 CTAATAGACTCACTATAGGAGCTC 119

RESULT 20
US-09-949-016-55437
Sequence 55437; Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55437
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-55437

Query Match 0.6%; Score 26; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAAATTAATTAATTAAGTAAA 3935
DB 500 AAAAAATTAATTAATTAAGTAAA 525

RESULT 21

US-09-949-016-13362/c
; Sequence 13362, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13362
; LENGTH: 285478
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(285478)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13362

Query Match 0.6%; Score 26; DB 3; Length 285478;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAAATTAATTAATTAAGTAAA 3935
DB 97296 AAAAAATTAATTAATTAAGTAAA 97271

RESULT 22

US-08-458-423A-11/c
; Sequence 11, Application US/08458423A
; Patent No. 5731144
; GENERAL INFORMATION:
; APPLICANT: PENELOPE J. TOOTHMAN
; APPLICANT: STEVEN RINGQUIST
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY TGFA NUCLEIC
; ACID LIGANDS AND INHIBITORS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,423A

FILING DATE: 2-JUNE-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991

FILING DATE: 8-SEPTEMBER-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

ATTORNEY/AGENT INFORMATION:

NAME: Diane H. McClearn

REGISTRATION NUMBER: 33,960

REFERENCE/DOCKET NUMBER: NEX 34-1

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-458-423A-11

Query Match 0.6%; Score 25; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCATATAGGAGCTC 48
DB 33 TATACGACTCATATAGGAGCTC 9

RESULT 23

US-08-458-424B-11/c
; Sequence 11, Application US/08458424B
; Patent No. 5731424
; GENERAL INFORMATION:
; APPLICANT: PENELOPE J. TOOTHMAN
; APPLICANT: STEVEN RINGQUIST
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY TGFA NUCLEIC
; ACID LIGANDS AND INHIBITORS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,424B
; FILING DATE: 2-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McLearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX 34-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-458-424B-11

Query Match 0.6%; Score 25; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 24 TAATACGACTCAGTATAGGAGCTC 48
DB 33 TAATACGACTCAGTATAGGAGCTC 9

RESULT 24
US-08-973-124-11/c
Sequence 11, Application US/08973124
Patent No. 6207816
GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594

FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-973-124-11

Query Match 0.6%; Score 25; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 24 TAATACGACTCAGTATAGGAGCTC 48
DB 33 TAATACGACTCAGTATAGGAGCTC 9

RESULT 25
PCT-US96-08014-11/c
Sequence 11, Application PC/TUS9608014
GENERAL INFORMATION:
APPLICANT: LARRY GOLD, NEBOJSA JANJIC, STEVEN RINGQUIST,
TITLE OF INVENTION: PAGRATIS/PENELOPE J. TOOTHMAN
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR (TGF), PLATELET-DERIVED
TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,633
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US96-08014-11

Query Match 0.6%; Score 25; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 33 TAATAGACTCACTATAGGAGCTC 9

RESULT 26
US-09-268-710-1
Sequence 1, Application US/09268710
Patent No. 6261773
GENERAL INFORMATION:
APPLICANT: Segawa, Masaya
APPLICANT: Kondo, Motohiro
APPLICANT: Takarada, Yutaka
TITLE OF INVENTION: Reagent for Nucleic Acid Amplification and Process for
FILE REFERENCE: 10089/8
CURRENT APPLICATION NUMBER: US/09/268,710
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: JP P1998/66988
EARLIER FILING DATE: 1998-03-17
EARLIER APPLICATION NUMBER: JP P1999/18434
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_binding
LOCATION: (28)..(47)
OTHER INFORMATION: DNA sequence complementary to a sequence of
OTHER INFORMATION: Mycobacterium tuberculosis 16S rRNA gene
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(27)
OTHER INFORMATION: promoter for T7 RNA polymerase
US-09-268-710-1

Query Match 0.6%; Score 25; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAGCT 47
DB 5 CTAATAGACTCACTATAGGAGCT 29

RESULT 27
US-07-931-473B-37
Sequence 37, Application US/07931473B
Patent No. 5270163
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/931,473B
FILING DATE: 19920817
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-931-473B-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 28
US-08-199-507B-55
Sequence 55, Application US/08199507B
Patent No. 5472641
GENERAL INFORMATION:
APPLICANT: JAYASENA, S. AND GOLD, L.
TITLE OF INVENTION: NUCLEIC ACID LIGAND INHIBITORS
TITLE OF INVENTION: OF HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado

COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,507B
FILING DATE: 22 FEBRUARY 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-199-507B-55

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTATAGGAGCTC 48
Db 9 TAATACGACTCATTATAGGAGCTC 33

RESULT 29
US-07-714-131C-37
Sequence 37, Application US/07714131C
Patent No. 5475096
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 344
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,131C
FILING DATE: June 10, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900

TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-714-131C-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTATAGGAGCTC 48
Db 9 TAATACGACTCATTATAGGAGCTC 33

RESULT 30
US-08-243-870-1
Sequence 1, Application US/08243870
Patent No. 5527894
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY M.
TITLE OF INVENTION: LIGANDS OF HIV-1 cat PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,870
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/953,694
FILING DATE: 29-SEPTEMBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-243-870-1

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTATAGGAGCTC 48
Db 9 TAATACGACTCATTATAGGAGCTC 33

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RESULT 31
US-08-442-572-58
; Sequence 58, Application US/08442572
; Patent No. 5587468
; GENERAL INFORMATION:
; APPLICANT: Allen, Patrick, and Gold, Larry
; TITLE OF INVENTION: High Affinity HIV
; TITLE OF INVENTION: Integrase Inhibitors
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratechun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,572
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/177,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-442-572-58
;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 24 TAATAGACTCACTATAGGAGCTC 48
| | | | | | | | | | | | | | | | | |
Db 9 TAATAGACTCACTATAGGAGCTC 33
```

```
RESULT 32
US-08-477-530-2
; Sequence 2, Application US/08477530
```

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; Patent No. 5635400
; GENERAL INFORMATION:
; APPLICANT: PATRICK ALLEN
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY HIV
; TITLE OF INVENTION: NUCLEOCAPSID NUCLEIC ACID LIGANDS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratechun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,530
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,474
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,172
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McClearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX 44-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
;
US-08-477-530-2
;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 24 TAATAGACTCACTATAGGAGCTC 48
| | | | | | | | | | | | | | | | | |
Db 9 TAATAGACTCACTATAGGAGCTC 33
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RESULT 33
US-08-477-530-2
; Sequence 2, Application US/08477530
; Patent No. 5635615
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: GENERAL INFORMATION:
: APPLICANT: PATRICK ALLEN
: APPLICANT: LARRY GOLD
: TITLE OF INVENTION: HIGH AFFINITY HIV
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESS: Swanson and Bratschun, L.L.C.
: STREET: 8400 East Prentice Avenue, Suite #200
: CITY: Denver
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80111
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
: COMPUTER: IBM compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 6.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,530
: FILING DATE: 7-JUNE-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/714,131
: FILING DATE: 10-JUNE-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/536,428
: FILING DATE: 11-JUNE-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/964,624
: FILING DATE: 21-OCTOBER-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/117,991
: FILING DATE: 8-SEPTEMBER-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/931,474
: FILING DATE: 17-AUGUST-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/361,795
: FILING DATE: 21-DECEMBER-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/477,172
: FILING DATE: 19-MAY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Diane H. McClearn
: REGISTRATION NUMBER: 33,960
: REFERENCE/DOCKET NUMBER: NEX 44-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 48 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: RNA
: US-08-477-530-2
:
Query Match      0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
OY      24 TAATACGACTCACTATAGGAGCTC 48
Db      9 TAATACGACTCACTATAGGAGCTC 33
:
RESULT 34
US-08-409-439A-1
: Sequence 1, Application US/08409439A
: Patent No. 5637461
: GENERAL INFORMATION:

```

```

: APPLICANT: GOLD, LARRY M.
: APPLICANT: TURK, CRAIG
: TITLE OF INVENTION: LIGANDS OF HIV-1 tat PROTEIN
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESS: Swanson & Bratschun, L.L.C.
: STREET: 8400 E. Prentice Avenue, Suite 200
: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80111
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
: COMPUTER: IBM compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 6.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/409,439A
: FILING DATE: 24-MARCH-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/953,694
: FILING DATE: 29-SEPTEMBER-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/714,131
: FILING DATE: 10-JUNE-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/536,428
: FILING DATE: 11-JUNE-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Barry J. Swanson
: REGISTRATION NUMBER: 33,215
: REFERENCE/DOCKET NUMBER: NEX03/D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 48 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-409-439A-1
:
Query Match      0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
OY      24 TAATACGACTCACTATAGGAGCTC 48
Db      9 TAATACGACTCACTATAGGAGCTC 33
:
RESULT 35
US-08-441-591-2
: Sequence 2, Application US/08441591
: Patent No. 5637682
: GENERAL INFORMATION:
: APPLICANT: NIEMLANDT, D., GOLD, L. AND WECKER, M.
: TITLE OF INVENTION: HIGH-AFFINITY
: TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
: TITLE OF INVENTION: TO THE TACHYKININ
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESS: Swanson & Bratschun, L.L.C.
: STREET: 8400 E. Prentice Avenue, Suite 200
: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80111
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage

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COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,591
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 9-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 36
US-08-384-708A-2
Sequence 2, Application US/08384708A
Patent No. 5639868
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Janjic, Nebojsa
TITLE OF INVENTION: High-Affinity RNA Ligands of Basic
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,708A

FILING DATE: 02-FEBRUARY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-384-708A-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 37
US-08-303-362A-2
Sequence 2, Application US/08303362A
Patent No. 5648214
GENERAL INFORMATION:
APPLICANT: NIEMULANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,362A
FILING DATE: 9-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-362A-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCCTATAGGAGCTC 48
DB 9 TAATACGACTCCTATAGGAGCTC 33

RESULT 38
US-08-477-830-2
Sequence 2, Application US/08477830
Patent No. 5654151
GENERAL INFORMATION:
APPLICANT: PATRICK ALLEN
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY HIV
TITLE OF INVENTION: NUCLEOSAPSID NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 830
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,474
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,795
FILING DATE: 21-DECEMBER-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,172
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McLearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX 44-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-477-830-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCCTATAGGAGCTC 48
DB 9 TAATACGACTCCTATAGGAGCTC 33

RESULT 39
US-08-412-110-37
Sequence 37, Application US/08412110
Patent No. 5670637
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Therk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 344
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,110
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-412-110-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTACTATAGGAGCTC 48
DB 9 TAATAGACTACTATAGGAGCTC 33

RESULT 40
US-08-409-442A-37
Sequence 37, Application US/08409442A
Patent No. 5696249
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,442A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-409-442A-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTACTATAGGAGCTC 48
DB 9 TAATAGACTACTATAGGAGCTC 33

RESULT 41
US-08-441-828-55
Sequence 55, Application US/08441828
Patent No. 5734034
GENERAL INFORMATION:
APPLICANT: JAYASENA, S. AND GOLD, L.
TITLE OF INVENTION: NUCLEIC ACID LIGAND INHIBITORS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,828
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,507
FILING DATE: 22 FEBRUARY 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-828-55

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTACTATAGGAGCTC 48
DB 9 TAATAGACTACTATAGGAGCTC 33

RESULT 42
US-08-361-795-58
Sequence 58, Application US/08361795
Patent No. 5756287
GENERAL INFORMATION:
APPLICANT: Allen, Patrick, and Gold, Larry
TITLE OF INVENTION: High Affinity HIV
INTEGRASE INHIBITORS
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,795
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-361-795-58

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAAATAGACTCCTATAGGAGCTC 48
Db 9 TAAATAGACTCCTATAGGAGCTC 33

RESULT 43
US-08-447-169A-2
Sequence 2, Application US/08447169A
Patent No. 5811533
GENERAL INFORMATION:
APPLICANT: JANJIC, N. and GOLD, L.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Place, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,169A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233,012
FILING DATE: 25-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205,515
FILING DATE: 03-MARCH-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-169A-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAAATAGACTCCTATAGGAGCTC 48
Db 9 TAAATAGACTCCTATAGGAGCTC 33

RESULT 44
US-08-469-609A-37
Sequence 37, Application US/08469609A
Patent No. 5843653
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,609A
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-609A-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TATACGACTCACTATAGGAGCTC 48
Db 9 TATACGACTCACTATAGGAGCTC 33

RESULT 45
US-08-233-012C-2
Sequence 2, Application US/08233012C
Patent No. 5849479
GENERAL INFORMATION:
APPLICANT: JANITC, N. and GOLD, L.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Place, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,012C
FILING DATE: 25-APRIL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA: 07/964,624
APPLICATION NUMBER: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-233-012C-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TATACGACTCACTATAGGAGCTC 48
Db 9 TATACGACTCACTATAGGAGCTC 33

RESULT 46
US-08-477-527A-208
Sequence 208, Application US/08477527A
Patent No. 5972599
GENERAL INFORMATION:
APPLICANT: DIANE TASET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA
US-08-477-527A-208

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TATACGACTCACTATAGGAGCTC 48

Db 9 TAATACGACTCATATAGGAGCTC 33

RESULT 47

US-08-481-710-208
; Sequence 208, Application US/08481710
; Patent No. 6028186
; GENERAL INFORMATION:
; APPLICANT: DIANE TASSSET
; APPLICANT: NIKOS PAGRATIS
; APPLICANT: SUMEDHA JAYASENA
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; TITLE OF INVENTION: OF CYTOKINES
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,710
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McClearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX41-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-481-710-208

Query Match 0.6%; Score 25; DB 3; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATATAGGAGCTC 48
; Sequence 2, Application US/08687421
; Patent No. 6177557
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Tasec, Diane

RESULT 48

US-09-143-190-37

; Sequence 37, Application US/09143190
; Patent No. 6110900
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Therk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,190
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/469,609
; FILING DATE: June 6, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,964
; FILING DATE: April 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/412,110
; FILING DATE: March 27, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,442
; FILING DATE: March 24, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-143-190-37

Query Match 0.6%; Score 25; DB 3; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATATAGGAGCTC 48
; Sequence 2, Application US/08687421
; Patent No. 6177557
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Tasec, Diane

RESULT 49

US-08-687-421-2

; Sequence 2, Application US/08687421
; Patent No. 6177557
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Tasec, Diane

TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-687-421-2

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGCACTCACTATAGGAGCTC 48
DB 9 TAATAGCACTCACTATAGGAGCTC 33

RESULT 50
US-09-502-344-37
Sequence 37, Application US/09502344
Patent No. 6331398
GENERAL INFORMATION:
APPLICANT: Larry Gold
ADDRESSEE: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/502,344
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-502-344-37

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGCACTCACTATAGGAGCTC 48
DB 9 TAATAGCACTCACTATAGGAGCTC 33

RESULT 51
US-09-860-474-2
Sequence 2, Application US/09860474
Patent No. 6696252
GENERAL INFORMATION:
APPLICANT: GOLD, L. and JANIC, N.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE LIGANDS
TO VASCULAR ENDOTHELIAL GROWTH
FACTOR (VEGF)
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
CITY: Highlands Ranch
STATE: Colorado

COUNTRY: USA
ZIP: 80129
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,474
FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/156,824
FILING DATE: 18-SEPTEMBER-1998
APPLICATION NUMBER: 08/447,169
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: 08/233,012
FILING DATE: 25-APRIL-1994
APPLICATION NUMBER: 08/205,515
FILING DATE: 03-MARCH-1994
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX14/CIP-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-860-474-2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-860-474-2
Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 24 TAATACGACTCATTATAGGAGCTC 48
DB 9 TAATACGACTCATTATAGGAGCTC 33
RESULT 52
US-08-442-423-2
Sequence 2, Application US/08442423
Patent No. 675392
GENERAL INFORMATION:
APPLICANT: Gold, Larry
TITLE OF INVENTION: High-Affinity RNA ligands of Basic
TITLE OF INVENTION: Fibroblast Growth Factors
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,423
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-442-423-2
Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 24 TAATACGACTCATTATAGGAGCTC 48
DB 9 TAATACGACTCATTATAGGAGCTC 33
RESULT 53
US-09-449-204-16
Sequence 16, Application US/09449204A
Patent No. 6927024
GENERAL INFORMATION:
APPLICANT: Sinitopoli, Dominick V.
APPLICANT: Williams, P. Mickey
APPLICANT: Meng, Yu-Ju G.
APPLICANT: Dodge, Anthony H.
APPLICANT: Sims, Paul W.
APPLICANT: Wong, Wei Lee Tan
TITLE OF INVENTION: PCR ASSAY
FILE REFERENCE: P1543R1
CURRENT APPLICATION NUMBER: US/09/449,204A
CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: US 60/110,259
EARLIER FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 16
LENGTH: 48
TYPE: DNA
ORGANISM: artificial sequence
FEATURES:
OTHER INFORMATION: Sequence source: synthetic primer
Patent No. 6927024
US-09-449-204-16

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 24 TAATACGACTCATTATAGGAGCTC 48
DB 9 TAATACGACTCATTATAGGAGCTC 33

RESULT 54
US-10-037-986-37
Sequence 37, Application US/10037986
Patent No. 693316
GENERAL INFORMATION:
APPLICANT: Larry Gold
Craig Therk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/037,986
FILING DATE: 18-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-10-037-986-37
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 TAATACGACTCATATAGGAGCTC 48
9 TAATACGACTCATATAGGAGCTC 33

RESULT 55
PCT-US95-05600-19
Sequence 19, Application PC/TUS9505600
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: NIEUWLANDT, DAN
APPLICANT: WECKER, MATTHEW
APPLICANT: SCHNEIDER, DANIEL J.

APPLICANT: FEIGON, JULI
APPLICANT: ALLEN, PATRICK
APPLICANT: SULENGER, BRUCE A.
APPLICANT: DOUDNA, JENNIFER, A.
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05600
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,863
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,632
FILING DATE: 24-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 09-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,795
FILING DATE: 21-DECEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 08-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX17/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05600-19
Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGACTACTATAGGAGCTC 48

Db 9 TAATAGACTACTATAGGAGCTC 33

RESULT 56

PCT-US95-05600-141

Sequence 141, Application PC/TUS9505600

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY

APPLICANT: NIEUMLANDT, DAN

APPLICANT: WECKER, MATTHEW

APPLICANT: SCHNEIDER, DANIEL J.

APPLICANT: FEIGON, JULI

APPLICANT: ALLEN, PATRICK

APPLICANT: SULENGER, BRUCE A.

APPLICANT: DOUDNA, JENNIFER A.

TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF

TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE

TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05600

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/238, 863

FILING DATE: 06-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/248, 632

FILING DATE: 24-MAY-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/303, 362

FILING DATE: 09-SEPTEMBER-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/361, 795

FILING DATE: 21-DECEMBER-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117, 991

FILING DATE: 08-SEPTEMBER-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931, 473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964, 624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536, 428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714, 131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536, 428

FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX17/PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 141:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US95-05600-141

Query Match 0.6%; Score 25; DB 6; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGACTACTATAGGAGCTC 48

Db 9 TAATAGACTACTATAGGAGCTC 33

RESULT 57

PCT-US96-09537-208

Sequence 208, Application PC/TUS9609537

GENERAL INFORMATION:

APPLICANT: NEXSTAR PHARMACEUTICALS, INC.

APPLICANT: DIANE TASSER

APPLICANT: NIKOS PAGRATIS

APPLICANT: SUMEDHA JAYASENA

APPLICANT: LARRY GOLD

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF

TITLE OF INVENTION: CYTOKINES

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.

STREET: 8400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09537

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477, 829

FILING DATE: 07-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/481, 710

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX14/PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 208:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

PCT-US96-09537-208

Query Match 0.6%; Score 25; DB 6; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATAGACTCACTATAGGAGCTC 48
|||||
DB 9 TATAGACTCACTATAGGAGCTC 33

RESULT 58

US-09-816-089A-7
Sequence 7, Application US/09816089A
Patent No. 6558906
GENERAL INFORMATION:
APPLICANT: OBOKATA, Junichi et al.
TITLE OF INVENTION: Methods of Screening Potential
TITLE OF INVENTION: Translational Regulatory Elements of Messenger RNA
FILE REFERENCE: 10235/9
CURRENT APPLICATION NUMBER: US/09/816,089A
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2000-291084
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 59
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-816-089A-7

Query Match 0.6%; Score 25; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GGCCTAATAGACTCACTATAGGGA 44
|||||
DB 4 GGCCTAATAGACTCACTATAGGGA 28

RESULT 59

US-09-816-089A-3
Sequence 3, Application US/09816089A
Patent No. 6558906
GENERAL INFORMATION:
APPLICANT: OBOKATA, Junichi et al.
TITLE OF INVENTION: Methods of Screening Potential
TITLE OF INVENTION: Translational Regulatory Elements of Messenger RNA
FILE REFERENCE: 10235/9
CURRENT APPLICATION NUMBER: US/09/816,089A
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2000-291084
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 63
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-816-089A-3

Query Match 0.6%; Score 25; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GGCCTAATAGACTCACTATAGGGA 44
|||||
DB 9 GGCCTAATAGACTCACTATAGGGA 33

RESULT 60

5436330-1
Patent No. 5436330
APPLICANT: TAIRA, KAZUNARI;ODA, MASANO;SHINSHI, HIDEAKI;
FURUKAWA, KENSUKE;MAEDA, HIDEKATSU
TITLE OF INVENTION: HAMMERHEAD RIBOZYMES WITH ENHANCED
STABILITY PROVIDED BY AN ADDITIONAL 3' HAIRPIN SEQUENCE
NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/111,444
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 499,787
FILING DATE: 27-MAR-1990
APPLICATION NUMBER:
FILING DATE:
SEQ ID NO:1
LENGTH: 136
5436330-1

Query Match 0.6%; Score 25; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATAGACTCACTATAGGAGCTC 48
|||||
DB 11 TATAGACTCACTATAGGAGCTC 35

RESULT 61

US-08-652-369A-2
Sequence 2, Application US/08652369A
Patent No. 5861268
GENERAL INFORMATION:
APPLICANT: Dean G. Tang, Kenneth V. Honn
TITLE OF INVENTION: Induction of Tumor
TITLE OF INVENTION: Cell Apoptosis With Chemical Inhibitors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 kb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (version
3.3)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,369A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Biomide 4.1-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 Bases
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:

DESCRIPTION: DNA primer for
DESCRIPTION: a segment of 12-lipoxygenase.
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
LIBRARY: Genomic
US-08-652-369A-2

Query Match 0.6%; Score 24; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 62
US-09-302-620B-109
Sequence 109, Application US/09302620B
Patent No. 6331420
GENERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
TITLE OF INVENTION: RELATING THERETO
FILE REFERENCE: 1010-16.seq
CURRENT APPLICATION NUMBER: US/09/302,620B
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 109
LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-09-302-620B-109

Query Match 0.6%; Score 24; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 63
US-08-755-587-203
Sequence 203, Application US/08755587
Patent No. 6045997
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
TITLE OF INVENTION: Susceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson

STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-755-587-203

Query Match 0.6%; Score 24; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 64
US-08-169-303-23
Sequence 23, Application US/08169303
Patent No. 5709998
GENERAL INFORMATION:
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF FAMILIAL
TITLE OF INVENTION: ADENOMATOUS POLYPOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,303
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.44447
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
US-08-169-303-23

Query Match 0.6%; Score 24; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 65
US-08-771-781-1
Sequence 1, Application US/08771781
Patent No. 6027886
GENERAL INFORMATION:
APPLICANT: LEYING, Hermann
APPLICANT: HINZPETER, Matthias
APPLICANT: WITTOR, Heiko
APPLICANT: FRITTON, Hans-Peter
TITLE OF INVENTION: METHOD FOR THE QUANTITATIVE
TITLE OF INVENTION: DETECTION OF SPECIFIC NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,781
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 48 680.3
FILING DATE: 23-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
US-08-771-781-1

Query Match 0.6%; Score 24; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 CCTAATACGACTCATTATAGGAG 45

DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 66
US-09-181-706-6
Sequence 6, Application US/09181706
Patent No. 6130068
GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. Dubose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,706
FILING DATE: October 28, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to a
APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: primer
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-181-706-6

Query Match 0.6%; Score 24; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 67
US-09-458-791-6
Sequence 6, Application US/09458791
Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie

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1 TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
2 RECEPTOR DNA AND POLYPEPTIDES
3
4 NUMBER OF SEQUENCES: 10
5
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Janis C. Henry
8 STREET: 51 University St.
9 CITY: Seattle
10 STATE: WA
11 COUNTRY: US
12 ZIP: 98101
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: MS-DOS/Windows 95
18 SOFTWARE: Word for Windows 95, 7.0a
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20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/458,791
22 FILING DATE: 10-Dec-1999
23 CLASSIFICATION: <Unknown>
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 08/958,598
27 FILING DATE: 28-OCT-1997
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Henry, Janis C
30 REGISTRATION NUMBER: 34,347
31 REFERENCE/DOCKET NUMBER: 2631
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (206)470-4189
34 TELEFAX: (206)233-0644
35
36 INFORMATION FOR SEQ ID NO: 6:
37
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 43 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: primer
44 HYPOTHEICAL: NO
45
46 ANTI-SENSE: NO
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48 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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50 US-09-458-791-6
51
52 Query Match 0.6%; Score 24; DB 3; Length 43;
53 Best Local Similarity 100.0%; Pred. No. 12;
54 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
55
56 QY 22 CCTAATACGACTCACTATAGGAG 45
57 |||||
58 Db 5 CCTAATACGACTCACTATAGGAG 28
59
60
61 RESULT 68
62 US-09-459-066-6
63 Sequence 6, Application US/09459066
64 Patent No. 6187909
65
66 GENERAL INFORMATION:
67 APPLICANT: Spr1999, Melanie
68 TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
69 TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
70 NUMBER OF SEQUENCES: 10
71 CORRESPONDENCE ADDRESS:
72 ADDRESSEE: Janis C. Henry
73 STREET: 51 University St.
74 CITY: Seattle
75 STATE: WA
76 COUNTRY: US
77 ZIP: 98101
78
79 COMPUTER READABLE FORM:
80 MEDIUM TYPE: Floppy disk
81 COMPUTER: IBM PC compatible
82 OPERATING SYSTEM: MS-DOS/Windows 95
83 SOFTWARE: Word for Windows 95, 7.0a
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85 CURRENT APPLICATION DATA:
86 APPLICATION NUMBER: US/09/459,066
87

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1      CLASSIFICATION:
2      PRIOR APPLICATION DATA:
3      APPLICATION NUMBER: 08/958,598
4      FILING DATE:
5      ATTORNEY/AGENT INFORMATION:
6      NAME: Henry, Janis C
7      REGISTRATION NUMBER: 34,347
8      REFERENCE/DOCKET NUMBER: 2631
9      TELECOMMUNICATION INFORMATION:
10     TELEPHONE: (206)470-4189
11     TELEFAX: (206)233-0644
12     INFORMATION FOR SEQ ID NO: 6:
13     SEQUENCE CHARACTERISTICS:
14     LENGTH: 43 base pairs
15     TYPE: nucleic acid
16     STRANDEDNESS: single
17     TOPOLOGY: linear
18     US-09-459-066-6
19     ANTI-SENSE: NO
20     HYPOTHETICAL: NO
21     MOLECULAR TYPE: primer
22     TOPOLOGY: linear
23     STRANDEDNESS: single
24     TYPE: nucleic acid
25     LENGTH: 43 base pairs
26     SEQUENCE CHARACTERISTICS:
27     INFORMATION FOR SEQ ID NO: 6:
28     TELEFAX: (206)233-0644
29     TELEPHONE: (206)470-4189
30     TELECOMMUNICATION INFORMATION:
31     REFERENCE/DOCKET NUMBER: 2631
32     REGISTRATION NUMBER: 34,347
33     NAME: Henry, Janis C
34     ATTORNEY/AGENT INFORMATION:
35     FILING DATE:
36     APPLICATION NUMBER: 08/958,598
37     PRIOR APPLICATION DATA:
38     FILING DATE:
39     CURRENT APPLICATION DATA:
40     SOFTWARE: Word for Windows 95, 7.0a
41     OPERATING SYSTEM: MS-DOS/Windows 95
42     COMPUTER: IBM PC compatible
43     MEDIUM TYPE: floppy disk
44     COMPUTER READABLE FORM:
45     ZIP: 98101
46     COUNTRY: US
47     STATE: WA
48     CITY: Seattle
49     STREET: 51 University St.
50     ADDRESSER: Janis C. Henry
51     CORRESPONDENCE ADDRESS:
52     NUMBER OF SEQUENCES: 10
53     TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
54     VIRAL ENCODED SEMAPHORIN PROTEIN
55     APPLICANT: Spriggs, Melanie
56     GENERAL INFORMATION:
57     Patent No. 6562949
58     Sequence 6, Application US/09459065
59     US-09-459-065-6
60     RESULT 69
61     Query Match 0.6%; Score 24; DB 3; Length 43;
62     Best Local Similarity 100.0%; Pred. No. 12;
63     Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
64     22 CCTATATGAGCTCAGTATAGGAG 45
65     |||||||
66     5 CCTATATGAGCTCAGTATAGGAG 28

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/ MOLECULE TYPE: primer
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
US-09-459-065-6

Query Match 0.6%; Score 24; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 70
US-08-623-428D-40
Sequence 40, Application US/08623428D
Patent No. 6312890
GENERAL INFORMATION:
APPLICANT: W. MARSTON LINEHAN, MICHAEL
LEHMAN, FARIDA LATIF AND BERTON
ZBAR

TITLE OF INVENTION: PARTIAL INTRON SEQUENCE
OF VHL DISEASE GENE AND ITS USE IN DIAGNOSIS
OF DISEASE CARRIERS

NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,428D
FILING DATE: 05-Sep-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/623,428
FILING DATE: MARCH 28, 1996

APPLICATION NUMBER: 08/061,889
FILING DATE: MAY 14, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Kachya M. Brown
REGISTRATION NUMBER: 34,556

REFERENCE/DOCKET NUMBER: 2026-4078US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-08-623-428D-40

Query Match 0.6%; Score 24; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 71
US-09-689-012-6
Sequence 6, Application US/09689012
Patent No. 6670135
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie K.
TITLE OF INVENTION: NOVEL SEMAPHORIN POLYPEPTIDES
FILE REFERENCE: 2634-US

CURRENT APPLICATION NUMBER: US/09/689,012
CURRENT FILING DATE: 2000-10-12

PRIOR APPLICATION NUMBER: PCT/US99/09831
PRIOR FILING DATE: 1999-05-05

PRIOR APPLICATION NUMBER: US 60/085,497
PRIOR FILING DATE: 1998-05-14

NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 44

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: PRIMER
US-09-689-012-6

Query Match 0.6%; Score 24; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 6 CCTAATACGACTCATTATAGGAG 29

RESULT 72
US-08-270-314-6
Sequence 6, Application US/08270314
Patent No. 5663888
GENERAL INFORMATION:
APPLICANT: CAMPBELL, Anthony K.

TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND
THEIR USE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA

COUNTRY: US
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,314
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 89 16806.6
FILING DATE: 22-JUL-1989

APPLICATION NUMBER: PCT/GB90/01131
FILING DATE: 23-JUL-1990

APPLICATION NUMBER: US 07/820,867
FILING DATE: 22-JAN-1992

ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573

TELEFAX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-270-314-6

Query Match      0.6%; Score 24; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATACGACTCACTATAGGAG 45
Db      3 CCTAATACGACTCACTATAGGAG 26

RESULT 73
US-08-270-314-9
; Sequence 9, Application US/08270314
; Patent No. 568388
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, Anthony K.
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND
; TITLE OF INVENTION: THEIR USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: US
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/270,314
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89 16806.6
; FILING DATE: 22-JUL-1989
; APPLICATION NUMBER: PCT/GB90/01131
; FILING DATE: 23-JUL-1990
; APPLICATION NUMBER: US 07/820,867
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 585-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-270-314-9

Query Match      0.6%; Score 24; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATACGACTCACTATAGGAG 45
Db      3 CCTAATACGACTCACTATAGGAG 26
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RESULT 74
US-09-225-302-6
; Sequence 6, Application US/09225302
; Patent No. 644065
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, ANTHONY KEITH
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
; FILE REFERENCE: 09/225,302
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: 08/957,135
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-225-302-6

Query Match      0.6%; Score 24; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATACGACTCACTATAGGAG 45
Db      3 CCTAATACGACTCACTATAGGAG 26

RESULT 75
US-09-225-302-9
; Sequence 9, Application US/09225302
; Patent No. 644065
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, ANTHONY KEITH
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
; FILE REFERENCE: 09/225,302
; CURRENT APPLICATION NUMBER: 08/957,135
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: 08/957,135
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-225-302-9

Query Match      0.6%; Score 24; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATACGACTCACTATAGGAG 45
Db      3 CCTAATACGACTCACTATAGGAG 26

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 00:39:54 : Search time 745 Seconds
(without alignments)
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Title: US-10-623-477-3

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Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

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Published Applications NA New:*
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3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB_seq.*
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	0.8	4162	7 US-10-755-092-26	Sequence 26, Appl
2	26	0.6	625	6 US-09-925-065A-275529	Sequence 275529,
3	26	0.6	625	6 US-09-925-065A-275530	Sequence 275530,
4	24	0.6	52	12 US-11-183-294-1	Sequence 1,
5	24	0.6	53	12 US-11-183-294-3	Sequence 3, Appl1
6	24	0.6	94	7 US-10-903-612B-138	Sequence 138, App
7	24	0.6	99	7 US-10-903-612B-146	Sequence 146, App
8	24	0.6	114	7 US-10-903-612B-141	Sequence 141, App
9	24	0.6	115	7 US-10-903-612B-144	Sequence 144, App
10	24	0.6	582	6 US-09-925-065A-269639	Sequence 269639,
11	24	0.6	585	6 US-09-925-065A-330079	Sequence 330079,
12	24	0.6	585	6 US-09-925-065A-330080	Sequence 330080,
13	23	0.5	28	12 US-11-169-809-11	Sequence 11, Appl
14	23	0.5	31	8 US-10-500-831-385	Sequence 385, App
15	23	0.5	46	12 US-11-148-593-2	Sequence 2,
16	23	0.5	47	8 US-10-773-440A-1	Sequence 1, Appl1
17	23	0.5	47	12 US-11-176-795-81	Sequence 81, Appl
18	23	0.5	49	8 US-10-500-831-138	Sequence 138, App
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25	23	0.5	49	8 US-10-500-831-229	Sequence 229, App
26	23	0.5	49	8 US-10-500-831-233	Sequence 233, App
27	23	0.5	49	12 US-11-176-795-72	Sequence 72, Appl
28	23	0.5	49	12 US-11-176-795-76	Sequence 76, Appl
29	23	0.5	50	7 US-10-991-803-20	Sequence 20, Appl
30	23	0.5	50	7 US-10-991-803-21	Sequence 21, Appl
31	23	0.5	50	7 US-10-014-128-20	Sequence 20, Appl
32	23	0.5	50	7 US-10-014-128-21	Sequence 21, Appl
33	23	0.5	50	8 US-10-500-831-197	Sequence 197, App
34	23	0.5	50	8 US-10-500-831-235	Sequence 235, App
35	23	0.5	50	8 US-10-500-831-243	Sequence 243, App
36	23	0.5	50	12 US-11-176-795-47	Sequence 47, Appl
37	23	0.5	50	12 US-11-176-795-51	Sequence 51, Appl
38	23	0.5	51	8 US-10-500-831-153	Sequence 153, App
39	23	0.5	51	8 US-10-500-831-163	Sequence 163, App
40	23	0.5	51	8 US-10-500-831-173	Sequence 173, App
41	23	0.5	51	8 US-10-500-831-178	Sequence 178, App
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43	23	0.5	51	8 US-10-500-831-200	Sequence 200, App
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45	23	0.5	51	8 US-10-500-831-212	Sequence 212, App
46	23	0.5	51	8 US-10-500-831-215	Sequence 215, App
47	23	0.5	51	8 US-10-500-831-217	Sequence 217, App
48	23	0.5	51	8 US-10-500-831-242	Sequence 242, App
49	23	0.5	51	8 US-10-500-831-251	Sequence 251, App
50	23	0.5	51	8 US-10-500-831-264	Sequence 264, App
51	23	0.5	51	8 US-10-500-831-269	Sequence 269, App
52	23	0.5	51	8 US-10-500-831-271	Sequence 271, App
53	23	0.5	51	8 US-10-500-831-285	Sequence 285, App
54	23	0.5	52	8 US-10-500-831-195	Sequence 195, App
55	23	0.5	52	8 US-10-500-831-248	Sequence 248, App
56	23	0.5	52	12 US-11-176-795-55	Sequence 55, Appl
57	23	0.5	53	8 US-10-500-831-135	Sequence 135, App
58	23	0.5	53	8 US-10-500-831-160	Sequence 160, App
59	23	0.5	53	8 US-10-500-831-181	Sequence 181, App
60	23	0.5	53	8 US-10-500-831-224	Sequence 224, App
61	23	0.5	53	8 US-10-500-831-254	Sequence 254, App
62	23	0.5	53	8 US-10-500-831-262	Sequence 262, App
63	23	0.5	53	8 US-10-500-831-277	Sequence 277, App
64	23	0.5	53	8 US-10-500-831-279	Sequence 279, App
65	23	0.5	53	12 US-11-176-795-55	Sequence 55, Appl
66	23	0.5	53	12 US-11-176-795-79	Sequence 79, Appl
67	23	0.5	54	8 US-10-500-831-235	Sequence 235, App
68	23	0.5	54	12 US-11-195-109-32	Sequence 12, Appl
69	23	0.5	55	8 US-10-500-831-166	Sequence 166, App
70	23	0.5	55	8 US-10-500-831-256	Sequence 256, App
71	23	0.5	55	8 US-10-500-831-260	Sequence 260, App
72	23	0.5	55	8 US-10-500-831-275	Sequence 275, App
73	23	0.5	56	8 US-10-500-831-157	Sequence 157, App
74	23	0.5	56	12 US-11-176-795-63	Sequence 63, Appl
75	23	0.5	57	8 US-10-500-831-187	Sequence 187, App
76	23	0.5	60	10 US-11-174-042-1	Sequence 11, Appl1
77	23	0.5	60	12 US-11-119-869-11	Sequence 11, Appl1
78	23	0.5	99	8 US-10-989-723-5	Sequence 5, Appl1
79	23	0.5	101	8 US-10-989-723-6	Sequence 8, Appl1
80	23	0.5	104	8 US-10-989-723-2	Sequence 2, Appl1
81	23	0.5	122	8 US-10-989-723-1	Sequence 1, Appl1
82	23	0.5	525	6 US-09-925-065A-18438	Sequence 18438, A
83	23	0.5	588	6 US-09-925-065A-892537	Sequence 892537,
84	23	0.5	594	6 US-09-925-065A-354079	Sequence 354079,
85	23	0.5	597	6 US-09-925-065A-620716	Sequence 620716,
86	23	0.5	597	6 US-09-925-065A-895007	Sequence 895007,
87	23	0.5	599	6 US-09-925-065A-894173	Sequence 894173,
88	23	0.5	614	6 US-09-925-065A-836169	Sequence 836169,
89	23	0.5	614	6 US-09-925-065A-836170	Sequence 836170,
90	23	0.5	650	6 US-09-925-065A-875759	Sequence 875759,
91	23	0.5	2219	12 US-11-151-601-24	Sequence 24, Appl
92	23	0.5	2838	12 US-11-151-601-14	Sequence 14, Appl
93	23	0.5	6860	8 US-10-949-720-406	Sequence 406, App

94 23 0.5 6921 8 US-10-949-720-420
95 23 0.5 7164 8 US-10-949-720-411
96 23 0.5 7387 12 US-11-154-421-28
97 23 0.5 7429 8 US-10-949-720-413
98 23 0.5 48000 12 US-11-159-597-20
99 22 0.5 23 12 US-11-128-440-53
100 22 0.5 26 12 US-11-089-805-1

Sequence 420, App
Sequence 411, App
Sequence 28, App
Sequence 413, App
Sequence 20, App
Sequence 53, App
Sequence 1, App

ALIGNMENTS

RESULT 1

US-10-755-092-26/c
Sequence 26, Application US/10755092
Publication No. US20060021095A1

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/755,092

FILING DATE: 08-Jan-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-Nov-2001

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-Apr-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-Jun-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-Sep-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-Oct-1991

ATTORNEY/AGENT INFORMATION:

NAME: Weigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 4162 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"

FEATURE:

NAME/KEY: exon

LOCATION: 1481..2366

FEATURE:

NAME/KEY: intron

LOCATION: 2367..2451

FEATURE:

NAME/KEY: exon

LOCATION: 2452..2602

FEATURE:

NAME/KEY: intron

LOCATION: 2603..2690

FEATURE:

NAME/KEY: exon

LOCATION: 2691..2804

FEATURE:

NAME/KEY: intron

LOCATION: 2805..2906

FEATURE:

NAME/KEY: exon

LOCATION: 2907..3075

FEATURE:

NAME/KEY: intron

LOCATION: 3076..3177

FEATURE:

NAME/KEY: exon

LOCATION: 3178..3304

FEATURE:

NAME/KEY: intron

LOCATION: 3305..3398

FEATURE:

NAME/KEY: exon

LOCATION: 3399..3498

FEATURE:

NAME/KEY: intron

LOCATION: 3499..3713

FEATURE:

NAME/KEY: exon

LOCATION: 3714..3811

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-10-755-092-26

Query Match

Best Local Similarity 0.8%; Score 32; DB 7; Length 4162;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGCGCTAATGACGCTCACTATAGGAGCTCGA 50

Db 4162 TGCGCTAATGACGCTCACTATAGGAGCTCGA 4131

RESULT 2

US-09-925-065A-275529

Sequence 275529, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16


```

; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275529
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-275529

Query Match      0.6%; Score 26; DB 6; Length 625;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3910 AAAAAATAAAAATAAATAAAGTAAA 3935
Db      161 AAAAAATAAAAATAAATAAAGTAAA 186

RESULT 3
US-09-925-065A-275530
; Sequence 275530, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David C.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 10837.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275530
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-275530

Query Match      0.6%; Score 26; DB 6; Length 625;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3910 AAAAAATAAAAATAAATAAAGTAAA 3935
Db      161 AAAAAATAAAAATAAATAAAGTAAA 186

RESULT 4
US-11-183-294-1
; Sequence 1, Application US/11183294
; Publication No. US20060019383A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Grasso, Luigi
; APPLICANT: Saes, Philip M.
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0475
; CURRENT APPLICATION NUMBER: US/11/183,294
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 09/760,285
; PRIOR FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
; US-11-183-294-1

Query Match      0.6%; Score 24; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATCGACTCACTATAGGAG 45
Db      5 CCTAATCGACTCACTATAGGAG 28

RESULT 5
US-11-183-294-3
; Sequence 3, Application US/11183294
; Publication No. US20060019383A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Grasso, Luigi
; APPLICANT: Saes, Philip M.
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0475
; CURRENT APPLICATION NUMBER: US/11/183,294
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 09/760,285
; PRIOR FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
; US-11-183-294-3

Query Match      0.6%; Score 24; DB 12; Length 53;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATCGACTCACTATAGGAG 45
Db      5 CCTAATCGACTCACTATAGGAG 28

RESULT 6
US-10-903-612B-138
; Sequence 138, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gilte, Sadeand
; APPLICANT: Bergo, Vladislav B.
; APPLICANT: Rothechild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-903-612B-138
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Query Match 0.6%; Score 24; DB 7; Length 94;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATACGACTCCTATAGGAG 45
|||||
Db 5 CCTAATACGACTCCTATAGGAG 28

RESULT 7

US-10-903-612B-146
; Sequence 146, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gile, Sadanand
; APPLICANT: Bergo, Vladislav B.
; APPLICANT: Rothschild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 146
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-146

Query Match 0.6%; Score 24; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATACGACTCCTATAGGAG 45
|||||
Db 5 CCTAATACGACTCCTATAGGAG 28

RESULT 8

US-10-903-612B-141
; Sequence 141, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gile, Sadanand
; APPLICANT: Bergo, Vladislav B.
; APPLICANT: Rothschild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-141

Query Match 0.6%; Score 24; DB 7; Length 114;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATACGACTCCTATAGGAG 45
|||||
Db 5 CCTAATACGACTCCTATAGGAG 28

RESULT 9
US-10-903-612B-144
; Sequence 144, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gile, Sadanand
; APPLICANT: Bergo, Vladislav B.
; APPLICANT: Rothschild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 144
; LENGTH: 115
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-144

Query Match 0.6%; Score 24; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATACGACTCCTATAGGAG 45
|||||
Db 5 CCTAATACGACTCCTATAGGAG 28

RESULT 10

US-09-925-065A-269639/c
; Sequence 269639, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269639
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-269639

Query Match 0.6%; Score 24; DB 6; Length 582;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3910 AAAAAATTAATTAATTAAGTA 3933
|||||
Db 425 AAAAAATTAATTAATTAAGTA 402

RESULT 11
US-09-925-065A-330079/c
; Sequence 330079, Application US/09925065A

```
Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330079
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-330079

Query Match      0.6%; Score 24; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2019 AATTTCTAGTAAATACATTTT 2042
Db      426 AATTTCTAGTAAATACATTTT 403

RESULT 12
US-09-925-065A-330080/C
; Sequence 330080, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330080
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-330080

Query Match      0.6%; Score 24; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2019 AATTTCTAGTAAATACATTTT 2042
Db      426 AATTTCTAGTAAATACATTTT 403

Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Hayashi, Toshihori
; TITLE OF INVENTION: METHOD OF DETECTING AND QUANTIFYING CYTOMEGALOVIRUS
; FILE REFERENCE: 274564USO
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: JP2004-194367
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: Synthetic DNA
US-11-169-809-11

Query Match      0.5%; Score 23; DB 12; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 CTAATACGACTCCTATATGGAG 45
Db      5 CTAATACGACTCCTATATGGAG 27

RESULT 14
US-10-500-831-385
; Sequence 385, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT FILING DATE: US/10/500,831
; PRIOR APPLICATION NUMBER: US/04-07-07
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 385
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: T7 promoter sequence
US-10-500-831-385

Query Match      0.5%; Score 23; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 CTAATACGACTCCTATATGGAG 45
Db      5 CTAATACGACTCCTATATGGAG 27

RESULT 15
US-11-148-593-2
; Sequence 2, Application US/11148593
; Publication No. US20060014182A1
; GENERAL INFORMATION:
; APPLICANT: Kuri, Norich
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES
```

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; FILE REFERENCE: 492692000701
; CURRENT APPLICATION NUMBER: US/11/148,593
; CURRENT FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: 10/096,221
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/274,236
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: 46
; OTHER INFORMATION: 3' thymine is biotinylated
US-11-148-593-2
```

```
Query Match          0.5%; Score 23; DB 12; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23  CTAATACGACTCACTATAGGAG 45
Db       7  CTAATACGACTCACTATAGGAG 29
```

```
RESULT 16
; Sequence 1, Application US/10773440A
; Publication No. US20050282170A1
; GENERAL INFORMATION:
; APPLICANT: Fradet, Yves
; APPLICANT: Chypre, Camille
; APPLICANT: Piche, Lyvon
; APPLICANT: Garon, Genevieve
; TITLE OF INVENTION: Method to Detect Prostate Cancer in a Sample
; FILE REFERENCE: 1619.0180001
; CURRENT APPLICATION NUMBER: US/10/773,440A
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/445,436
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-773-440A-1
```

```
Query Match          0.5%; Score 23; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23  CTAATACGACTCACTATAGGAG 45
Db       5  CTAATACGACTCACTATAGGAG 27
```

```
RESULT 17
US-11-176-795-81
; Sequence 81, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
```

```
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Listeria monocytogenes
US-11-176-795-81
```

```
Query Match          0.5%; Score 23; DB 12; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23  CTAATACGACTCACTATAGGAG 45
Db       5  CTAATACGACTCACTATAGGAG 27
```

```
RESULT 18
; Sequence 138, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS B6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-138
```

```
Query Match          0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23  CTAATACGACTCACTATAGGAG 45
Db       5  CTAATACGACTCACTATAGGAG 27
```

```
RESULT 19
US-10-500-831-139
; Sequence 139, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS B6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-139
```

```
Query Match          0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      23 CTAATAGCACTCACTATAGGAG 45
|||
Db      5 CTAATAGCACTCACTATAGGAG 27

RESULT 20
US-10-500-831-140
; Sequence 140, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-140

Query Match      0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 CTAATAGCACTCACTATAGGAG 45
|||
Db      5 CTAATAGCACTCACTATAGGAG 27

RESULT 21
US-10-500-831-141
; Sequence 141, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-141

Query Match      0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 CTAATAGCACTCACTATAGGAG 45
|||
Db      5 CTAATAGCACTCACTATAGGAG 27

RESULT 22
US-10-500-831-175
; Sequence 175, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 175
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 18
US-10-500-831-175

Query Match      0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 CTAATAGCACTCACTATAGGAG 45
|||
Db      5 CTAATAGCACTCACTATAGGAG 27

RESULT 23
US-10-500-831-221
; Sequence 221, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 221
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 52
US-10-500-831-221

Query Match      0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 CTAATAGCACTCACTATAGGAG 45
|||
Db      5 CTAATAGCACTCACTATAGGAG 27

RESULT 24
US-10-500-831-227
; Sequence 227, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
```


FILE OF INVENTION: MOLECULES
FILE REFERENCE: INVIT1290-4
CURRENT APPLICATION NUMBER: US/10/991,803
CURRENT FILING DATE: 2004-11-17
PRIOR APPLICATION NUMBER: US 60/520,946
PRIOR FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 10/014,128
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/326,092
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/254,510
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PRIMER T7top
US-10-991-803-20

Query Match 0.5%; Score 23; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TAATAGACTCCTATAGGAGC 46
|||||
8 TAATAGACTCCTATAGGAGC 30

RESULT 30
US-10-991-803-21/c
Sequence 21, Application US/10991803
Publication No. US2006008817A1
GENERAL INFORMATION:
APPLICANT: INVITROGEN CORPORATION
APPLICANT: CARRINO, John
APPLICANT: FAN, James
APPLICANT: BENNETT, Robert P.
APPLICANT: CHESNUT, Jonathan D.
APPLICANT: GLEESON, Martin A.
APPLICANT: MADDEN, Knut R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING RECOMBINANT NUCLEIC ACID
FILE REFERENCE: INVIT1290-4
CURRENT APPLICATION NUMBER: US/10/991,803
CURRENT FILING DATE: 2004-11-17
PRIOR APPLICATION NUMBER: US 60/520,946
PRIOR FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 10/014,128
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/326,092
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/254,510
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PRIMER T7bottom
US-10-991-803-21

Query Match 0.5%; Score 23; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TAATAGACTCCTATAGGAGC 46
|||||
43 TAATAGACTCCTATAGGAGC 21

RESULT 31
US-10-014-128-20
Sequence 20, Application US/10014128
Publication No. US20060029935A1
GENERAL INFORMATION:
APPLICANT: INVITROGEN CORPORATION
APPLICANT: CARRINO, John
APPLICANT: FAN, James
APPLICANT: BENNETT, Robert
APPLICANT: CHESNUT, Jonathan
APPLICANT: GLEESON, Martin
APPLICANT: MADDEN, Knut
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR RAPIDLY GENERATING
FILE REFERENCE: INVIT1290-2
CURRENT APPLICATION NUMBER: US/10/014,128
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/254,510
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/326,092
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 50
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: PRIMER T7top
US-10-014-128-20

Query Match 0.5%; Score 23; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TAATAGACTCCTATAGGAGC 46
|||||
8 TAATAGACTCCTATAGGAGC 30

RESULT 32
US-10-014-128-21/c
Sequence 21, Application US/10014128
Publication No. US20060029935A1
GENERAL INFORMATION:
APPLICANT: INVITROGEN CORPORATION
APPLICANT: CARRINO, John
APPLICANT: FAN, James
APPLICANT: BENNETT, Robert
APPLICANT: CHESNUT, Jonathan
APPLICANT: GLEESON, Martin
APPLICANT: MADDEN, Knut
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR RAPIDLY GENERATING
FILE REFERENCE: INVIT1290-2
CURRENT APPLICATION NUMBER: US/10/014,128
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/254,510
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/326,092
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 50
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: PRIMER T7bottom
US-10-014-128-21

```
Query Match          0.5%; Score 23; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGCACTCACTATAGGAGC 46
Db 43 TAATAGCACTCACTATAGGAGC 21

RESULT 33
US-10-500-831-197
; Sequence 197, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.700520S00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human papillomavirus type 33
US-10-500-831-197

Query Match          0.5%; Score 23; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 34
US-10-500-831-239
; Sequence 239, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.700520S00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-500-831-239

Query Match          0.5%; Score 23; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 35
US-10-500-831-245

; Sequence 245, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.700520S00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 245
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human papillomavirus type 39
US-10-500-831-245

Query Match          0.5%; Score 23; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 36
US-11-176-795-47
; Sequence 47, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-11-176-795-47

Query Match          0.5%; Score 23; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 37
US-11-176-795-51
; Sequence 51, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 50
; TYPE: DNA
```


ORGANISM: *Nisseria gonorrhoea*
US-11-176-795-51

Query Match 0.5%; Score 23; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 38
US-10-500-831-137

Sequence 137, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 51
TYPE: DNA
ORGANISM: Human papillomavirus type 16
US-10-500-831-137

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 39
US-10-500-831-163

Sequence 163, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 163
LENGTH: 51
TYPE: DNA
ORGANISM: Human papillomavirus type 18
US-10-500-831-163

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 40
US-10-500-831-173

Sequence 173, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 173
LENGTH: 51
TYPE: DNA
ORGANISM: Human papillomavirus type 18
US-10-500-831-173

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 41
US-10-500-831-178

Sequence 178, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 178
LENGTH: 51
TYPE: DNA
ORGANISM: Human papillomavirus type 31
US-10-500-831-178

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 42
US-10-500-831-184

Sequence 184, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07

```
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 184
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 31
US-10-500-831-184
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATACGACTCACTATAGGAG 45
Db      5 CTAATACGACTCACTATAGGAG 27
```

```
RESULT 43
US-10-500-831-200
; Sequence 200, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 33
US-10-500-831-200
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATACGACTCACTATAGGAG 45
Db      5 CTAATACGACTCACTATAGGAG 27
```

```
RESULT 44
US-10-500-831-209
; Sequence 209, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 33
US-10-500-831-209
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATACGACTCACTATAGGAG 45
Db      5 CTAATACGACTCACTATAGGAG 27
```

```
RESULT 45
US-10-500-831-212
; Sequence 212, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 212
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 35
US-10-500-831-212
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATACGACTCACTATAGGAG 45
Db      5 CTAATACGACTCACTATAGGAG 27
```

```
RESULT 46
US-10-500-831-215
; Sequence 215, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 35
US-10-500-831-215
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATACGACTCACTATAGGAG 45
Db      5 CTAATACGACTCACTATAGGAG 27
```

RESULT 47

```
US-10-500-831-217
; Sequence 217, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500, 831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 35
US-10-500-831-217

Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTATACGACTCACTATAGGAG 45
Db      5 CTATACGACTCACTATAGGAG 27

RESULT 48
US-10-500-831-242
; Sequence 242, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500, 831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 242
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-500-831-242

Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTATACGACTCACTATAGGAG 45
Db      5 CTATACGACTCACTATAGGAG 27

RESULT 49
US-10-500-831-251
; Sequence 251, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500, 831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 251
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 35
US-10-500-831-251

Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTATACGACTCACTATAGGAG 45
Db      5 CTATACGACTCACTATAGGAG 27

RESULT 50
US-10-500-831-264
; Sequence 264, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500, 831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 264
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
US-10-500-831-264

Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTATACGACTCACTATAGGAG 45
Db      5 CTATACGACTCACTATAGGAG 27

RESULT 51
US-10-500-831-269
; Sequence 269, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500, 831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 269
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 51
US-10-500-831-269

Query Match          0.5%; Score 23; DB 8; Length 51;
```

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 52

US-10-500-831-271
; Sequence 271, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:

APPLICANT: Frank KARLSEN

TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

FILE REFERENCE: B0192.700520S00

CURRENT APPLICATION NUMBER: US/10/500,831

CURRENT FILING DATE: 2004-07-07

PRIOR APPLICATION NUMBER: GB 0200258.2

PRIOR FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: GB 0214124.0

PRIOR FILING DATE: 2002-06-19

NUMBER OF SEQ ID NOS: 387

SOFTWARE: PatentIn version 3.2

SEQ ID NO 271

LENGTH: 51

TYPE: DNA

ORGANISM: Human papillomavirus type 51

US-10-500-831-271

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 53

US-10-500-831-285

; Sequence 285, Application US/10500831

; Publication No. US20050244813A1

; GENERAL INFORMATION:

APPLICANT: Frank KARLSEN

TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

FILE REFERENCE: B0192.700520S00

CURRENT APPLICATION NUMBER: US/10/500,831

CURRENT FILING DATE: 2004-07-07

PRIOR APPLICATION NUMBER: GB 0200258.2

PRIOR FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: GB 0214124.0

PRIOR FILING DATE: 2002-06-19

NUMBER OF SEQ ID NOS: 387

SOFTWARE: PatentIn version 3.2

SEQ ID NO 285

LENGTH: 51

TYPE: DNA

ORGANISM: Human papillomavirus type 56

US-10-500-831-285

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 54

US-10-500-831-195

; Sequence 195, Application US/10500831

; Publication No. US20050244813A1

; GENERAL INFORMATION:

APPLICANT: Frank KARLSEN

TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

FILE REFERENCE: B0192.700520S00

CURRENT APPLICATION NUMBER: US/10/500,831

CURRENT FILING DATE: 2004-07-07

PRIOR APPLICATION NUMBER: GB 0200258.2

PRIOR FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: GB 0214124.0

PRIOR FILING DATE: 2002-06-19

NUMBER OF SEQ ID NOS: 387

SOFTWARE: PatentIn version 3.2

SEQ ID NO 195

LENGTH: 52

TYPE: DNA

ORGANISM: Human papillomavirus type 31

US-10-500-831-195

Query Match 0.5%; Score 23; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 55

US-10-500-831-248

; Sequence 248, Application US/10500831

; Publication No. US20050244813A1

; GENERAL INFORMATION:

APPLICANT: Frank KARLSEN

TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

FILE REFERENCE: B0192.700520S00

CURRENT APPLICATION NUMBER: US/10/500,831

CURRENT FILING DATE: 2004-07-07

PRIOR APPLICATION NUMBER: GB 0200258.2

PRIOR FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: GB 0214124.0

PRIOR FILING DATE: 2002-06-19

NUMBER OF SEQ ID NOS: 387

SOFTWARE: PatentIn version 3.2

SEQ ID NO 248

LENGTH: 52

TYPE: DNA

ORGANISM: Human papillomavirus type 39

US-10-500-831-248

Query Match 0.5%; Score 23; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 56

US-11-176-795-59

; Sequence 59, Application US/11176795

; Publication No. US2005025517A1

; GENERAL INFORMATION:

APPLICANT: Gardes, John C

APPLICANT: Marmaro, Jeffrey M

TITLE OF INVENTION: Method and Device for Multiplex Amplification System

FILE REFERENCE: 1

CURRENT APPLICATION NUMBER: US/11/176,795

CURRENT FILING DATE: 2005-07-07

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 59

LENGTH: 52
TYPE: DNA
ORGANISM: Coliform Bacteria
US-11-176-795-59

Query Match 0.5%; Score 23; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 4 CTAATAGCACTCACTATAGGAG 26

RESULT 57
US-10-500-831-135
Sequence 135, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:

APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 135
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus
US-10-500-831-135

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 58
US-10-500-831-160
Sequence 160, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 160
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus type 16
US-10-500-831-160

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 59
US-10-500-831-181
Sequence 181, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 181
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus type 31
US-10-500-831-181

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 60
US-10-500-831-224
Sequence 224, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 224
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus type 52
US-10-500-831-224

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 61
US-10-500-831-254
Sequence 254, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00

```

1 CURRENT APPLICATION NUMBER: US/10/500,831
2
3 CURRENT FILING DATE: 2004-07-07
4
5 PRIOR APPLICATION NUMBER: GB 0200258.2
6
7 PRIOR FILING DATE: 2002-01-07
8
9 PRIOR APPLICATION NUMBER: GB 0214124.0
10
11 PRIOR FILING DATE: 2002-06-19
12
13 NUMBER OF SEQ ID NOS: 387
14
15 SOFTWARE: PatentIn version 3.2
16
17 SEQ ID NO 254
18
19 LENGTH: 53
20
21 TYPE: DNA
22
23 ORGANISM: Human papillomavirus type 45
24
25 US-10-500-831-254

```

Query Match	0.5%;	Score 23;	DB 8;	Length 53;
Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy		23	CTAATACGACTCACTATAGG	45
Db		5	CTAATACGACTCACTATAGG	27

```

RESULT 62
US-10-500-831-262
; Sequence 262: Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.700520S00
; CURRENT APPLICATION NUMBER: US/10/500, 831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 262
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
; US-10-500-831-262

```

Query Match	0.5%;	Score 23;	DB 8;	Length 53;
Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy 23 CTAATACGACTCACTATAGGAG 45
|||
5 CTAATACGACTCACTATAGGAG 27

```

RESULT 63
US-10-500-831-277
; Sequence 277, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70062US00
; CURRENT APPLICATION NUMBER: US/10/500, 831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: patentlin version 3.2
; SEQ ID NO 277
;
; LENGTH: 53
; TYPE: DNA

```

ORGANISM: Human papillomavirus type 56
US-10-500-831-277

Query Match	0.5%	Score 23;	DB 8;	Length 53;
Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		
Matches 23; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	23	CTAATAGCACTCACTATAGGAG	45
Db	5	CTAATAGCACTCACTATAGGAG	27

```

RESULT 64
US-10-500-831-279
Sequence 279, Application US/105000831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: FRANK KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 MRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500, 831
CURRENT FILING DATE: 2004-07-07
PRIORITY APPLICATION NUMBER: GB 0200258.2
PRIORITY FILING DATE: 2002-01-07
PRIORITY APPLICATION NUMBER: GB 0214124.0
PRIORITY FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 279
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus type 56
US-10-500-831-279

```

Query Match	0.5%	Score 23;	DB 8;	Length 53;
Best Local Similarity	100.0%;	Pred. NO. 1.8e+02;		
Matches 23; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

```

RESULT 65
US-11-176-795-55
; Sequence 55. Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Coliform Bacteria
; US-11-176-795-55

```

Query Match	0.5%	Score 23;	DB 12;	Length 53;
Best Local Similarity	100.0%	Pred. No. 1.8e+02;		
Matches 23; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy		23	CTAATACGACTCACTATAAGGAG	45
Db		5	CTAATACGACTCACTATAAGGAG	27

RESULT 66
US-11-176-795-75

```
/ Sequence 79, Application US/11176795
/ Publication No. US20050255517A1
/ GENERAL INFORMATION:
/ APPLICANT: Gerdes, John C
/ APPLICANT: Marmaro, Jeffrey M
/ TITLE OF INVENTION: Method and Device for Multiplex Amplification System
/ FILE REFERENCE: 1
/ CURRENT APPLICATION NUMBER: US/11/176,795
/ CURRENT FILING DATE: 2005-07-07
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 79
/ LENGTH: 53
/ TYPE: DNA
/ ORGANISM: Escherichia coli
US-11-176-795-79

Query Match          0.5%; Score 23; DB 12; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 23 CTATACGACTCACTATAGGAG 45
Db 5 CTATACGACTCACTATAGGAG 27

```
RESULT 67
US-10-500-831-235
/ Sequence 235, Application US/10500831
/ Publication No. US20050244813A1
/ GENERAL INFORMATION:
/ APPLICANT: Frank KARLSEN
/ TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
/ FILE REFERENCE: B0192.70052US00
/ CURRENT APPLICATION NUMBER: US/10/500,831
/ CURRENT FILING DATE: 2004-07-07
/ PRIOR APPLICATION NUMBER: GB 0200258.2
/ PRIOR FILING DATE: 2002-01-07
/ PRIOR APPLICATION NUMBER: GB 0214124.0
/ PRIOR FILING DATE: 2002-06-19
/ NUMBER OF SEQ ID NOS: 387
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 235
/ LENGTH: 54
/ TYPE: DNA
/ ORGANISM: Human papillomavirus
US-10-500-831-235

Query Match          0.5%; Score 23; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 23 CTATACGACTCACTATAGGAG 45
Db 5 CTATACGACTCACTATAGGAG 27

```
RESULT 68
US-11-195-109-32
/ Sequence 32, Application US/11195109
/ Publication No. US20050265975A1
/ GENERAL INFORMATION:
/ APPLICANT: Miles, Vincent J.
/ APPLICANT: Mathews, Michael B.
/ APPLICANT: Katze, Michael G.
/ APPLICANT: Witherell, Gary
/ APPLICANT: Watson, Julia C.
/ TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
/ TITLE OF INVENTION: OF VIRAL REPLICATION
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
```

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/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036/2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/195,109
/ FILING DATE: 01-Aug-2005
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/867,798
/ FILING DATE: 14-Jun-2004
/ APPLICATION NUMBER: US/10/109,368
/ FILING DATE: 27-Mar-2002
/ APPLICATION NUMBER: US/08/221,816
/ FILING DATE: 01-Apr-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7960-030
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864
/ TELE: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 54 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-11-195-109-32

Query Match          0.5%; Score 23; DB 12; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 23 CTATACGACTCACTATAGGAG 45
Db 8 CTATACGACTCACTATAGGAG 30

```
RESULT 69
US-10-500-831-166
/ Sequence 166, Application US/10500831
/ Publication No. US20050244813A1
/ GENERAL INFORMATION:
/ APPLICANT: Frank KARLSEN
/ TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
/ FILE REFERENCE: B0192.70052US00
/ CURRENT APPLICATION NUMBER: US/10/500,831
/ CURRENT FILING DATE: 2004-07-07
/ PRIOR APPLICATION NUMBER: GB 0200258.2
/ PRIOR FILING DATE: 2002-01-07
/ PRIOR APPLICATION NUMBER: GB 0214124.0
/ PRIOR FILING DATE: 2002-06-19
/ NUMBER OF SEQ ID NOS: 387
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 166
/ LENGTH: 55
/ TYPE: DNA
/ ORGANISM: Human papillomavirus type 18
US-10-500-831-166

Query Match          0.5%; Score 23; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 23 CTATACGACTCACTATAGGAG 45

Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 70
US-10-500-831-256
; Sequence 256, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:

; APPLICANT: Frank KARLSEN

; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

; FILE REFERENCE: B0192.70052US00

; CURRENT APPLICATION NUMBER: US/10/500,831

; CURRENT FILING DATE: 2004-07-07

; PRIOR APPLICATION NUMBER: GB 0200258.2

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: GB 0214124.0

; PRIOR FILING DATE: 2002-06-19

; NUMBER OF SEQ ID NOS: 387

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 256

; LENGTH: 55

; TYPE: DNA

; ORGANISM: Human papillomavirus type 45

US-10-500-831-256

Query Match 0.5%; Score 23; DB 8; Length 55;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45

Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 71
US-10-500-831-260
; Sequence 260, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:

; APPLICANT: Frank KARLSEN

; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

; FILE REFERENCE: B0192.70052US00

; CURRENT APPLICATION NUMBER: US/10/500,831

; CURRENT FILING DATE: 2004-07-07

; PRIOR APPLICATION NUMBER: GB 0200258.2

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: GB 0214124.0

; PRIOR FILING DATE: 2002-06-19

; NUMBER OF SEQ ID NOS: 387

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 260

; LENGTH: 55

; TYPE: DNA

; ORGANISM: Human papillomavirus type 45

US-10-500-831-260

Query Match 0.5%; Score 23; DB 8; Length 55;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45

Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 72
US-10-500-831-275
; Sequence 275, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:

; APPLICANT: Frank KARLSEN

; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

US-10-500-831-275

Query Match 0.5%; Score 23; DB 8; Length 55;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45

Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 73
US-10-500-831-157
; Sequence 157, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:

; APPLICANT: Frank KARLSEN

; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

; FILE REFERENCE: B0192.70052US00

; CURRENT APPLICATION NUMBER: US/10/500,831

; CURRENT FILING DATE: 2004-07-07

; PRIOR APPLICATION NUMBER: GB 0200258.2

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: GB 0214124.0

; PRIOR FILING DATE: 2002-06-19

; NUMBER OF SEQ ID NOS: 387

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 157

; LENGTH: 56

; TYPE: DNA

; ORGANISM: Human papillomavirus type 16

US-10-500-831-157

Query Match 0.5%; Score 23; DB 8; Length 56;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45

Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 74
US-11-176-795-63
; Sequence 63, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:

; APPLICANT: Marmaro, Jeffrey M

; TITLE OF INVENTION: Method and Device for Multiplex Amplification System

; FILE REFERENCE: 1

; CURRENT APPLICATION NUMBER: US/11/176,795

; CURRENT FILING DATE: 2005-07-07

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 63

; LENGTH: 56

; TYPE: DNA

; ORGANISM: Coliform Bacteria

US-11-176-795-63

Query Match 0.5%; Score 23; DB 8; Length 56;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45

Db 5 CTAATAGCACTCACTATAGGAG 27

Query Match 0.5%; Score 23; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATACGACTCTACTATAGGAG 45
|||
Db 5 CTATACGACTCTACTATAGGAG 27

RESULT 75

US-10-500-831-187
; Sequence 187, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 187
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Human papillomavirus type 31
US-10-500-831-187

Query Match 0.5%; Score 23; DB 8; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATACGACTCTACTATAGGAG 45
|||
Db 5 CTATACGACTCTACTATAGGAG 27

Search completed: February 28, 2006, 03:47:17
Job time : 747 secs

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QY 1621 CATTCTTATCAATTTTATGTAATAATAAACACGACTATAGGCTACAGGTT 1680
DB 1621 CATTCTTATCAATTTTATGTAATAATAAACACGACTATAGGCTACAGGTT 1680
QY 1681 GGATTTAAGGATTTATGCTTCTAGTCGAGGAAATTTTGTATGATTAACATCGTG 1740
DB 1681 GGATTTAAGGATTTATGCTTCTAGTCGAGGAAATTTTGTATGATTAACATCGTG 1740
QY 1741 GGAATAAATCCAGCCTAATATGCTCAATTAAGATTAATGATTTAAATGCTTTAATCA 1800
DB 1741 GGAATAAATCCAGCCTAATATGCTCAATTAAGATTAATGATTTAAATGCTTTAATCA 1800
QY 1801 TTTAAATTAAGGTTTGTGCTTTTAAAGGTACACCGCTTAATGCTCAATGAGAAAT 1860
DB 1801 TTTAAATTAAGGTTTGTGCTTTTAAAGGTACACCGCTTAATGCTCAATGAGAAAT 1860
QY 1861 ATTAACCTTGATCGAAATTCGAAATATCTTTTAAACATTAAGAAATTTTGCAGATT 1920
DB 1861 ATTAACCTTGATCGAAATTCGAAATATCTTTTAAACATTAAGAAATTTTGCAGATT 1920
QY 1921 TTTAAATTAAGGCTACATTTATGCGTTCAATTAATATGTTTCCAGTAAAGTTGAGGT 1980
DB 1921 TTTAAATTAAGGCTACATTTATGCGTTCAATTAATATGTTTCCAGTAAAGTTGAGGT 1980
QY 1981 TTTAAACCATGAATGTTTTGATTTAAATAACATTAATTTTCTAGTAATTAACATT 2040
DB 1981 TTTAAACCATGAATGTTTTGATTTAAATAACATTAATTTTCTAGTAATTAACATT 2040
QY 2041 TTTAAACGCTGATCCAGATGTAATAGTGACAAATCGTAAACATTTTGTCTG 2100
DB 2041 TTTAAACGCTGATCCAGATGTAATAGTGACAAATCGTAAACATTTTGTCTG 2100
QY 2101 AATCTGTTTAAATCTCTGCTGACACTTGACGACATTTGACACGACTATACATA 2160
DB 2101 AATCTGTTTAAATCTCTGCTGACACTTGACGACATTTGACACGACTATACATA 2160
QY 2161 TTTGAAAGCAAAATATCCACAGGAGTATGAGGTATGATCCCATTAATCTTTTGT 2220
DB 2161 TTTGAAAGCAAAATATCCACAGGAGTATGAGGTATGATCCCATTAATCTTTTGT 2220
QY 2221 CTTTGTATTTAAGAAACAAATATTTATCAGGAAACAAACGTTCTGCTAGAGGTA 2280
DB 2221 CTTTGTATTTAAGAAACAAATATTTATCAGGAAACAAACGTTCTGCTAGAGGTA 2280
QY 2281 TTAAGTATAGATTAATAACAAATTTAATTAATTAATTAATTAATTAATTAATTAAT 2340
DB 2281 TTAAGTATAGATTAATAACAAATTTAATTAATTAATTAATTAATTAATTAATTAAT 2340
QY 2341 ACCATCTTGAACATTAATTAATTAATTAATTTTATTAATTAATTAATTAATTAAT 2400
DB 2341 ACCATCTTGAACATTAATTAATTAATTAATTTTATTAATTAATTAATTAATTAAT 2400
QY 2401 AAAAAATGCAAAAGAAAGATTAATTTAAGTCAAAATTAATTAAGTATGAGTAT 2460
DB 2401 AAAAAATGCAAAAGAAAGATTAATTTAAGTCAAAATTAATTAAGTATGAGTAT 2460
QY 2461 TCTTCAAGCAAAACGCGCCGCTAGAGGTCTTATCTTACATTAAGCTGGGTTGGCAG 2520
DB 2461 TCTTCAAGCAAAACGCGCCGCTAGAGGTCTTATCTTACATTAAGCTGGGTTGGCAG 2520
QY 2521 ACATCATAGGCGCTAGATTAATTTAGCTTTAAGTACGTAAGCTTTAACAATCTAGT 2580
DB 2521 ACATCATAGGCGCTAGATTAATTTAGCTTTAAGTACGTAAGCTTTAACAATCTAGT 2580
QY 2581 TAGTCTCACTGTAACAAACAAATTCATTCGTAACATTAATTAACAAATCTAGT 2640
DB 2581 TAGTCTCACTGTAACAAACAAATTCATTCGTAACATTAATTAACAAATCTAGT 2640
QY 2641 GTACTAGATTAAGCTAGATATACATCGTTTTTGGCAAAATTTCTAACTAATCTATACAA 2700
DB 2641 GTACTAGATTAAGCTAGATATACATCGTTTTTGGCAAAATTTCTAACTAATCTATACAA 2700
QY 2701 CAAACTTGAAATGTTGTTGTAATTTATCTTAAACAAAGTTTGAATGTGCAATGGG 2760

DB 2701 CAAACTTGAAATGTTGTTGTAATTTATCTTAACAAAGTTTGAATGTGCAATGGG 2760
QY 2761 AGCTACACTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAAGT 2820
DB 2761 AGCTACACTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAAGT 2820
QY 2821 ATTTAAACCAACAAATTTTATTTGCTGTAAGGTACAAACATGTCATATATAGAGA 2880
DB 2821 ATTTAAACCAACAAATTTTATTTGCTGTAAGGTACAAACATGTCATATATAGAGA 2880
QY 2881 CAGCATGTTTATACAAATATGTTGATGTTAATGAAATCAATTAATTAATACGATTA 2940
DB 2881 CAGCATGTTTATACAAATATGTTGATGTTAATGAAATCAATTAATTAATACGATTA 2940
QY 2941 GCGACTCACTGGTTTAAATGTTTGAAGATTAATTAATAAATGAATTCAGAGATA 3000
DB 2941 GCGACTCACTGGTTTAAATGTTTGAAGATTAATTAATAAATGAATTCAGAGATA 3000
QY 3001 CAGAGCTATATATGCTGGGCTATTAGAGCGGTGACAAAGTTGCTGTAATTTCTAC 3060
DB 3001 CAGAGCTATATATGCTGGGCTATTAGAGCGGTGACAAAGTTGCTGTAATTTCTAC 3060
QY 3061 GGTGCGATTAAGAAATTTTGAATTTTCTTCAACCTTTATGAACTTCTGATAGTTT 3120
DB 3061 GGTGCGATTAAGAAATTTTGAATTTTCTTCAACCTTTATGAACTTCTGATAGTTT 3120
QY 3121 TGTGGAATTAATATTTGTAATTCGTAATTTTGTCTTAATTAAGTATCGTAATTTCA 3180
DB 3121 TGTGGAATTAATATTTGTAATTCGTAATTTTGTCTTAATTAAGTATCGTAATTTCA 3180
QY 3181 CGATTAAGAAAGCTTCTTTTATTTAATTTGATTTAAACCTTTGTTTGGAAATGACT 3240
DB 3181 CGATTAAGAAAGCTTCTTTTATTTAATTTGATTTAAACCTTTGTTTGGAAATGACT 3240
QY 3241 CATACAAAGGTTAAGTTGATGATATCCAAATTTCAAAATGTTTGCAGAGTGCCTTC 3300
DB 3241 CATACAAAGGTTAAGTTGATGATATCCAAATTTCAAAATGTTTGCAGAGTGCCTTC 3300
QY 3301 GAGTGTCTTACCAACATCGTACCACTCGTATGGGTTATATAGGTTTTTTCTTCTT 3360
DB 3301 GAGTGTCTTACCAACATCGTACCACTCGTATGGGTTATATAGGTTTTTTCTTCTT 3360
QY 3361 TTTTCAATGCTTTATTAATTTGAACACTTAATTTCTTTTAAATTAATGTTAAAGT 3420
DB 3361 TTTTCAATGCTTTATTAATTTGAACACTTAATTTCTTTTAAATTAATGTTAAAGT 3420
QY 3421 CTTGAATTTCTGTTGATTTTAAACCAAGGTTTCAATCTCTGTCGCAAAAAA 3480
DB 3421 CTTGAATTTCTGTTGATTTTAAACCAAGGTTTCAATCTCTGTCGCAAAAAA 3480
QY 3481 AAAAGGTTTCAATTAATTAAGATCTAAATTTTGAAGTTCAAGTTTAATGATGCT 3540
DB 3481 AAAAGGTTTCAATTAATTAAGATCTAAATTTTGAAGTTCAAGTTTAATGATGCT 3540
QY 3541 GAAAGTTATGAATGATGCAAGTTTGCACAGATGCTGATGATCAATCAAAA 3600
DB 3541 GAAAGTTATGAATGATGCAAGTTTGCACAGATGCTGATGATCAATCAAAA 3600
QY 3601 CATGCAATCAAAATTAATTTGCTGTTAGCAAGAAAGATTAATTAACGAAAT 3660
DB 3601 CATGCAATCAAAATTAATTTGCTGTTAGCAAGAAAGATTAATTAACGAAAT 3660
QY 3661 CGTTAACCACTTAATAATCTTAGAATTAATTTGATGATTAATTTCTGTAAGAGAGG 3720
DB 3661 CGTTAACCACTTAATAATCTTAGAATTAATTTGATGATTAATTTCTGTAAGAGAGG 3720
QY 3721 TATCATATCTTACAAAAAACTCATTTCAATTAATTAATGTTGCTCAATGTTACCA 3780
DB 3721 TATCATATCTTACAAAAAACTCATTTCAATTAATTAATGTTGCTCAATGTTACCA 3780
QY 3781 AGTATGTTTGTGCTGATCAAGTTGATTTGTAATCTGCTCTTAAGCATTAAGTTCTAAG 3840

Db 3781 AGATGTTTTGGTCATCAGTTGATGTAACTGCTCTTAGACCATATAGTCTAAG 3840
Qy 3841 TTTTAAATGTTTCAAGACTTTACAAAATATAATATAAGGGAATTTGAGG 3900
Db 3841 TTTTAAATGTTTCAAGACTTTACAAAATATAATATAAGGGAATTTGAGG 3900
Qy 3901 CTAAGACGAAAAATATAATATAATATAAGTAAGAAAGCTCTTCTCAATAGAAC 3960
Db 3901 CTAAGACGAAAAATATAATATAATATAAGTAAGAAAGCTCTTCTCAATAGAAC 3960
Qy 3961 AGATCCCAACGGAATCAACAGCAAAATTTGTGCTTGTCTCTCTCTTAATATATC 4020
Db 3961 AGATCCCAACGGAATCAACAGCAAAATTTGTGCTTGTCTCTCTCTTAATATATC 4020
Qy 4021 CTTCAAAAAACCTCTCTATCTATCTCTTAAGCCCCCTTCCCTGTTTCTCAACGCA 4080
Db 4021 CTTCAAAAAACCTCTCTATCTCTTAATCTCTTAAGCCCCCTTCCCTGTTTCTCAACGCA 4080
Qy 4081 CAAAGAAAAACAAGTTTGAGAAAAATGTGTGTTGTTGTAACCAATGATGGGT 4140
Db 4081 CAAAGAAAAACAAGTTTGAGAAAAATGTGTGTTGTTGTAACCAATGATGGGT 4140
Qy 4141 TTTAGCTTACTCTGAGAGATTATAGAAGAAAGAGTGAATCATTAATAGAAGA 4200
Db 4141 TTTAGCTTACTCTGAGAGATTATAGAAGAAAGAGTGAATCATTAATAGAAGA 4200
Qy 4201 AGAAGACAGAAACCAAAAAAGAACCC 4228
Db 4201 AGAAGACAGAAACCAAAAAAGAACCC 4228

RESULT 2

US-10-059-911-3
; Sequence 3, Application US/10059911
; Publication No. US20030159180A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods for Altering Organ Mass in Plants
; FILE REFERENCE: 023070-090730US
; CURRENT APPLICATION NUMBER: US/10/059,911
; NUMBER OF FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4228
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AINTEGUMENTA (ANT) promoter, 5'-upstream sequence
; OTHER INFORMATION: of ANT gene
US-10-059-911-3

Query Match 93.1%; Score 3936; DB 6; Length 4228;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 4226; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 GTGACTCTAGGCTCTCACTGCTTAATAGCACTCACTAATAGGAGCTCGAGATCCCTTA 60
Db 1 GTGACTCTAGGCTCTCACTGCTTAATAGCACTCACTAATAGGAGCTCGAGATCCCTTA 60
Qy 61 GTTAGAAAAAATCTTCTTTAGTGTGTCGTGTGTTTAACTTCAATATATAGTATC 120
Db 61 GTTAGAAAAAATCTTCTTTAGTGTGTCGTGTGTTTAACTTCAATATATAGTATC 120
Qy 121 ACATGTGATTCACAATATATATATATGAAATTTGAAATTTATTCATATATAGTATGAT 180
Db 121 ACATGTGATTCACAATATATATATGAAATTTGAAATTTATTCATATATAGTATGAT 180
Qy 181 TAATATATATAGCTGATTAACCAACCAAAATGTTTCTGTTTATAGATATGATTTATAT 240
Db 181 TAATATATATAGCTGATTAACCAACCAAAATGTTTCTGTTTATAGATATGATTTATAT 240

Qy 241 GTTGCACTTGAATATAGATTAATATAAACTGGTTTATTTTAAATCCGTACCATTAAC 300
Db 241 GTTGCACTTGAATATAGATTAATATAAACTGGTTTATTTTAAATCCGTACCATTAAC 300
Qy 301 AAAAGTGAACCAAAACGAGATCCATGTTTGTGTTTACTTGTGTTTAAACAGATTAAT 360
Db 301 AAAAGTGAACCAAAACGAGATCCATGTTTGTGTTTACTTGTGTTTAAACAGATTAAT 360
Qy 361 ATGATTAATGAGATTAATCTTTACTAATATATAATATTTGGAAAAACAACTTA 420
Db 361 ATGATTAATGAGATTAATCTTTACTAATATATAATATTTGGAAAAACAACTTA 420
Qy 421 ATATGTTGAGTGTCTCAAGGCTCACTGTTCAAGAAATTAATCTGTTTATCTACTTGAA 480
Db 421 ATATGTTGAGTGTCTCAAGGCTCACTGTTCAAGAAATTAATCTGTTTATCTACTTGAA 480
Qy 481 CTAGAAATTGATATACATTAACACGTGAATATTTTAACGACCGTACATTAACATGAT 540
Db 481 CTAGAAATTGATATACATTAACACGTGAATATTTTAACGACCGTACATTAACATGAT 540
Qy 541 CGATCAAAATCAAAATTTATGAGACTAGAAATCCAGATGAGATGACCTTACAGAAAT 600
Db 541 CGATCAAAATCAAAATTTATGAGACTAGAAATCCAGATGAGATGACCTTACAGAAAT 600
Qy 601 TACACAGCTAAGAAATTTGACAAAGAGTGAAGAAAAATAGTTCTAATCAATTTAAAAA 660
Db 601 TACACAGCTAAGAAATTTGACAAAGAGTGAAGAAAAATAGTTCTAATCAATTTAAAAA 660
Qy 661 TATGATTTCACTTACGATGATATATTAATTAACATTAACGAGTATGATTAATATTTT 720
Db 661 TATGATTTCACTTACGATGATATATTAATTAACATTAACGAGTATGATTAATATTTT 720
Qy 721 TGTGTTTGTGTTTACGATTAATAGAAATGTTGTTTAAATTTGTTTACTTA 780
Db 721 TGTGTTTGTGTTTACGATTAATAGAAATGTTGTTTAAATTTGTTTACTTA 780
Qy 781 AACTGTTTATGTTTAACTATATATATGTTCTTCCGATGTTAAATTTGAAACAAACCTGTA 840
Db 781 AACTGTTTATGTTTAACTATATATATGTTCTTCCGATGTTAAATTTGAAACAAACCTGTA 840
Qy 841 TACAAATTAATGTTAAAGCCATGCAATTAATAAAATCCAGCGGTATGAATCTCAGAAAT 900
Db 841 TACAAATTAATGTTAAAGCCATGCAATTAATAAAATCCAGCGGTATGAATCTCAGAAAT 900
Qy 901 TATGTTAAGTCTACAAATTTTCTTTAGATTTAGTAAAGTTGAGCAAAATTAATGATTA 960
Db 901 TATGTTAAGTCTACAAATTTTCTTTAGATTTAGTAAAGTTGAGCAAAATTAATGATTA 960
Qy 961 CCTTGACAGGGGTATTAAGGTCATGATGTCAGATCTCAGCATGAAGCCAAAGTCGTC 1020
Db 961 CCTTGACAGGGGTATTAAGGTCATGATGTCAGATCTCAGCATGAAGCCAAAGTCGTC 1020
Qy 1021 TCTGTCTTAAAGATATCTACAGCTGCTTCCCTGTGAATAGAGAATAATGTAATGATGA 1080
Db 1021 TCTGTCTTAAAGATATCTACAGCTGCTTCCCTGTGAATAGAGAATAATGTAATGATGA 1080
Qy 1081 GAGATCCCATCTAGGCTTCAAGTTTGCCTGTCGCGCACTTTGGCGGTGTTGACT 1140
Db 1081 GAGATCCCATCTAGGCTTCAAGTTTGCCTGTCGCGCACTTTGGCGGTGTTGACT 1140
Qy 1141 TTTTCTTATGTCGTTGTTTGACTAATTTTCTCAGAGTGAAGTGAATCAAGAAACT 1200
Db 1141 TTTTCTTATGTCGTTGTTTGACTAATTTTCTCAGAGTGAAGTGAATCAAGAAACT 1200
Qy 1201 AATATTGAAAAAGAAAAAGAAAAAGCAAGAAATATATGTCGAAAGCATTAATGAC 1260
Db 1201 AATATTGAAAAAGAAAAAGAAAAAGCAAGAAATATATGTCGAAAGCATTAATGAC 1260
Qy 1261 ACTAAATTTGATTTATTAATAATGTTATATGTTTGTGGAATTTATATCATTTACCA 1320
Db 1261 ACTAAATTTGATTTATTAATAATGTTATATATGTTTGTGGAATTTATATCATTTACCA 1320

QY 1321 AATCAAGAGAGAGAGGACCTTGGCTTATGATTTCCCTCTAAACAATGCT 1380
| | | | |
Db 1321 AATCAAGAGAGAGAGGACCTTGGCTTATGATTTCCCTCTAAACAATGCT 1380
QY 1381 CCCACTATCTTTTATCTTCAACAATAATCATTCACAGAAAATCTGTCTGTATC 1440
| | | | |
Db 1381 CCCACTATCTTTTATCTTCAACAATAATCATTCACAGAAAATCTGTCTGTATC 1440
QY 1441 ACTTTCATGCAAAATTAACATAATTTGGATTTTGTCAAGTTCTGTCTTTTAA 1500
| | | | |
Db 1441 ACTTTCATGCAAAATTAACATAATTTGGATTTTGTCAAGTTCTGTCTTTTAA 1500
QY 1501 TCGATTAATTTGGTAATCTATATGATGATATACATCCAGCTATCAATAATGAT 1560
| | | | |
Db 1501 TCGATTAATTTGGTAATCTATATGATGATATACATCCAGCTATCAATAATGAT 1560
QY 1561 CTCCTCTGCTTATCAATAATTAACACACATTAAGCTATCAAGCTAATAATTA 1620
| | | | |
Db 1561 CTCCTCTGCTTATCAATAATTAACACACATTAAGCTATCAAGCTAATAATTA 1620
QY 1621 CATCTCTTATCAATTTTATATGATTAATAAACAACGACTATAGCTACAGATT 1680
| | | | |
Db 1621 CATCTCTTATCAATTTTATATGATTAATAAACAACGACTATAGCTACAGATT 1680
QY 1681 GGTAATTAAGGATTAATGCTCTAGTCAAGAAATTTTGTATGATTAACATCTGTG 1740
| | | | |
Db 1681 GGTAATTAAGGATTAATGCTCTAGTCAAGAAATTTTGTATGATTAACATCTGTG 1740
QY 1741 GGAATAAATATCAGCTTAATATGCTCAATTAAGATTAATGATTAATGCTTAATCA 1800
| | | | |
Db 1741 GGAATAAATATCAGCTTAATATGCTCAATTAAGATTAATGATTAATGCTTAATCA 1800
QY 1801 TTAATAATTAAGATTTTGTCTTTTAAAGTTTACACGCTTAATTCATTAAGAGAT 1860
| | | | |
Db 1801 TTAATAATTAAGATTTTGTCTTTTAAAGTTTACACGCTTAATTCATTAAGAGAT 1860
QY 1861 ATTAACCTTGAATGCAAAATTCCTTTTAAACATTAAGAAAATTTTCAGCATTT 1920
| | | | |
Db 1861 ATTAACCTTGAATGCAAAATTCCTTTTAAACATTAAGAAAATTTTCAGCATTT 1920
QY 1921 TTAATAATTAAGGATTAATGCTTCAATTAATATGTTTCAAGTAAATTTTGAAGT 1980
| | | | |
Db 1921 TTAATAATTAAGGATTAATGCTTCAATTAATATGTTTCAAGTAAATTTTGAAGT 1980
QY 1981 TTAACAATGAATGTTTTTGAATTAATAAACAATTAATTTCTAGTAATTAACATTT 2040
| | | | |
Db 1981 TTAACAATGAATGTTTTTGAATTAATAAACAATTAATTTCTAGTAATTAACATTT 2040
QY 2041 TTTTAACGCTCAATGCAATTTGTATTAAGTGAACAATTCGAAAACATTTTCTTGT 2100
| | | | |
Db 2041 TTTTAACGCTCAATGCAATTTGTATTAAGTGAACAATTCGAAAACATTTTCTTGT 2100
QY 2101 AATCTGTTTAAATTTCTCTGCTGCAATCTTGACGCAATTTGACAAAGCATTAACATA 2160
| | | | |
Db 2101 AATCTGTTTAAATTTCTCTGCTGCAATCTTGACGCAATTTGACAAAGCATTAACATA 2160
QY 2161 TTGAAGAGAAAATTCACAGAGATGATAGGGTTAATCCACATTCMAATCTTTTGT 2220
| | | | |
Db 2161 TTGAAGAGAAAATTCACAGAGATGATAGGGTTAATCCACATTCMAATCTTTTGT 2220
QY 2221 CTTTGTATTTATGAAAAACAATTTTATCAAGAAAAACGTTTCTTCTAGTGATA 2280
| | | | |
Db 2221 CTTTGTATTTATGAAAAACAATTTTATCAAGAAAAACGTTTCTTCTAGTGATA 2280
QY 2281 TTAAGATTAAGATTAATCAAAATTTTAATTAATGATTAATTAATTAATTAATTA 2340
| | | | |
Db 2281 TTAAGATTAAGATTAATCAAAATTTTAATTAATGATTAATTAATTAATTAATTA 2340
QY 2341 ACGATCTTCAACATTAATTAATGCAATTTTATTTTATTAATTAATTAATTAATTA 2400
| | | | |
Db 2341 ACGATCTTCAACATTAATTAATGCAATTTTATTTTATTAATTAATTAATTAATTA 2400
QY 2401 AAAAAATGCAAAAGAGATATATTTTAAGTCAAGTAATTAAGATGATGATGAT 2460
| | | | |

Db 2401 AAAAAATGCAAAAGAGATATATTTTAAGTCAAGTAATTAAGATGATGATGAT 2460
| | | | |
QY 2461 TCTTACGAAAACGGCCCGTAGAGTGTCTTATCTTACATTAACGCTGGTGTGCA 2520
| | | | |
Db 2461 TCTTACGAAAACGGCCCGTAGAGTGTCTTATCTTACATTAACGCTGGTGTGCA 2520
QY 2521 ACATCATAGGCGCTACATTAATTTAGCTTTACGTACGTAAAGCTTTACATATCTAGT 2580
| | | | |
Db 2521 ACATCATAGGCGCTACATTAATTTAGCTTTACGTACGTAAAGCTTTACATATCTAGT 2580
QY 2581 TAGTTCTCATCTGCAACAACAACAATCCAAATTCCTTAACATATATATACAAATCTACTA 2640
| | | | |
Db 2581 TAGTTCTCATCTGCAACAACAACAATCCAAATTCCTTAACATATATATACAAATCTACTA 2640
QY 2641 GTACTAGATTAACGCTACGATATACATGCTTTTGGCAAAATTTCTAAATCTATACAA 2700
| | | | |
Db 2641 GTACTAGATTAACGCTACGATATACATGCTTTTGGCAAAATTTCTAAATCTATACAA 2700
QY 2701 CAACCTGAATGTTTGTATTTGTAATTTATCTTAAACCAAGTTTGAATGTGCAATGGG 2760
| | | | |
Db 2701 CAACCTGAATGTTTGTATTTGTAATTTATCTTAAACCAAGTTTGAATGTGCAATGGG 2760
QY 2761 AGCTACACTCTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAAGT 2820
| | | | |
Db 2761 AGCTACACTCTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAAGT 2820
QY 2821 ATTTAAACCAACAAATTTTAATTTGTGCTGAAGTACCAACATGTCATATATAGAGA 2880
| | | | |
Db 2821 ATTTAAACCAACAAATTTTAATTTGTGCTGAAGTACCAACATGTCATATATAGAGA 2880
QY 2881 CAGCATGTTTATTAACAATAATGTTGATGATTTGGAATCAATATTAATTAAGATTA 2940
| | | | |
Db 2881 CAGCATGTTTATTAACAATAATGTTGATGATTTGGAATCAATATTAATTAAGATTA 2940
QY 2941 GCGACTCACTGGTTTATATGTTTGAAGATTAATGAATTAATAAATGAATTAAGAT 2999
| | | | |
Db 2941 GCGACTCACTGGTTTATATGTTTGAAGATTAATGAATTAATAAATGAATTAAGAT 2999
QY 3000 ACAGAGCTATATATGTCGGGTCATTTAGAGCCGTGACCAAAAGTTTGTCTGTAATTTCTA 3059
| | | | |
Db 3000 ACAGAGCTATATATGTCGGGTCATTTAGAGCCGTGACCAAAAGTTTGTCTGTAATTTCTA 3059
QY 3060 CGGTGCGTCATTAAGAAATTTTGACCTTTTCTCACCCCTTTATAGACTTCTGTATAGTTT 3119
| | | | |
Db 3060 CGGTGCGTCATTAAGAAATTTTGACCTTTTCTCACCCCTTTATAGACTTCTGTATAGTTT 3119
QY 3120 TTGTGGAATTAATATATTTGATTTGTAATTTTGTCTTAATTAATGATCGTAATTTTC 3179
| | | | |
Db 3120 TTGTGGAATTAATATATTTGATTTGTAATTTTGTCTTAATTAATGATCGTAATTTTC 3179
QY 3180 ACGATTAAGAAAACCTCTTTTATTAATTTGAATTAACCTTTTGTGAAAATGAC 3239
| | | | |
Db 3180 ACGATTAAGAAAACCTCTTTTATTAATTTGAATTAACCTTTTGTGAAAATGAC 3239
QY 3240 TCATACACAAGGTTAAAGTTGATGATCAATTTCAAAAAGTTTCGAGAGTGCGTT 3299
| | | | |
Db 3240 TCATACACAAGGTTAAAGTTGATGATCAATTTCAAAAAGTTTCGAGAGTGCGTT 3299
QY 3300 CGAGTGTCTTACCAACATCGTACCACTCGTAAAGGTTTATTAAGGTTTCTTCT 3359
| | | | |
Db 3300 CGAGTGTCTTACCAACATCGTACCACTCGTAAAGGTTTATTAAGGTTTCTTCT 3359
QY 3360 TTTTCAATGCTTATTAATTAATGAACACTTAATTTCTTTTAAATTAATTAAGTTAAGAA 3419
| | | | |
Db 3360 TTTTCAATGCTTATTAATTAATGAACACTTAATTTCTTTTAAATTAATTAAGTTAAGAA 3419
QY 3420 TCTTGAATTTTGTGATTTTAAACAAGGTTTCAATCTTCTAGCACAAAAAAAA 3479
| | | | |
Db 3420 TCTTGAATTTTGTGATTTTAAACAAGGTTTCAATCTTCTAGCACAAAAAAAA 3479
QY 3480 AAAAAAGTTTCAATTAATTAAGAAATTTTGAATGCAAGGTTTATGATAGC 3539
| | | | |

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Db 3480 AAAAGGTTTCATTATATTAAGAATCTAATTTTTGAGTCAAGATTAAATGATAGC 3539
Qy 3540 TGAAGGTTATGATGATTTGCAAGTTCAGAAAGCGATGATGATCAATATCAAAA 3599
Db 3540 TGAAGGTTATGATGATTTGCAAGTTCAGAAAGCGATGATGATCAATATCAAAA 3599
Qy 3600 ACATGATCAAAATTAATATTCGTCTTACAGAGAAAGATTTGAATTAACAGAA 3659
Db 3600 ACATGATCAAAATTAATATTCGTCTTACAGAGAAAGATTTGAATTAACAGAA 3659
Qy 3660 TCGTTAACCACTTAAATATTTGTAGTATTAATTTCTGTAAAGAGAG 3719
Db 3660 TCGTTAACCACTTAAATATTTGTAGTATTAATTTCTGTAAAGAGAG 3719
Qy 3720 GTATCATATTTTCAAAAAAATCTCATTTAGATTAATATGATGATCAATGATACC 3779
Db 3720 GTATCATATTTTCAAAAAAATCTCATTTAGATTAATATGATGATCAATGATACC 3779
Qy 3780 AAGTATGTTTCTGTCATCATGTTGATTTGAATCTGCTCTTACGATATAGTTCTAA 3839
Db 3780 AAGTATGTTTCTGTCATCATGTTGATTTGAATCTGCTCTTACGATATAGTTCTAA 3839
Qy 3840 GTTTAAATGTTTCAAAAGCTTTACAAAATAATATATATATATATATATATATAT 3899
Db 3840 GTTTAAATGTTTCAAAAGCTTTACAAAATAATATATATATATATATATATATAT 3899
Qy 3900 GCTTAAAGCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
Db 3900 GCTTAAAGCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
Qy 3960 CAGATCCCAAGGATTCAGAAAGATTTGCTTCTCTTCTCTTATTAATATAT 4019
Db 3960 CAGATCCCAAGGATTCAGAAAGATTTGCTTCTCTTCTCTTATTAATATATAT 4019
Qy 4020 CCTCTCAAAAACCTCTCTATATCTCTCTTAAAGCCCCCTCTCTTCTCTTAA 4079
Db 4020 CCTCTCAAAAACCTCTCTATATCTCTCTTAAAGCCCCCTCTCTTCTCTTAA 4079
Qy 4080 ACAAAGAAAAAACAAGTTGAGAAAAATGCTGTCTGTGTAACCAATGATGGG 4139
Db 4080 ACAAAGAAAAAACAAGTTGAGAAAAATGCTGTCTGTGTAACCAATGATGGG 4139
Qy 4140 TTTTACCTTACTCTTGAAGATTTATAGAAAGAAAGATGATATATAGAAAG 4199
Db 4140 TTTTACCTTACTCTTGAAGATTTATAGAAAGAAAGATGATATATAGAAAG 4199
Qy 4200 AAGAGAGCAGAAACCAAAAAAGAAACC 4228
Db 4200 AAGAGAGCAGAAACCAAAAAAGAAACC 4228
```

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RESULT 3
US-10-059-911-1
; Sequence 1, Application US/10059911
; Publication No. US20030159180A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; TITLE OF INVENTION: Methods for the University of California
; FILE REFERENCE: 023070-090730US
; CURRENT APPLICATION NUMBER: US/10/059,911
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2148
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AINTEGUMENTA (ANT) cDNA
; NAME/KEY: CDS
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; LOCATION: (269)..(1936)
; OTHER INFORMATION: Arabidopsis AINTEGUMENTA (ANT)
US-10-059-911-1
Query Match 6.3%; Score 268; DB 6; Length 2148;
Best Local Similarity 100.0%; Pred. No. 5e-108;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3961 AGATCCCAAGGATTCAGAAAGATTTGCTTCTCTTCTCTTATTAATATATC 4020
Db 1 AGATCCCAAGGATTCAGAAAGATTTGCTTCTCTTCTCTTATTAATATATC 60
Qy 4021 CTCTCAAAAACCTCTCTATATCTCTTAAAGCCCCCTTCTCTTCTCTACGCA 4080
Db 61 CTCTCAAAAACCTCTCTATATCTCTTAAAGCCCCCTTCTCTTCTCTACGCA 120
Qy 4081 CAAAGAAAAACAAGTTGAGAAAAATGCTGTCTGTGTAACCAATGATGGGT 4140
Db 121 CAAAGAAAAACAAGTTGAGAAAAATGCTGTCTGTGTAACCAATGATGGGT 180
Qy 4141 TTTAGCTTACTCTTGAAGATTTATAGAAAGAAAGATGATATATAGAAAG 4200
Db 181 TTTAGCTTACTCTTGAAGATTTATAGAAAGAAAGATGATATATAGAAAG 240
Qy 4201 AAGAGAGCAGAAACCAAAAAAGAAACC 4228
Db 241 AAGAGAGCAGAAACCAAAAAAGAAACC 268
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RESULT 4
US-10-623-477-1
; Sequence 1, Application US/10623477
; Publication No. US20050132445A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; TITLE OF INVENTION: Methods for the University of California
; FILE REFERENCE: 023070-090720US
; CURRENT APPLICATION NUMBER: US/10/623,477
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US/09/479,855
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2148
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: CDS
; LOCATION: (269)..(1936)
; OTHER INFORMATION: AINTEGUMENTA (ANT) cDNA
; OTHER INFORMATION: AINTEGUMENTA (ANT)
US-10-623-477-1
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Query Match 6.3%; Score 268; DB 9; Length 2148;
Best Local Similarity 100.0%; Pred. No. 5e-108;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3961 AGATCCCAAGGATTCAGAAAGATTTGCTTCTCTTCTCTTATTAATATC 4020
Db 1 AGATCCCAAGGATTCAGAAAGATTTGCTTCTCTTCTCTTATTAATATC 60
Qy 4021 CTCTCAAAAACCTCTCTATATCTCTTAAAGCCCCCTTCTCTTCTCTACGCA 4080
Db 61 CTCTCAAAAACCTCTCTATATCTCTTAAAGCCCCCTTCTCTTCTCTACGCA 120
Qy 4081 CAAAGAAAAACAAGTTGAGAAAAATGCTGTCTGTGTAACCAATGATGGGT 4140
Db 121 CAAAGAAAAACAAGTTGAGAAAAATGCTGTCTGTGTAACCAATGATGGGT 180
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SEQUENCE DESCRIPTION: SEQ ID NO: 26;
US-09-988-462-26

Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGCTATATAGACTCACTATAGGAGCTCGA 50
DB 4162 TGGCTATATAGACTCACTATAGGAGCTCGA 4131

RESULT 7

US-10-431-252-17/c
Sequence 17, Application US/10431252
Publication No. US20030226166A1
GENERAL INFORMATION:
APPLICANT: Li, Zhongqun
TITLE OF INVENTION: S-ADENOSYL-L-METHIONINE SYNTHETASE PROMOTER AND
TITLE OF INVENTION: ITS USE IN EXPRESSION OF TRANSGENIC GENES IN PLANTS
FILE REFERENCE: BB1205 US CIP
CURRENT APPLICATION NUMBER: US/10/431,252
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: US 60/113,045
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: US 09/464,528
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 6975
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid
FEATURE:
NAME/KEY: unsure
LOCATION: (3367)
OTHER INFORMATION: n = a, c, g or t
US-10-431-252-17

Query Match 0.6%; Score 27; DB 6; Length 6975;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAGCTCG 49
DB 4123 CTAATACGACTCACTATAGGAGCTCG 4097

RESULT 8

US-09-925-065A-275529
Sequence 275529, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 275529
LENGTH: 625
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-275529

Query Match 0.6%; Score 26; DB 4; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAATTAATAATTAATAAGTAAA 3935
DB 161 AAAAATTAATAATTAATAAGTAAA 186

RESULT 9

US-09-925-065A-275530
Sequence 275530, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 275530
LENGTH: 625
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-275530

Query Match 0.6%; Score 26; DB 4; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAATTAATAATTAATAAGTAAA 3935
DB 161 AAAAATTAATAATTAATAAGTAAA 186

RESULT 10

US-10-223-646-58
Sequence 58, Application US/10223646
Publication No. US20030140372A1
GENERAL INFORMATION:
APPLICANT: Shen, Jennie B.
TITLE OF INVENTION: GENES FOR DESATURASES TO ALTER LIPID PROFILES IN CORN
FILE REFERENCE: BB-1137
CURRENT APPLICATION NUMBER: US/10/223,646
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US/09/326,285
PRIOR FILING DATE: 1999-06-07
PRIOR APPLICATION NUMBER: 60/088,987
PRIOR FILING DATE: JUNE 11, 1998
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Microsoft Office 97
SEQ ID NO 58
LENGTH: 6337

TYPE: DNA
ORGANISM: Zea mays
US-10-223-646-58

Query Match 0.6%; Score 26; DB 6; Length 6337;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAGCTC 48
Db 6312 CTAATACGACTCACTATAGGAGCTC 6337

RESULT 11
US-10-087-192-2011/c
Sequence 2011, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morrie, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 2011
LENGTH: 96499
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(96499)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-2011

Query Match 0.6%; Score 26; DB 5; Length 96499;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3914 ATAAATATAATTAATTAAGTAAAGAA 3939
Db 1233 ATAAATATAATTAATTAAGTAAAGAA 1208

RESULT 12
US-10-322-281-456/c
Sequence 456, Application US/10322281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morrie
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
PRIOR APPLICATION NUMBER: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 456
LENGTH: 301477
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(301477)
OTHER INFORMATION: n = A,T,C or G
US-10-322-281-456

Query Match 0.6%; Score 26; DB 7; Length 301477;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3910 AAAAAATATAATTAATTAAGTAA 3935
Db 105296 AAAAAATATAATTAATTAAGTAA 105271

RESULT 13
US-10-223-666-11/c
Sequence 11, Application US/10223666
Publication No. US20030180744A1
GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratechun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/223,666
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,763
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-10-223-666-11

Query Match 0.6%; Score 25; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 33 TAATAGACTCACTATAGGAGCTC 9

RESULT 14
US-09-449-204-16
Sequence 16, Application US/09449204A
Patent No. US20020051974A1
GENERAL INFORMATION:
APPLICANT: Sincropl, Dominick V.
APPLICANT: Williams, P. Mickey
APPLICANT: Meng, Yu-Ju G. H.
APPLICANT: Dodge, Anthony H.
APPLICANT: Sims, Paul W.
APPLICANT: Wong, Wei Lee Tan
TITLE OF INVENTION: PCR ASSAY
FILE REFERENCE: P1543R1
CURRENT APPLICATION NUMBER: US/09/449,204A
CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: US 60/110,259
EARLIER FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 16
LENGTH: 48
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Sequence source: synthetic primer
US-09-449-204-16

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 15
US-09-860-474-2
Sequence 2, Application US/09860474
Publication No. US20030032785A1
GENERAL INFORMATION:
APPLICANT: GOLD, L. and JANJIC, N.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE LIGANDS
TO VASCULAR ENOTHELIAL GROWTH
FACTOR (VEGF)
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
CITY: Highlands Ranch
STATE: Colorado
COUNTRY: USA
ZIP: 80129
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,474

FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/156,824
FILING DATE: 18-SEPTEMBER-1998
APPLICATION NUMBER: 08/447,169
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: 08/233,012
FILING DATE: 25-APRIL-1994
APPLICATION NUMBER: 08/205,515
FILING DATE: 03-MARCH-1994
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX14/CIP-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-860-474-2

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 16
US-10-037-986-37
Sequence 37, Application US/10037986
Publication No. US20030157467A1
GENERAL INFORMATION:
APPLICANT: Larry Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/037,986
FILING DATE: 18-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995

APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-037-986-37

Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TAATACGACTCATTAGGAGCTC 48
Db 9 TAATACGACTCATTAGGAGCTC 33

RESULT 17
US-10-409-565-2
Sequence 2, Application US/10409565
Publication No. US20030176680A1
GENERAL INFORMATION:
APPLICANT: GOLD, L. and JANJIC, N.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE LIGANDS
TO VASCULAR ENDOTHELIAL GROWTH
FACTOR (VEGF)
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
CITY: Highlands Ranch
STATE: Colorado
COUNTRY: USA
ZIP: 80129
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/409,565
FILING DATE: 07-Apr-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/860,474
FILING DATE: 18-May-2001
APPLICATION NUMBER: 09/156,824
FILING DATE: 18-SEPTEMBER-1998
APPLICATION NUMBER: 08/447,169
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: 08/233,012
FILING DATE: 25-APRIL-1994
APPLICATION NUMBER: 08/205,515
FILING DATE: 03-MARCH-1994
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEX14/CIP-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-409-565-2

Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TAATACGACTCATTAGGAGCTC 48
Db 9 TAATACGACTCATTAGGAGCTC 33

RESULT 18
US-10-408-085-37
Sequence 37, Application US/10408085
Publication No. US20030198989A1
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/408,085
FILING DATE: 03-Apr-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/037,986
FILING DATE: 18-Oct-2001
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEX01/C7

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-408-085-37

Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
DB 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 19
US-10-885-403-2
Sequence 2, Application US/10885403
Publication No. US20050043265A1
GENERAL INFORMATION:
APPLICANT: Gold, Larry
TITLE OF INVENTION: High-Affinity RNA Ligands of Basic
Fibroblast Growth Factors
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/885,403
FILING DATE: 06-Jul-2004
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/442,423
FILING DATE: 16-MAY-1995
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-885-403-2
Query Match 0.6%; Score 25; DB 8; Length 48;

Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
DB 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 20
US-09-816-089A-7
Sequence 7, Application US/09816089A
Publication No. US20020086299A1
GENERAL INFORMATION:
APPLICANT: OBOKATA, Junichi et al.
TITLE OF INVENTION: Methods of Screening Potential
TITLE OF INVENTION: Translational Regulatory Elements of Messenger RNA
FILE REFERENCE: 10235/9
CURRENT APPLICATION NUMBER: US/09/816,089A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2000-291084
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 59
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-816-089A-7

Query Match 0.6%; Score 25; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GGCCTAATACGACTCACTATAGGGA 44
DB 4 GGCCTAATACGACTCACTATAGGGA 28

RESULT 21
US-09-816-089A-3
Sequence 3, Application US/09816089A
Publication No. US20020086299A1
GENERAL INFORMATION:
APPLICANT: OBOKATA, Junichi et al.
TITLE OF INVENTION: Methods of Screening Potential
TITLE OF INVENTION: Translational Regulatory Elements of Messenger RNA
FILE REFERENCE: 10235/9
CURRENT APPLICATION NUMBER: US/09/816,089A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2000-291084
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 63
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-816-089A-3

Query Match 0.6%; Score 25; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GGCCTAATACGACTCACTATAGGGA 44
DB 9 GGCCTAATACGACTCACTATAGGGA 33

RESULT 22

```
US-09-976-800-109
; Sequence 109, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
US-09-976-800-109

Query Match      0.6%; Score 24; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28

RESULT 24
US-10-139-031-109
; Sequence 109, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
US-10-139-031-109

Query Match      0.6%; Score 24; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-10-138-905-109

Query Match 0.6%; Score 24; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATCGACTCACTATAGGAG 45
Db 5 CCTAATCGACTCACTATAGGAG 28

RESULT 26
US-10-138-916-109

Sequence 109, Application US/10138916
Publication No. US20030073220A1

GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornelt, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,916
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 09/976,800
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/302,602
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-10-138-916-109

Query Match 0.6%; Score 24; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATCGACTCACTATAGGAG 45
Db 5 CCTAATCGACTCACTATAGGAG 28

RESULT 27
US-10-139-296-109

Sequence 109, Application US/10139296
Publication No. US20030148486A1

GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornelt, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE

TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,296
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-10-139-296-109

Query Match 0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATCGACTCACTATAGGAG 45
Db 5 CCTAATCGACTCACTATAGGAG 28

RESULT 28
US-10-139-218-109

Sequence 109, Application US/10139218
Publication No. US20030153060A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornelt, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,218
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-10-139-218-109

Query Match 0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATCGACTCACTATAGGAG 45
Db 5 CCTAATCGACTCACTATAGGAG 28

RESULT 29
US-10-405-660-109

Sequence 109, Application US/10405660
Publication No. US20030186411A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley

Query Match 0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATCGACTCACTATAGGAG 45
Db 5 CCTAATCGACTCACTATAGGAG 28

RESULT 29
US-10-405-660-109


```

; APPLICANT: Behoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/405,660
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
US-10-405-660-109
```

```

Query Match      0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Cy      22 CCTAATAGCACTCACTAATAGGAG 45
      |||
      5 CCTAATAGCACTCACTAATAGGAG 28
```

```

RESULT 30
; Sequence 109, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Behoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,898
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
US-10-138-898-109
```

```

Query Match      0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Cy      22 CCTAATAGCACTCACTAATAGGAG 45
      |||
      5 CCTAATAGCACTCACTAATAGGAG 28
```

```

RESULT 31
US-10-294-055-6
; Sequence 6, Application US/10294055
; Publication No. US20030095968A1
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; RECEPTOR DNA AND POLYPEPTIDES
```

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
```

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/294,055
FILING DATE: 13-NO. US20030095968A1-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/958,598
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 470-4189
TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: primer

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-294-055-6

```

Query Match      0.6%; Score 24; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Cy      22 CCTAATAGCACTCACTAATAGGAG 45
      |||
      5 CCTAATAGCACTCACTAATAGGAG 28
```

```

RESULT 32
US-10-983-198-33
; Sequence 33, Application US/10983198
; Publication No. US20050130203A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qingyun
; APPLICANT: McDonald, Terrence
; APPLICANT: Bonner, Timothy P.
; APPLICANT: Ng, Gordon
; APPLICANT: Kolakowski, Lee F., Jr.
; APPLICANT: Clark, Janet
; APPLICANT: Bonner, Tom I.
; TITLE OF INVENTION: NOVEL GABAB RECEPTOR DNA SEQUENCES
; FILE REFERENCE: 20052YP
; CURRENT APPLICATION NUMBER: US/10/983,198
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/601,582
```

;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: PCT/US99/02361
;; PRIOR FILING DATE: 1999-02-03
;; PRIOR APPLICATION NUMBER: 60/073,767
;; PRIOR FILING DATE: 1998-02-05
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 33
;; LENGTH: 43
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
US-10-983-198-33

Query Match 0.6%; Score 24; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAAATACGACTCCTATAGGAGCT 47
Db 6 TAAATACGACTCCTATAGGAGCT 29

RESULT 33
US-10-740-773-6
;; Sequence 6, Application US/10740773
;; Publication No. US20040180825A1
;; GENERAL INFORMATION:
;; APPLICANT: Spriggs, Melanie K.
;; TITLE OF INVENTION: NOVEL SEMAPHORIN POLYPEPTIDES
;; FILE REFERENCE: 2634-US
;; CURRENT APPLICATION NUMBER: US/10/740,773
;; CURRENT FILING DATE: 2003-12-19
;; PRIOR APPLICATION NUMBER: US/09/689,012
;; PRIOR FILING DATE: 2000-10-12
;; PRIOR APPLICATION NUMBER: PCT/US99/09831
;; PRIOR FILING DATE: 1999-05-05
;; PRIOR APPLICATION NUMBER: US 60/085,497
;; PRIOR FILING DATE: 1998-05-14
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 6
;; LENGTH: 44
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: PRIMER
US-10-740-773-6

Query Match 0.6%; Score 24; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
Db 6 CCTAATACGACTCCTATAGGAG 29

RESULT 34
US-10-154-801-6
;; Sequence 6, Application US/10154801
;; Publication No. US20020151014A1
;; GENERAL INFORMATION:
;; APPLICANT: CAMPBELL, ANTHONY KEITH
;; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
;; FILE REFERENCE: 09/225,302
;; CURRENT APPLICATION NUMBER: US/10/154,801
;; CURRENT FILING DATE: 2002-05-28
;; PRIOR APPLICATION NUMBER: 08/957,135
;; PRIOR FILING DATE: 1998-09-14
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 45

;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-154-801-6

Query Match 0.6%; Score 24; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
Db 3 CCTAATACGACTCCTATAGGAG 26

RESULT 35
US-10-154-801-9
;; Sequence 9, Application US/10154801
;; Publication No. US20020151014A1
;; GENERAL INFORMATION:
;; APPLICANT: CAMPBELL, ANTHONY KEITH
;; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
;; FILE REFERENCE: 09/225,302
;; CURRENT APPLICATION NUMBER: US/10/154,801
;; CURRENT FILING DATE: 2002-05-28
;; PRIOR APPLICATION NUMBER: 08/957,135
;; PRIOR FILING DATE: 1998-09-14
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 9
;; LENGTH: 45
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-154-801-9

Query Match 0.6%; Score 24; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
Db 3 CCTAATACGACTCCTATAGGAG 26

RESULT 36
US-09-816-089A-6
;; Sequence 6, Application US/09816089A
;; Publication No. US20020086299A1
;; GENERAL INFORMATION:
;; APPLICANT: OBOKATA, Junichi et al.
;; TITLE OF INVENTION: Methods of Screening Potential
;; FILE REFERENCE: 10235/9
;; CURRENT APPLICATION NUMBER: US/09/816,089A
;; CURRENT FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: JP 2000-291084
;; PRIOR FILING DATE: 2000-09-25
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 48
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer
US-09-816-089A-6

Query Match 0.6%; Score 24; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 GGCTATAGACTACTATAGG 43
Db 4 GGCTATAGACTACTATAGG 27

RESULT 37

US-10-094-507-32
; Sequence 32, Application US/10094507
; Publication No. US2003014353A1
; GENERAL INFORMATION:
; APPLICANT: Sommer, Steve S.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION WITH DIRECT SEQUENCING
; FILE REFERENCE: 27709-42A
; CURRENT APPLICATION NUMBER: US/10/094,507
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Replication segment
US-10-094-507-32

Query Match 0.6%; Score 24; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CCTATAGACTACTATAGGAG 45

Db 5 CCTATAGACTACTATAGGAG 28

RESULT 38

US-09-976-800-59
; Sequence 59, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-976-800-59

Query Match 0.6%; Score 24; DB 3; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CCTATAGACTACTATAGGAG 45

Db 5 CCTATAGACTACTATAGGAG 28

RESULT 39
US-09-976-800-71
; Sequence 71, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-976-800-71

Query Match 0.6%; Score 24; DB 3; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CCTATAGACTACTATAGGAG 45

Db 5 CCTATAGACTACTATAGGAG 28

RESULT 40

US-09-976-800-75
; Sequence 75, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-976-800-75

Query Match 0.6%; Score 24; DB 3; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CCTATAGACTACTATAGGAG 45

Db 5 CCTATAGACTACTATAGGAG 28

Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
|||||
Db 5 CCTAATACGACTCATTATAGGAG 28

RESULT 41

US-10-138-838-59
; Sequence 59, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-838-59

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
|||||
Db 5 CCTAATACGACTCATTATAGGAG 28

RESULT 42

US-10-138-838-71
; Sequence 71, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03

PRIOR APPLICATION NUMBER: US/09/976,800

PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 49
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-838-71

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
|||||
Db 5 CCTAATACGACTCATTATAGGAG 28

RESULT 43

US-10-138-838-75
; Sequence 75, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-838-75

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
|||||
Db 5 CCTAATACGACTCATTATAGGAG 28

RESULT 44

US-10-139-031-59
; Sequence 59, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark

```

: APPLICANT: Madduri, Kriehna M.
: APPLICANT: Cornett, Cathy A.
: APPLICANT: Brenner, Alfred A.
: APPLICANT: Tang, Maria
: APPLICANT: Loper, John C.
: APPLICANT: Gleeson, Martin
: TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
: TITLE OF INVENTION: P450 OXIDOREDUCTASE
: TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
: FILE REFERENCE: 1010-16
: CURRENT APPLICATION NUMBER: US/10/139,031
: PRIOR FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: US/09/976,800
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 59
: LENGTH: 49
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-59

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28

RESULT 45
US-10-139-031-71
: Sequence 71, Application US/10139031
: Publication No. US20030049822A1
: GENERAL INFORMATION:
: APPLICANT: Wilson, Ron C.
: APPLICANT: Craft, David L.
: APPLICANT: Ertich, Dudley
: APPLICANT: Eshoo, Mark
: APPLICANT: Madduri, Krishna M.
: APPLICANT: Cornett, Cathy A.
: APPLICANT: Brenner, Alfred A.
: APPLICANT: Tang, Maria
: APPLICANT: Loper, John C.
: APPLICANT: Gleeson, Martin
: TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
: TITLE OF INVENTION: P450 OXIDOREDUCTASE
: TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
: FILE REFERENCE: 1010-16
: CURRENT APPLICATION NUMBER: US/10/139,031
: CURRENT FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: US/09/976,800
: PRIOR FILING DATE: 2001-10-12
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 71
: LENGTH: 49
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-71

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28
```

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Db      5 CCTAATAGACTCACTATAGGAG 28

RESULT 46
US-10-139-031-75
: Sequence 75, Application US/10139031
: Publication No. US20030049822A1
: GENERAL INFORMATION:
: APPLICANT: Wilson, Ron C.
: APPLICANT: Craft, David L.
: APPLICANT: Ertich, Dudley
: APPLICANT: Eshoo, Mark
: APPLICANT: Madduri, Krishna M.
: APPLICANT: Cornett, Cathy A.
: APPLICANT: Brenner, Alfred A.
: APPLICANT: Tang, Maria
: APPLICANT: Loper, John C.
: APPLICANT: Gleeson, Martin
: TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
: TITLE OF INVENTION: P450 OXIDOREDUCTASE
: TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
: FILE REFERENCE: 1010-16
: CURRENT APPLICATION NUMBER: US/10/139,031
: CURRENT FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: US/09/976,800
: PRIOR FILING DATE: 2001-10-12
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 75
: LENGTH: 49
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-75

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28

RESULT 47
US-10-138-905-59
: Sequence 59, Application US/10138905
: Publication No. US20030068800A1
: GENERAL INFORMATION:
: APPLICANT: Wilson, Ron C.
: APPLICANT: Craft, David L.
: APPLICANT: Ertich, Dudley
: APPLICANT: Eshoo, Mark
: APPLICANT: Madduri, Krishna M.
: APPLICANT: Cornett, Cathy A.
: APPLICANT: Brenner, Alfred A.
: APPLICANT: Tang, Maria
: APPLICANT: Loper, John C.
: APPLICANT: Gleeson, Martin
: TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
: TITLE OF INVENTION: P450 OXIDOREDUCTASE
: TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
: FILE REFERENCE: 1010-16
: CURRENT APPLICATION NUMBER: US/10/138,905
: CURRENT FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: US/09/976,800
: PRIOR FILING DATE: 2001-10-12
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 59
: LENGTH: 49
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-59

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28
```

/ SEQ ID NO 59
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-59

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATTAGGAG 45
DB 5 CCTAATACGACTCCTATTAGGAG 28

RESULT 48

US-10-138-905-71
/ Sequence 71, Application US/10138905
/ Publication No. US20030068800A1
/ GENERAL INFORMATION:
/ APPLICANT: Wilson, Ron C.
/ APPLICANT: Craft, David L.
/ APPLICANT: Birch, Dudley
/ APPLICANT: Bahoo, Mark
/ APPLICANT: Madduri, Krishna M.
/ APPLICANT: Cornelt, Cathy A.
/ APPLICANT: Brenner, Alfred A.
/ APPLICANT: Tang, Maria
/ APPLICANT: Loper, John C.
/ APPLICANT: Gleeson, Martin
/ TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
/ TITLE OF INVENTION: P450 OXIDOREDUCTASE
/ TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
/ FILE REFERENCE: 1010-16
/ CURRENT APPLICATION NUMBER: US/10/138,905
/ CURRENT FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US/09/976,800
/ PRIOR FILING DATE: 2001-10-12
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 71
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-71

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATTAGGAG 45
DB 5 CCTAATACGACTCCTATTAGGAG 28

RESULT 49

US-10-138-905-75
/ Sequence 75, Application US/10138905
/ Publication No. US20030068800A1
/ GENERAL INFORMATION:
/ APPLICANT: Wilson, Ron C.
/ APPLICANT: Craft, David L.
/ APPLICANT: Birch, Dudley
/ APPLICANT: Bahoo, Mark
/ APPLICANT: Madduri, Krishna M.
/ APPLICANT: Cornelt, Cathy A.
/ APPLICANT: Brenner, Alfred A.
/ APPLICANT: Tang, Maria

/ APPLICANT: Loper, John C.
/ APPLICANT: Gleeson, Martin
/ TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
/ TITLE OF INVENTION: P450 OXIDOREDUCTASE
/ TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
/ FILE REFERENCE: 1010-16
/ CURRENT APPLICATION NUMBER: US/10/138,905
/ CURRENT FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US/09/976,800
/ PRIOR FILING DATE: 2001-10-12
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 75
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-75

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATTAGGAG 45
DB 5 CCTAATACGACTCCTATTAGGAG 28

RESULT 50

US-10-138-916-59
/ Sequence 59, Application US/10138916
/ Publication No. US20030073220A1
/ GENERAL INFORMATION:
/ APPLICANT: Wilson, Ron C.
/ APPLICANT: Craft, David L.
/ APPLICANT: Birch, Dudley
/ APPLICANT: Bahoo, Mark
/ APPLICANT: Madduri, Krishna M.
/ APPLICANT: Cornelt, Cathy A.
/ APPLICANT: Brenner, Alfred A.
/ APPLICANT: Tang, Maria
/ APPLICANT: Loper, John C.
/ APPLICANT: Gleeson, Martin
/ TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
/ TITLE OF INVENTION: P450 OXIDOREDUCTASE
/ TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
/ FILE REFERENCE: 1010-16
/ CURRENT APPLICATION NUMBER: US/10/138,916
/ CURRENT FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US/09/976,800
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US/09/302,602
/ PRIOR FILING DATE: 1999-04-30
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 59
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-916-59

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATTAGGAG 45
DB 5 CCTAATACGACTCCTATTAGGAG 28

```
RESULT 51
US-10-138-916-71
; Sequence 71, Application US/10138916
; Publication No. US20030073220A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYP1B1
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,916
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/976,800
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/302,602
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-916-71

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATAGCACTCACTAATAGGAG 45
Db      5 CCTAATAGCACTCACTAATAGGAG 28

RESULT 52
US-10-138-916-75
; Sequence 75, Application US/10138916
; Publication No. US20030073220A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYP1B1
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,916
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/976,800
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/302,602
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
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```
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-916-75

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATAGCACTCACTAATAGGAG 45
Db      5 CCTAATAGCACTCACTAATAGGAG 28

RESULT 53
US-10-139-296-59
; Sequence 59, Application US/10139296
; Publication No. US20030148486A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYP1B1
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,296
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-296-59

Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATAGCACTCACTAATAGGAG 45
Db      5 CCTAATAGCACTCACTAATAGGAG 28

RESULT 54
US-10-139-296-71
; Sequence 71, Application US/10139296
; Publication No. US20030148486A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
```

APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,296
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-296-71

Query Match 0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTGACTATAGGAG 45
DB 5 CCTAATACGACTGACTATAGGAG 28

RESULT 55
US-10-139-296-75
Sequence 75, Application US/10139296
Publication No. US20030148486A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,296
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-296-75

Query Match 0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTGACTATAGGAG 45
DB 5 CCTAATACGACTGACTATAGGAG 28

RESULT 56

US-10-139-218-59
Sequence 59, Application US/10139218
Publication No. US20030153060A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,218
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-218-59

Query Match 0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTGACTATAGGAG 45
DB 5 CCTAATACGACTGACTATAGGAG 28

RESULT 57
US-10-139-218-71
Sequence 71, Application US/10139218
Publication No. US20030153060A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,218
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:


```
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-218-71
Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATAGACTCACTATAGGAG 45
      |||||
      5 CCTAATAGACTCACTATAGGAG 28

RESULT 58
US-10-139-218-75
; Sequence 75, Application US/10139218
; Publication No. US20030153060A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139, 218
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-218-75
Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATAGACTCACTATAGGAG 45
      |||||
      5 CCTAATAGACTCACTATAGGAG 28

RESULT 59
US-10-405-660-59
; Sequence 59, Application US/10405660
; Publication No. US20030186411A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDU
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
```

```
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/405,660
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-405-660-59
Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATAGACTCACTATAGGAG 45
      |||||
      5 CCTAATAGACTCACTATAGGAG 28

RESULT 60
US-10-405-660-71
; Sequence 71, Application US/10405660
; Publication No. US20030186411A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDU
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/405,660
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-405-660-71
Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATAGACTCACTATAGGAG 45
      |||||
      5 CCTAATAGACTCACTATAGGAG 28

RESULT 61
US-10-405-660-75
; Sequence 75, Application US/10405660
; Publication No. US20030186411A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
```

```

; APPLICANT: Birch, Dudley
; APPLICANT: Behoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/405,660
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-405-660-75
```

```

Query Match          0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      22 CCTAATACGACTCATTATAGGAG 45
Db      5 CCTAATACGACTCATTATAGGAG 28

RESULT 62
US-10-138-898-59
; Sequence 59, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Behoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,898
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-898-59
```

```

Query Match          0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      22 CCTAATACGACTCATTATAGGAG 45
Db      5 CCTAATACGACTCATTATAGGAG 28
```

```

RESULT 63
US-10-138-898-71
; Sequence 71, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Behoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,898
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-898-71
```

```

Query Match          0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      22 CCTAATACGACTCATTATAGGAG 45
Db      5 CCTAATACGACTCATTATAGGAG 28

RESULT 64
US-10-138-898-75
; Sequence 75, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Behoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,898
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
```

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-898-75
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Query Match          0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      22 CCTAATACGACTCACTATAGGAG 45
DB      5 CCTAATACGACTCACTATAGGAG 28
```

```
RESULT 65
US-10-212-476-16
; Sequence 16; Application US/10212476
; Publication No. US20030157509A1
; GENERAL INFORMATION:
; APPLICANT: MIRZABEKOV, ANDREI
; APPLICANT: GUSCHIN, DMITRY Y.
; APPLICANT: SHIK, VALENTINE
; APPLICANT: DROBYSHEV, ALEKSEI
; APPLICANT: FOTIN, ALEXANDER
; APPLICANT: YERSHOV, GENNADIY
; APPLICANT: LYSOV, YU
; TITLE OF INVENTION: CUSTOMIZED OLIGONUCLEOTIDE MICROCHIPS THAT CONVERT
; TITLE OF INVENTION: MULTIPLE GENETIC INFORMATION TO SIMPLE PATTERNS, ARE
; FILE REFERENCE: 21416/90184
; CURRENT APPLICATION NUMBER: US/10/212,476
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US/09/261,115
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Reverse primer
US-10-212-476-16
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```
Query Match          0.6%; Score 24; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
DB      7 CCTAATACGACTCACTATAGGAG 30
```

```
RESULT 66
US-10-094-507-1
; Sequence 1; Application US/10094507
; Publication No. US20030143553A1
; GENERAL INFORMATION:
; APPLICANT: Sommer, Steve S.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION WITH DIRECT SEQUENCING
; FILE REFERENCE: 27709-A22A
; CURRENT APPLICATION NUMBER: US/10/094,507
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 51
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Replication segment
US-10-094-507-1
```

```
Query Match          0.6%; Score 24; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
DB      5 CCTAATACGACTCACTATAGGAG 28
```

```
RESULT 67
US-09-760-285-1
; Sequence 1; Application US/09760285
; Publication No. US20030091997A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaidis, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sasse, Philip M
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0017
; CURRENT APPLICATION NUMBER: US/09/760,285
; CURRENT FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-09-760-285-1
```

```
Query Match          0.6%; Score 24; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
DB      5 CCTAATACGACTCACTATAGGAG 28
```

```
RESULT 68
US-10-079-429-65
; Sequence 65; Application US/10079429
; Publication No. US20030027177A1
; GENERAL INFORMATION:
; APPLICANT: Haselcline et al.
; TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
; FILE REFERENCE: P106P3D1
; CURRENT APPLICATION NUMBER: US/10/079,429
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US95/01035
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/468,024
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/465,769
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/294,312
; PRIOR FILING DATE: 1994-08-23
; PRIOR APPLICATION NUMBER: 08/210,143
; PRIOR FILING DATE: 1994-03-16
; PRIOR APPLICATION NUMBER: 08/187,757
; PRIOR FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 65
; LENGTH: 52
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer useful for amplifying codons 1 to 863 hMLH3
US-10-079-429-65
```

```
Query Match          0.6%; Score 24; DB 5; Length 52;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATCGACTCACTATAGGAG 45
Db      5 CCTAATCGACTCACTATAGGAG 28
```

RESULT 69

```
US-10-369-845-1
; Sequence 1, Application US/10369845
; Publication No. US20030186441A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi M
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
; FILE REFERENCE: MOR-0005
; CURRENT APPLICATION NUMBER: US/10/369,845
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US/09/708,200
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-10-369-845-1
```

```
Query Match          0.6%; Score 24; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATCGACTCACTATAGGAG 45
Db      5 CCTAATCGACTCACTATAGGAG 28
```

RESULT 70

```
US-09-976-800-69
; Sequence 69, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Esnoff, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleason, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
```

```
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-976-800-69
```

```
Query Match          0.6%; Score 24; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATCGACTCACTATAGGAG 45
Db      5 CCTAATCGACTCACTATAGGAG 28
```

RESULT 71

```
US-09-760-285-3
; Sequence 3, Application US/09760285
; Publication No. US20030091997A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi M
; APPLICANT: Sasse, Philip M
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0017
; CURRENT APPLICATION NUMBER: US/09/760,285
; CURRENT FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-760-285-3
```

```
Query Match          0.6%; Score 24; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATCGACTCACTATAGGAG 45
Db      5 CCTAATCGACTCACTATAGGAG 28
```

RESULT 72

```
US-10-079-429-56
; Sequence 56, Application US/10079429
; Publication No. US20030027177A1
; GENERAL INFORMATION:
; APPLICANT: Haefliger et al.
; TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
; FILE REFERENCE: P106P3D1
; CURRENT APPLICATION NUMBER: US/10/079,429
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US95/01035
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/468,024
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/465,769
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/294,312
; PRIOR FILING DATE: 1994-08-23
; PRIOR APPLICATION NUMBER: 08/210,143
; PRIOR FILING DATE: 1994-03-16
; PRIOR APPLICATION NUMBER: 08/187,757
; PRIOR FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
```

```

; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer useful for amplifying codons 1 to 500 of hmlh2
US-10-079-429-56
```

```

Query Match          0.6%; Score 24; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 73

```

US-10-138-838-69
; Sequence 69, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138, 838
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976, 800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-838-69
```

```

Query Match          0.6%; Score 24; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 74

```

US-10-139-031-69
; Sequence 69, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
```

```

; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139, 031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976, 800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-69
```

```

Query Match          0.6%; Score 24; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 75

```

US-10-138-905-69
; Sequence 69, Application US/10138905
; Publication No. US20030068800A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138, 905
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976, 800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-69
```

```

Query Match          0.6%; Score 24; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

Search completed: February 28, 2006, 02:31:37

Job time : 3141 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 20:09:32 ; Search time 1581 Seconds
(without alignments)
17823.100 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtcgactctcggcctcactg.....agaaacccaagaagaacc 4228

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

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3: genesegq20008:*
4: genesegq2001aa:*
5: genesegq2001ba:*
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8: genesegq2003aa:*
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10: genesegq2003ca:*
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12: genesegq2004aa:*
13: genesegq2004ba:*
14: genesegq2005a:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4228	100.0	4228	10	Adg25137 Thalecres
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3	4107	97.1	4227	3	AAAS9221 Promoter
4	3936	93.1	4228	10	Adg88432 Arabidops
5	268	6.3	2148	3	AAAS9220
6	268	6.3	2148	8	ABX13437
7	268	6.3	2148	10	ADG85135
8	268	6.3	2148	10	ADG88430 Arabidops
9	268	6.3	2148	14	AEAL7180 A. thalia
10	55	1.3	1421	12	ADMA2796 DNA encod
11	55	1.3	1421	14	ADY55721 Mouse odo
12	55	1.3	1421	14	AEBS6275
13	55	1.3	2408	2	AAT30737 Rat ctyp
14	55	1.3	3049	6	ABN81284 Beet prom
15	55	1.3	3869	8	ABZ82143 Arabidops
16	55	1.3	11630	4	AA502362 Galactosy
17	55	1.3	16905	12	ADOS9305 Mouse kan
18	55	1.3	27048	4	AA502354 Porcine G
19	46	1.1	4026	4	AA502355 Porcine G

20	37	0.9	1905	12	AD061538	Ad061538 Transcrip
21	28	0.7	3484	2	AAV34987	AAV34987 Arabidops
22	27	0.6	1205	3	AAAT94303	AAAT94303 BGM3 gene
23	27	0.6	6975	3	AAAS1053	AAAS1053 Plasmid p
24	27	0.6	7038	3	AAAS5633	AAAS5633 2-hybrid
25	27	0.6	8815	3	AAAS5630	AAAS5630 Desinat
26	27	0.6	11240	14	AEAG2089	AEAG2089 Replicat
27	27	0.6	21178	13	ADU81180	ADU81180 Thale cre
28	27	0.6	22635	13	ADU81181	ADU81181 Thale cre
29	26	0.6	38	3	AAAC60777	AAAC60777 Candidate
30	26	0.6	40	2	AAAH88214	AAAH88214 Oligonuc
31	26	0.6	43	14	AEBO0576	AEBO0576 Drosophi
32	26	0.6	239	3	AAT36342	AAT36342 Human imm
33	26	0.6	6337	3	AAZ35182	AAZ35182 Corn del
34	26	0.6	6337	10	ADAD4515	ADAD4515 Plasmid p
35	26	0.6	96499	11	ACN45188	ACN45188 Mouse gen
36	26	0.6	301477	13	ABD33362	ABD33362 Human can
37	25	0.6	45	10	ADCG4226	ADCG4226 Identific
38	25	0.6	47	2	AAV45614	AAV45614 Primer fo
39	25	0.6	47	3	AAZ44303	AAZ44303 M. tuberc
40	25	0.6	47	4	AAAF77539	AAAF77539 M. tuberc
41	25	0.6	48	2	AAQ52391	AAQ52391 PCR prime
42	25	0.6	48	2	AAQ62710	AAQ62710 Primer fo
43	25	0.6	48	2	AAQ63026	AAQ63026 Primer us
44	25	0.6	48	2	AAQ63022	AAQ63022 Substance
45	25	0.6	48	2	AAT06077	AAT06077 HIV-1 int
46	25	0.6	48	2	AAT73197	AAT73197 HIV-1 int
47	25	0.6	48	2	AAQ98306	AAQ98306 SELEX pri
48	25	0.6	48	2	AAQ89173	AAQ89173 VEGF RNA
49	25	0.6	48	2	AAQ89176	AAQ89176 VEGF RNA
50	25	0.6	48	2	AAT07688	AAT07688 Amplifica
51	25	0.6	48	2	AAT84603	AAT84603 RNA ligas
52	25	0.6	48	2	AAT79124	AAT79124 3' primer
53	25	0.6	48	2	AAT87307	AAT87307 SELEX PCR
54	25	0.6	48	2	AAV00777	AAV00777 PCR prime
55	25	0.6	48	2	AAV14558	AAV14558 Primer fo
56	25	0.6	48	2	AAV79637	AAV79637 HSV-1 DNA
57	25	0.6	48	3	AAAS2737	AAAS2737 HSV-1 DNA
58	25	0.6	48	4	AAAF70540	AAAF70540 SELEX exp
59	25	0.6	48	6	ABAD4075	ABAD4075 PCR prime
60	25	0.6	48	6	ABK61113	ABK61113 SELEX pro
61	25	0.6	48	10	ADPF67501	ADPF67501 SELEX CDN
62	25	0.6	48	12	ADG39049	ADG39049 cDNA prim
63	25	0.6	59	6	ABL88785	ABL88785 HIV-1 rev
64	25	0.6	59	6	ABL41041	ABL41041 GUS mRNA
65	25	0.6	63	6	ABL41037	ABL41037 GUS mRNA
66	25	0.6	123	12	ADN14395	ADN14395 PCR prime
67	25	0.6	136	2	AAQ23256	AAQ23256 Plasmid p
68	25	0.6	243934	14	ADZ13446	ADZ13446 Human can
69	24	0.6	29	2	AAK00218	AAK00218 T7 RNA po
70	24	0.6	29	6	ABK31899	ABK31899 Bacteriop
71	24	0.6	29	10	ADC44990	ADC44990 T7 promot
72	24	0.6	29	10	ADC45560	ADC45560 T7 promot
73	24	0.6	29	10	ADBS2071	ADBS2071 T7 promot
74	24	0.6	29	10	ADP72378	ADP72378 Bacteriop
75	24	0.6	29	10	ADP71818	ADP71818 T7 promot
76	24	0.6	29	10	ADP11700	ADP11700 T7 promot
77	24	0.6	29	12	ADBE64235	ADBE64235 T7 promot
78	24	0.6	29	12	ADU26617	ADU26617 Bacteriop
79	24	0.6	29	12	ADQ76186	ADQ76186 Chemokine
80	24	0.6	38	2	AAQ12513	AAQ12513 Portion o
81	24	0.6	41	2	AAT69676	AAT69676 Upstearm
82	24	0.6	43	2	AAZ06993	AAZ06993 Murine GA
83	24	0.6	43	2	AAAS5564	AAAS5564 VESPR DNA
84	24	0.6	43	3	AAAC63725	AAAC63725 Human VES
85	24	0.6	43	3	AAZ29445	AAZ29445 PCR prime
86	24	0.6	43	4	AAAF76949	AAAF76949 Human EST
87	24	0.6	43	5	AAAF25253	AAAF25253 PCR prime
88	24	0.6	43	5	AAAL57778	AAAL57778 PCR prime
89	24	0.6	44	3	AAT90930	AAT90930 Primer fo
90	24	0.6	44	3	AAZ40171	AAZ40171 PCR prime
91	24	0.6	46	12	ADT60084	ADT60084 Oligonuc
92	24	0.6	47	2	AAT34362	AAT34362 TDH conta

C	93	24	0.6	47	2	AAT34360	Aatc34360 TDH conta
	94	24	0.6	47	2	AAT91751	Aatc91751 Primer BB
	95	24	0.6	47	2	AAx28398	Aax28398 Primer fo
	96	24	0.6	47	2	AAx87786	Aax87786 T7 promot
	97	24	0.6	47	2	AAZ25623	Aaz25623 Staphy10c
	98	24	0.6	47	3	AAC58766	Aac58766 Oligonuc1
	99	24	0.6	48	2	AAV07636	Aav07636 Human 1eu
	100	24	0.6	48	3	AAZ89013	Aaz89013 Human Fac

ALIGNMENTS

RESULT 1

ADG25137 standard; DNA, 4228 BP.

XX	ADG25137	
XX	ADG25137;	
XX	26-FEB-2004 (first entry)	
XX	Thalecress Aintegumenta, ANT, gene promoter.	
XX	Thalecress; ds; promoter; Aintegumenta; ANT; AP2 domain; plant;	
XX	seed mass; asexual reproduction; reduced fertility.	
XX	Arabidopsis thaliana.	
XX	US6639128-B1.	
XX	28-OCT-2003.	
XX	07-JAN-2000; 2000US-00479855.	
XX	08-JAN-1999; 99US-00227421.	
XX	(NASC-) NAT SCI FOUND.	
XX	Fischer RL, Mizukami Y;	
XX	WPI; 2003-842795/78.	
XX	New nucleic acid, useful in conferring desired traits on plants, such as	
XX	increased seed mass, asexual reproduction or reduced fertility.	
XX	disclosure, SEQ ID NO 3; 25bp; English.	
XX	The invention relates to an isolated nucleic acid comprising a	
XX	polynucleotide encoding a polypeptide having at least 90% identity with	
XX	Canola Aintegumenta, ANT, (appearing as ADG25139) as determined using a	
XX	BLAST algorithm and comprising two AP2 domains. Also included are an	
XX	expression cassette comprising a plant promoter operably linked to a	
XX	heterologous polynucleotide encoding the polypeptide, a vector comprising	
XX	the expression cassette, a plant comprising the plant promoter operably	
XX	linked to the heterologous polynucleotide, a method of asexually	
XX	reproducing a plant and a method of reducing fertility in a plant. The	
XX	nucleic acid is useful in conferring desired traits on plants, such as	
XX	increased seed mass, asexual reproduction or reduced fertility. The	
XX	present sequence is the promoter region of teh Thalecress Aintegumenta,	
XX	ANT, gene.	
XX	Sequence 4228 BP; 1489 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;	
XX	Query Match 100.0%; Score 4228; DB 10; Length 4228;	
XX	Best Local Similarity 100.0%; Pred. No. 0;	
XX	Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GTGACCTTAGGCTCACTGCTTAATAGACTCACTATAGGAGCTCGAGATCCTTTA	60
DB	1 GTGACCTTAGGCTCACTGCTTAATAGACTCACTATAGGAGCTCGAGATCCTTTA	60
QY	61 GTTAGAAAACTTTCTTGATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	120

DB	61 GTTAGAAAACTTTCTTGATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	120
QY	121 ACATGTGATATGCAAT	180
DB	121 ACATGTGATATGCAAT	180
QY	181 TAAT	240
DB	181 TAAT	240
QY	241 GTTGCACTTGAT	300
DB	241 GTTGCACTTGAT	300
QY	301 AAAAGTGACCAAAAGAGATCCATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	360
DB	301 AAAAGTGACCAAAAGAGATCCATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	360
QY	361 ATGATATATGGAAGATTAAT	420
DB	361 ATGATATATGGAAGATTAAT	420
QY	421 ATATGTGAGTGTCTTCACTGCTCACTGCTCACTGCTCACTGCTCACTGCTCACTGCT	480
DB	421 ATATGTGAGTGTCTTCACTGCTCACTGCTCACTGCTCACTGCTCACTGCTCACTGCT	480
QY	481 CTAGAGGTGAT	540
DB	481 CTAGAGGTGAT	540
QY	541 CGATCAATATCAAT	600
DB	541 CGATCAATATCAAT	600
QY	601 TACACAGCTAAGATTTGTACAAAGAGTGCAGAAATAGATTTCTAATTTAAAAAGA	660
DB	601 TACACAGCTAAGATTTGTACAAAGAGTGCAGAAATAGATTTCTAATTTAAAAAGA	660
QY	661 TATGATTTCACTTACGATTTGATTTTACCTTACGATTTGATTTTACCTTACGATTTT	720
DB	661 TATGATTTCACTTACGATTTGATTTTACCTTACGATTTGATTTTACCTTACGATTTT	720
QY	721 TGTGTTGTTTTACGATTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA	780
DB	721 TGTGTTGTTTTACGATTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA	780
QY	781 AACTCGTTTATGTTACTAT	840
DB	781 AACTCGTTTATGTTACTAT	840
QY	841 TACAATTTATGTTAGCCATTTGCAATTTAAAAATCCAGCGGTATATATCTCAGAAAT	900
DB	841 TACAATTTATGTTAGCCATTTGCAATTTAAAAATCCAGCGGTATATATCTCAGAAAT	900
QY	901 TATGTTAAGTCTACAAATTTCTTTAGATTTAGTAAAGTTTGAACAATATATATATAT	960
DB	901 TATGTTAAGTCTACAAATTTCTTTAGATTTAGTAAAGTTTGAACAATATATATATAT	960
QY	961 CCTTGACGGGTATTAAGGTCACTGATGTGAGACTCAGATGAGAACCAAGAGTCTGTC	1020
DB	961 CCTTGACGGGTATTAAGGTCACTGATGTGAGACTCAGATGAGAACCAAGAGTCTGTC	1020
QY	1021 TCTGTCTTAAGATATCTACAGCTGCTTCCCTGTGATATAGAGAAATTTGATATGA	1080
DB	1021 TCTGTCTTAAGATATCTACAGCTGCTTCCCTGTGATATAGAGAAATTTGATATGA	1080
QY	1081 GAGATCCCATTAAGGTTTCAAGTTTCCCTGCGCACTTGGGGGTTTGTGACT	1140
DB	1081 GAGATCCCATTAAGGTTTCAAGTTTCCCTGCGCACTTGGGGGTTTGTGACT	1140
QY	1141 TTTTTCCTATATGCTGTTGATTAATTTCTCAGAGTGAAGTGTATCAAGAAACT	1200
DB	1141 TTTTTCCTATATGCTGTTGATTAATTTCTCAGAGTGAAGTGTATCAAGAAACT	1200

QY 1201 AATATTCGAAAAAGAAAAAGGCAAGAAACCTATTGTGAAAAAGCATTAATGAC 1260
DB 1201 AATATTCGAAAAAGAAAAAGGCAAGAAACCTATTGTGAAAAAGCATTAATGAC 1260
QY 1261 ACTAATAATTGGATTATTAATAATGATATGTTGGTGAATTTAATCAATTACAA 1320
DB 1261 ACTAATAATTGGATTATTAATAATGATATGTTGGTGAATTTAATCAATTACAA 1320
QY 1321 AATCAAG 1380
DB 1321 AATCAAG 1380
QY 1381 CCGCATATCTCTTTTAACTTCCCAAAATCATTCACAGAGAAATCTGTCTGATC 1440
DB 1381 CCGCATATCTCTTTTAACTTCCCAAAATCATTCACAGAGAAATCTGTCTGATC 1440
QY 1441 ACTTCATGCAAAATTAACCTAAATTTGGATTTTGTCAAGTTCTGTGTTTAAAG 1500
DB 1441 ACTTCATGCAAAATTAACCTAAATTTGGATTTTGTCAAGTTCTGTGTTTAAAG 1500
QY 1501 TCGATTAATTTGATTAATTAATGATGATGATTAATCAATCCAACTAATCAATTAATGAT 1560
DB 1501 TCGATTAATTTGATTAATTAATGATGATGATTAATCAATCCAACTAATCAATTAATGAT 1560
QY 1561 CTCCTCTGCTTATCAATTAATTAACCACTTAAGCTAATCAAGCTAATTAATTAACCA 1620
DB 1561 CTCCTCTGCTTATCAATTAATTAACCACTTAAGCTAATCAAGCTAATTAATTAACCA 1620
QY 1621 CATTCCTTAATCAATTTTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
DB 1621 CATTCCTTAATCAATTTTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
QY 1681 GGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
DB 1681 GGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
QY 1741 GGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
DB 1741 GGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
QY 1801 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1860
DB 1801 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1860
QY 1861 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1920
DB 1861 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1920
QY 1921 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1980
DB 1921 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1980
QY 1981 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
DB 1981 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
QY 2041 TTTAACCGTTCATCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2100
DB 2041 TTTAACCGTTCATCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2100
QY 2101 AATCTGTTTAAATTTCTCTGTCTGATCAATTAATTAATTAATTAATTAATTAATTAATTA 2160
DB 2101 AATCTGTTTAAATTTCTCTGTCTGATCAATTAATTAATTAATTAATTAATTAATTAATTA 2160
QY 2161 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2220
DB 2161 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2220
QY 2221 CTTTGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2280
DB 2221 CTTTGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2280

QY 2281 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2340
DB 2281 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2340
QY 2341 ACCATCTTCATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2400
DB 2341 ACCATCTTCATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2400
QY 2401 AAAAAATGCAAAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2460
DB 2401 AAAAAATGCAAAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2460
QY 2461 TCTTCAGCAAAAG 2520
DB 2461 TCTTCAGCAAAAG 2520
QY 2521 ACATCAATGAGGAG 2580
DB 2521 ACATCAATGAGGAG 2580
QY 2581 TAGTTCATCTGATCAAAAG 2640
DB 2581 TAGTTCATCTGATCAAAAG 2640
QY 2641 GTACTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2700
DB 2641 GTACTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2700
QY 2701 CAAATCTGAATGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2760
DB 2701 CAAATCTGAATGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2760
QY 2761 AGCTACACTGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2820
DB 2761 AGCTACACTGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2820
QY 2821 ATTTAAACCAAAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2880
DB 2821 ATTTAAACCAAAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2880
QY 2881 CAGATGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2940
DB 2881 CAGATGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2940
QY 2941 GCGATCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3000
DB 2941 GCGATCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3000
QY 3001 CAGAGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3060
DB 3001 CAGAGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3060
QY 3061 GGTGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3120
DB 3061 GGTGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3120
QY 3121 TGTGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3180
DB 3121 TGTGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3180
QY 3181 CGATTAAGAAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3240
DB 3181 CGATTAAGAAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3240
QY 3241 CATACCAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3300
DB 3241 CATACCAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3300
QY 3301 GAGTGTCTTACCAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3360
DB 3301 GAGTGTCTTACCAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3360
QY 3361 TTTTCAATGCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3420


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Qy 541 CGATCAATAAATAATATATAGACTAGATCCAGATGAGATGACTCTGACGAAATA 600
Db 541 CGATCAATAAATAATATATAGACTAGATCCAGATGAGATGACTCTGACGAAATA 600
Qy 601 TACACAGCTAAGATTTGTACAGAGAGTCCGAAAAATAGATCTTAATCATTTAAAAAGA 660
Db 601 TACACAGCTAAGATTTGTACAGAGAGTCCGAAAAATAGATCTTAATCATTTAAAAAGA 660
Qy 661 TATGATTTCACTTACGATGATATTAACATTAACGAGTAGTACATACATATATTTT 720
Db 661 TATGATTTCACTTACGATGATATTAACATTAACGAGTAGTACATACATATATTTT 720
Qy 721 TGTTTTGTTTTACCAGTAATAGAAATGTGTGTTAAAAATATGTTTTTACTAA 780
Db 721 TGTTTTGTTTTACCAGTAATAGAAATGTGTGTTAAAAATATGTTTTTACTAA 780
Qy 781 AACTGTTTTATGTTAATATATATGCTTCCGATGTAATTTGAAACAAACGTGA 840
Db 781 AACTGTTTTATGTTAATATATATGCTTCCGATGTAATTTGAAACAAACGTGA 840
Qy 841 TACAAATTAATGTTAAGCCATTCGAATTAATAAAATCCAGGGTAGTAATCCTCAGAAAT 900
Db 841 TACAAATTAATGTTAAGCCATTCGAATTAATAAAATCCAGGGTAGTAATCCTCAGAAAT 900
Qy 901 TATGTTAAGTCAACAATTTTCTCTTAGATTAAGTTAGAGTTGAGACAAATTTATGATA 960
Db 901 TATGTTAAGTCAACAATTTTCTCTTAGATTAAGTTAGAGTTGAGACAAATTTATGATA 960
Qy 961 CCTTGACGGGGTAAAGGTCACTGATGTCAGACTCAGACTCAGAGCCAAAGAGTGTGTC 1020
Db 961 CCTTGACGGGGTAAAGGTCACTGATGTCAGACTCAGACTCAGAGCCAAAGAGTGTGTC 1020
Qy 1021 TCTGTCTTAAGATATCTACAGCTGCTTCGCTGTGATAGAGAAATGAATGAATGA 1080
Db 1021 TCTGTCTTAAGATATCTACAGCTGCTTCGCTGTGATAGAGAAATGAATGAATGA 1080
Qy 1081 GAGATCCCATCTAGCCCTTTCACGTTTGCGTTCCTCCGTCGCAACTTTGGCGGTGTGA 1140
Db 1081 GAGATCCCATCTAGCCCTTTCACGTTTGCGTTCCTCCGTCGCAACTTTGGCGGTGTGA 1140
Qy 1141 TTTTCTTAATGCTGTTTGAATAATTTTCTCAGAGTGAAGTGTATCAAGAAAT 1200
Db 1141 TTTTCTTAATGCTGTTTGAATAATTTTCTCAGAGTGAAGTGTATCAAGAAAT 1200
Qy 1201 AATATTCGAAAAAGAAAAAGGCAAGAAAACTATGTGCAAAAAGCATTAATGAC 1260
Db 1201 AATATTCGAAAAAGAAAAAGGCAAGAAAACTATGTGCAAAAAGCATTAATGAC 1260
Qy 1261 ACTTAAATTTGATATTAATAATGATATATGTTGTGTAATTTATCATTTACCA 1320
Db 1261 ACTTAAATTTGATATTAATAATGATATATGTTGTGTAATTTATCATTTACCA 1320
Qy 1321 AATCAAGAGAGAGAGAGGAGCTCTTCGTCCTATGATTTCCCTCTAAACAACGTCT 1380
Db 1321 AATCAAGAGAGAGAGAGGAGCTCTTCGTCCTATGATTTCCCTCTAAACAACGTCT 1380
Qy 1381 CCGCATATCTTTTATCTTCCAAACAATCATTCACGAGAAAAATCTGTCTGTATC 1440
Db 1381 CCGCATATCTTTTATCTTCCAAACAATCATTCACGAGAAAAATCTGTCTGTATC 1440
Qy 1441 ACTTTCAATGCAAAATTAACATAATTTTGTGATTTTGTCAAGTTCTTGCTTTTAA 1500
Db 1441 ACTTTCAATGCAAAATTAACATAATTTTGTGATTTTGTCAAGTTCTTGCTTTTAA 1500
Qy 1501 TCGATTAATTTGTAATCTATATGATGATATACATCCAGCTATCAATATATGAT 1560
Db 1501 TCGATTAATTTGTAATCTATATGATGATATACATCCAGCTATCAATATATGAT 1560
Qy 1561 CTCCTTGTCTTATCAATAATTAACACCACTTAGCTAATCAAGCTAATAATTAACA 1620
Db 1561 CTCCTTGTCTTATCAATAATTAACACCACTTAGCTAATCAAGCTAATAATTAACA 1620
Qy 1621 CATTCCTTATCAATTTTATATAGTATAAATAAACAACGACTATAGGCTACAGATT 1680
Db 1621 CATTCCTTATCAATTTTATATAGTATAAATAAACAACGACTATAGGCTACAGATT 1680
Qy 1681 GGTATTAAGGATTAATGCTTCTAGTCGAGAGAAATTTTGTATGATTAACACTGTG 1740
Db 1681 GGTATTAAGGATTAATGCTTCTAGTCGAGAGAAATTTTGTATGATTAACACTGTG 1740
Qy 1741 GGAATAAATTCACGCTTAATATGCTCATTTAAAGATTAATGATTAATGCTTAATCA 1800
Db 1741 GGAATAAATTCACGCTTAATATGCTCATTTAAAGATTAATGATTAATGCTTAATCA 1800
Qy 1801 TTAATAAAGGTTTTGCTTTAAAGTTACACCGCTTAATTCATCATTAAGAGAT 1860
Db 1801 TTAATAAAGGTTTTGCTTTAAAGTTACACCGCTTAATTCATCATTAAGAGAT 1860
Qy 1861 ATTACTTGTATCCAAATTCGAAATATCTTTTAAACATTAAGAAATTTTCAGCATTT 1920
Db 1861 ATTACTTGTATCCAAATTCGAAATATCTTTTAAACATTAAGAAATTTTCAGCATTT 1920
Qy 1921 TTAATAAAGGATCATTTATGAGTTCAATTAATGTTTCCAGTAAAGTTGAGGT 1980
Db 1921 TTAATAAAGGATCATTTATGAGTTCAATTAATGTTTCCAGTAAAGTTGAGGT 1980
Qy 1981 TTAACCAATGAATGTTTTTGAATTTAAABAAACATTAATTTCTAGTATTAACACT 2040
Db 1981 TTAACCAATGAATGTTTTTGAATTTAAABAAACATTAATTTCTAGTATTAACACT 2040
Qy 2041 TTTAACGCTCATCCAGATGTAATTAAGTGAACAATCTGAAACATTTTCTTCTCTG 2100
Db 2041 TTTAACGCTCATCCAGATGTAATTAAGTGAACAATCTGAAACATTTTCTTCTCTG 2100
Qy 2101 AATCTGTTTAAATCTCTCTGCTGCACTTCTGCAAGCATTTGACAAAGCTATACATA 2160
Db 2101 AATCTGTTTAAATCTCTCTGCTGCACTTCTGCAAGCATTTGACAAAGCTATACATA 2160
Qy 2161 TTGAAAGCAAAATTCACACAGAGGATGATGAGGTAAATCCACATCAATCTTTTGT 2220
Db 2161 TTGAAAGCAAAATTCACACAGAGGATGATGAGGTAAATCCACATCAATCTTTTGT 2220
Qy 2221 CTTTGTATTTATGAAAAAACAATATTTATCAGAAAAAAACGTTCTCTCTAGTGTGA 2280
Db 2221 CTTTGTATTTATGAAAAAACAATATTTATCAGAAAAAAACGTTCTCTCTAGTGTGA 2280
Qy 2281 TAAATTAAGATTAATTAACAATTTAATTAATCTAGTAAATGATTAATCTTCAAACTT 2340
Db 2281 TAAATTAAGATTAATTAACAATTTAATTAATCTAGTAAATGATTAATCTTCAAACTT 2340
Qy 2341 ACCATCTTCAACATTAATTAATGATCAATTTTATTTTAACTAATAACTCCACTA 2400
Db 2341 ACCATCTTCAACATTAATTAATGATCAATTTTATTTTAACTAATAACTCCACTA 2400
Qy 2401 AAAAAATGCAAAAGAGAGATATATTTTAAGTCAAGATTAATAAGTGAAGGATGAT 2460
Db 2401 AAAAAATGCAAAAGAGAGATATATTTTAAGTCAAGATTAATAAGTGAAGGATGAT 2460
Qy 2461 TCTTCAACAAAACGGCGCCGTAAGAGTGTCTTATCTTCAATTAACAGCTGGGTGTG 2520
Db 2461 TCTTCAACAAAACGGCGCCGTAAGAGTGTCTTATCTTCAATTAACAGCTGGGTGTG 2520
Qy 2521 ACATCATAGGCGCTTACGATATTTTGAAGCTTTACGTACGTAAGAGCTTTAATCAT 2580
Db 2521 ACATCATAGGCGCTTACGATATTTTGAAGCTTTACGTACGTAAGAGCTTTAATCAT 2580
Qy 2581 TAGTTCATCTGTACAAACAACAATCAATTCGTAACATATATACAAATCTACTA 2640
Db 2581 TAGTTCATCTGTACAAACAACAATCAATTCGTAACATATATACAAATCTACTA 2640
Qy 2641 GTACTAATTAACGCTACGTAATACATGCTTTTTCGAAATTTCTAAATCTATACAA 2700
Db 2641 GTACTAATTAACGCTACGTAATACATGCTTTTTCGAAATTTCTAAATCTATACAA 2700
Qy 2701 CAAACTGAATGTTTGTGTAATTAATGCTTAAACAAGTTTGAATGTGATGGG 2760
Db 2701 CAAACTGAATGTTTGTGTAATTAATGCTTAAACAAGTTTGAATGTGATGGG 2760
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D	b	270	CAAACTTGAATGTTTGTGTTTAATTACTTTAAACCAAGTTTGAATTGTGACTGGG	2760
Q	y	2761	AGCTACACTGTAAGTCCCTTTTTCCTTCAATCGACCGGTAAAGT	2820
D	b	2761	AGCTACACTGTAAGTCCCTTTTTCCTTCAATCGACCGGTAAAGT	2820
Q	y	2821	ATTTAAACCAAAATTTTAATTTGTGCTGGAAGTACAAACGTCAATATATAGA	2880
D	b	2821	ATTTAAACCAAAATTTTAATTTGTGCTGGAAGTACAAACGTCAATATATAGA	2880
Q	y	2881	CAGCATCGTTATACAAATAATGTCGTTATGGAAATCAATATTAATACGAATTA	2940
D	b	2881	CAGCATCGTTATACAAATAATGTCGTTATGGAAATCAATATTAATACGAATTA	2940
Q	y	2941	GCGACTCATCTTGTTTAATAGTTTGGAAAGATTAATAAATAATGAAATTC	3000
D	b	2941	GCGACTCATCTTGTTTAATAGTTTGGAAAGATTAATAAATAATGAAATTC	3000
Q	y	3001	CAGAGCTATATATGTCGGGTCAATTAAGACCGGTGACCAAAAGTTTCGTCTAC	3060
D	b	3001	CAGAGCTATATATGTCGGGTCAATTAAGACCGGTGACCAAAAGTTTCGTCTAC	3060
Q	y	3061	GGTGGGTCAATGAATAATTTTGGACCTTTCTCACCCCTTTATGAACTTCGTATAGTTT	3120
D	b	3061	GGTGGGTCAATGAATAATTTTGGACCTTTCTCACCCCTTTATGAACTTCGTATAGTTT	3120
Q	y	3121	TGTGGATTAATATATTTGTATTCGTATATTTTGTCTAATATGATACGTAAATCA	3180
D	b	3121	TGTGGATTAATATATTTGTATTCGTATATTTTGTCTAATATGATACGTAAATCA	3180
Q	y	3181	CGATTAAGAAAGACTTCTTTTATTTTAAATTTGATTTTAAACCTTTGTTTGGAAATGACT	3240
D	b	3181	CGATTAAGAAAGACTTCTTTTATTTTAAATTTGATTTTAAACCTTTGTTTGGAAATGACT	3240
Q	y	3241	CATACACAAAGTTTAAAGTTGATGATGCCAATTTACAAAAATGTTTCGAGAGCGTCC	3300
D	b	3241	CATACACAAAGTTTAAAGTTGATGATGCCAATTTACAAAAATGTTTCGAGAGCGTCC	3300
Q	y	3301	GAGTGTCTACACACATCGTACCAACTCGTATGGGTTATATATAGTTTCTTCTT	3360
D	b	3301	GAGTGTCTACACACATCGTACCAACTCGTATGGGTTATATATAGTTTCTTCTT	3360
Q	y	3361	TTTCCAAATGCTTTATATATGACCAACTCTAAATTTCTTTTAAATATAGTTAAGAAAT	3420
D	b	3361	TTTCCAAATGCTTTATATATGACCAACTCTAAATTTCTTTTAAATATAGTTAAGAAAT	3420
Q	y	3421	CTTGAATTTTCTGTGATTTTAAACCAAGTTTCAATCTCTTACACAAAAA	3480
D	b	3421	CTTGAATTTTCTGTGATTTTAAACCAAGTTTCAATCTCTTACACAAAAA	3480
Q	y	3481	AAAAGTTTTCAATATTTAAAGATCTAAATTTTGTAGTCAAGATTTATGATAGCT	3540
D	b	3481	AAAAGTTTTCAATATTTAAAGATCTAAATTTTGTAGTCAAGATTTATGATAGCT	3540
Q	y	3541	GAAGAATTATGATGATTTGCAAGTTTGCACAGATGTCATATGATACATACAAAA	3600
D	b	3541	GAAGAATTATGATGATTTGCAAGTTTGCACAGATGTCATATGATACATACAAAA	3600
Q	y	3601	CATGCATCAAAATTAATATTCGTGCTTACGAAAGAAACGATTAATAATCAAAAT	3660
D	b	3601	CATGCATCAAAATTAATATTCGTGCTTACGAAAGAAACGATTAATAATCAAAAT	3660
Q	y	3661	CGTTAACCACTTAAATAATCTTGAAGATATATTTGTAGTATATTTCTGTAGAGAGG	3720
D	b	3661	CGTTAACCACTTAAATAATCTTGAAGATATATTTGTAGTATATTTCTGTAGAGAGG	3720
Q	y	3721	TATCATATCTTACAAAAAATCAATTCAGATTAATAATATGTTGTCCATCGTTACCA	3780
D	b	3721	TATCATATCTTACAAAAAATCAATTCAGATTAATAATATGTTGTCCATCGTTACCA	3780
Q	y	3781	AGTATGTTTTGCTGTCACTAGTGTATGTATCTGCTCTTAGCCATATATGTTCTAAG	3840
D	b	3781	AGTATGTTTTGCTGTCACTAGTGTATGTATCTGCTCTTAGCCATATATGTTCTAAG	3840

Oy	3841	TTTTTAATGTTTCAAGACTTTATACAAAATTAATAATTAATTAAGTGAATTTGTAGCG	3900
Db	3841	TTTTTAATGTTTCAAGACTTTATACAAAATTAATAATTAATTAAGTGAATTTGTAGCG	3900
Oy	3901	CTAAAGACGAAAAATAAATAATTAATAAGTAAAGAAAGCGTCTTCTCAATAAGAACAC	3960
Db	3901	CTAAAGACGAAAAATAAATAATTAATAAGTAAAGAAAGCGTCTTCTCAATAAGAACAC	3960
Oy	3961	AGATCCACGAGATTCAAAACGAAATTTGTGCTTGTCTCTCTTAATTAATATC	4020
Db	3961	AGATCCACGAGATTCAAAACGAAATTTGTGCTTGTCTCTCTTAATTAATATC	4020
Oy	4021	CTCTCAAAAACCCCTCTATATCCCTCTAAAGCCCCCTCTCTGTGTTCTACACGCCAA	4080
Db	4021	CTCTCAAAAACCCCTCTATATCCCTCTAAAGCCCCCTCTCTGTGTTCTACACGCCAA	4080
Oy	4081	CAAGAAAAAACAAGATTGAGAAAATGATGTTGCTGTGTATACCAATGATTTGGGT	4140
Db	4081	CAAGAAAAAACAAGATTGAGAAAATGATGTTGCTGTGTATACCAATGATTTGGGT	4140
Oy	4141	TTTATGCTTACTACTTCGAGAGATTATTAAGAAAGATGAAGATTCATTATTAAGAAAGA	4200
Db	4141	TTTATGCTTACTACTTCGAGAGATTATTAAGAAAGATGAAGATTCATTATTAAGAAAGA	4200
Oy	4201	AGAGAACGACAAACCAAAAAAAGAAACC	4228
Db	4201	AGAGAACGACAAACCAAAAAAAGAAACC	4228
RESULT 3			
ID	AAAS9221	standard; cDNA; 4227 BP.	
XX	AAAS9221;		
AC	07-NOV-2000	(first entry)	
DT			
XX	Promoter sequence of the Arabidopsis aintegumenta (ANT) gene.		
DE			
XX	Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility;		
XX	asexual reproduction; plant; male sterile plant; female sterile plant;		
KW	early flowering; promoter; ss.		
XX			
OS	Arabidopsis sp.		
XX			
PN	WO200040694-A2.		
XX			
PD	13-JUL-2000.		
XX			
PF	07-JAN-2000; 2000WO-US000465.		
XX			
PR	08-JAN-1999; 99US-00227421.		
XX			
RA	(REGC) UNIV CALIFORNIA.		
XX			
PI	Fischer RL, Mizukami Y;		
XX			
DR	WPI; 2000-465969/40.		
PT			
PT	Modulating growth and cell proliferation in a plant used to alter organ		
PT	mass, control fertility and enhance asexual reproduction in plants		
PT	comprises modulating ANT activity and selecting plants with altered cell		
PT	number.		
XX			
PS	Claim 4; Page 41-43; 54pp; English.		
XX			
CC	The present sequence represents a promoter of an aintegumenta (ANT) gene.		
CC	The ANT gene is expressed and functions not only in developing ovules but		
CC	also in various developing organs. Growth and cell proliferation in plant		
CC	can be modulated by modulating ANT activity. Modulation of ANT activity		
CC	is used to alter organ mass, control fertility and enhance asexual		
CC	reproduction in plants. Increased ANT activity can be used to produce		

CC male or female sterile plants. Inhibition of AMT activity can be used to
CC truncate vegetative growth, resulting in early flowering

XX Sequence 4227 BP; 1488 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;

Query Match 97.1%; Score 4107; DB 3; Length 4227;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;
Matches 4227; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GTGACTCTAGGCTCACTGGCTTAATACGACTCACTAATAGGAGCTCGAGATCCTTTA 60
DB 1 GTGACTCTAGGCTCACTGGCTTAATACGACTCACTAATAGGAGCTCGAGATCCTTTA 60
QY 61 GTTAGAAAAAATCTTCTTTGTAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 GTTAGAAAAAATCTTCTTTGTAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ACATGATATCACTAT 180
DB 121 ACATGATATCACTAT 180
QY 181 TAAATATATATACGTGACATTAACCAACCAATGTTCTGCTTTATGATATGTTCTATAT 240
DB 181 TAAATATATATACGTGACATTAACCAACCAATGTTCTGCTTTATGATATGTTCTATAT 240
QY 241 GTTGCACTTAT 300
DB 241 GTTGCACTTAT 300
QY 301 AAAAGTGAACCAAAAGAGATCCATGTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 AAAAGTGAACCAAAAGAGATCCATGTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 ATGATATATGAAAGATTAATCTTACTAATATATATATATATATATATATATATATATAT 420
DB 361 ATGATATATGAAAGATTAATCTTACTAATATATATATATATATATATATATATATATAT 420
QY 421 ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGATATATCTGTTATCTTACTTGA 480
DB 421 ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGATATATCTGTTATCTTACTTGA 480
QY 481 CTGAAGTGTATATACATAAAGCGTGAATTTTAAAGACCGTATCAATCAATATATATATAT 540
DB 481 CTGAAGTGTATATACATAAAGCGTGAATTTTAAAGACCGTATCAATCAATATATATATAT 540
QY 541 CGATCAAAATCAAAATTTAT 600
DB 541 CGATCAAAATCAAAATTTAT 600
QY 601 TACAAGCTAAGATTTTGAACAGAGAGTGAAGATATATATATATATATATATATATATAT 660
DB 601 TACAAGCTAAGATTTTGAACAGAGAGTGAAGATATATATATATATATATATATATATAT 660
QY 661 TATGATTTGATTAAGGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTTT 720
DB 661 TATGATTTGATTAAGGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTTT 720
QY 721 TGTGTTGTTTACCGATTAATATAGAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 721 TGTGTTGTTTACCGATTAATATAGAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY 781 AACTCGTTTATGTTAACTAT 840
DB 781 AACTCGTTTATGTTAACTAT 840
QY 841 TACAATTAATGTTAAAGCAATTTGAAATTAATTAATTAATTAATTAATTAATTAATTTT 900
DB 841 TACAATTAATGTTAAAGCAATTTGAAATTAATTAATTAATTAATTAATTAATTTT 900
QY 901 TATGTTAAGTCTACAAATTTTCTTGTATATATATATATATATATATATATATATATATAT 960
DB 901 TATGTTAAGTCTACAAATTTTCTTGTATATATATATATATATATATATATATATATATAT 960

QY 961 CTTTGAGGGGTATTAAGGTCACTGCACTATGCACTCAGATGAAAGAGTGTGCT 1020
DB 961 CTTTGAGGGGTATTAAGGTCACTGCACTATGCACTCAGATGAAAGAGTGTGCT 1020
QY 1021 TCTGTCTTAAAGATATCTACAGCTGTGCTCGCTGTGATATAGAAAGAAATTTGATATGA 1080
DB 1021 TCTGTCTTAAAGATATCTACAGCTGTGCTCGCTGTGATATAGAAAGAAATTTGATATGA 1080
QY 1081 GAGATCCCATCTAGCGTTTACGTTTGCCTTCCGTGCGAATCTTGCGGTTGTGACT 1140
DB 1081 GAGATCCCATCTAGCGTTTACGTTTGCCTTCCGTGCGAATCTTGCGGTTGTGACT 1140
QY 1141 TTTTCTTATATGCTGTTTGTGCTAATTTTCTCAGATGAGATGATATCAAGAAACT 1200
DB 1141 TTTTCTTATATGCTGTTTGTGCTAATTTTCTCAGATGAGATGATATCAAGAAACT 1200
QY 1201 AATATTCGAAAAGAAAAGAAAAGAAAAGCAAGAAAATCAATTTGCGAAAAGACATTAATGAC 1260
DB 1201 AATATTCGAAAAGAAAAGAAAAGAAAAGCAAGAAAATCAATTTGCGAAAAGACATTAATGAC 1260
QY 1261 ACTTAAATGATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
DB 1261 ACTTAAATGATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
QY 1321 AATCAAGAAAG 1380
DB 1321 AATCAAGAAAG 1380
QY 1381 CCCGATCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440
DB 1381 CCCGATCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440
QY 1441 ACTTCAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
DB 1441 ACTTCAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
QY 1501 TCGATATTTTGTATATCTAT 1560
DB 1501 TCGATATTTTGTATATCTAT 1560
QY 1561 CTCCTTGTCTTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
DB 1561 CTCCTTGTCTTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
QY 1621 CATCTCTTATCAATTTTAT 1680
DB 1621 CATCTCTTATCAATTTTAT 1680
QY 1681 GGTATTAAGGATATATGCTTCTAGTCGAAGAAATTTTGTATATATATATATATATATATAT 1740
DB 1681 GGTATTAAGGATATATGCTTCTAGTCGAAGAAATTTTGTATATATATATATATATATATAT 1740
QY 1741 GGAAGAAAATTCAGCGCTTAT 1800
DB 1741 GGAAGAAAATTCAGCGCTTAT 1800
QY 1801 TTAATAATTAAGGTTTGTCTTTTAAAGTTTAAAGCTTAAATCACTATAGAGAAAT 1860
DB 1801 TTAATAATTAAGGTTTGTCTTTTAAAGTTTAAAGCTTAAATCACTATAGAGAAAT 1860
QY 1861 ATTATCTTATATGAAATTTCCAAATATCTTTTAAACATTAAGAAATTTTGCAGATTT 1920
DB 1861 ATTATCTTATATGAAATTTCCAAATATCTTTTAAACATTAAGAAATTTTGCAGATTT 1920
QY 1921 TTAATAATTAAGGTTTAT 1980
DB 1921 TTAATAATTAAGGTTTAT 1980
QY 1981 TTAACCAATGAATGTTTGTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
DB 1981 TTAACCAATGAATGTTTGTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
QY 2041 TTTAACCGTCAATCAGATTTGAT 2100

D	2041	TTTTACGTCATCCAGATGTAATAGACAAATCGAAAACTTTTTTTCTTG	2100
Q	2101	AATCTGTTAAATTCCTGCTGCATCTACTGAGGCACTTGACCAAGCATATACATA	2160
D	2101	AATCTGTTT-AAATCTCTGCTGCATCTACTGAGGCACTTGACCAAGCATATACATA	2159
Q	2161	TTGAAAGCAAAATNTCCACGAGGATGATAGGTTAGATCCCACTCAATCTTTGT	2220
D	2160	TTGAAAGCAAAATNTCCACGAGGATGATAGGTTAGATCCCACTCAATCTTTGT	2219
Q	2221	CTTTGTTATTTATGAAAACAAAATTTATCAGAAAAAAACGTTCTCTAGTGTA	2280
D	2220	CTTTGTTATTTATGAAAACAAAATTTATCAGAAAAAAACGTTCTCTAGTGTA	2279
Q	2281	TAGTATTAAGTAAATAACAAATTTTATCTTATGTTAATGTAATTTACTATCTCAACT	2340
D	2280	TAGTATTAAGTAAATAACAAATTTTATCTTATGTTAATGTAATTTACTATCTCAACT	2339
Q	2341	ACCATCTTCAACATTATATATGATCAATTTTATTTTTTTACTAACTACTCCACTA	2400
D	2340	ACCATCTTCAACATTATATATGATCAATTTTATTTTTTTTACTAACTACTCCACTA	2399
Q	2401	AAAAATGCAAAAGAGATATATATTTTAAGTCAAAAGTAATTAAAGATGGGTGAT	2460
D	2400	AAAAATGCAAAAGAGATATATATTTTAAGTCAAAAGTAATTAAAGATGGGTGAT	2459
Q	2461	TCTTCAGCAAAAGGGCCGCTAGAGGTCCTTATCCACATTAACAGTGGGTGTGCAG	2520
D	2460	TCTTCAGCAAAAGGGCCGCTAGAGGTCCTTATCCACATTAACAGTGGGTGTGCAG	2519
Q	2521	ACATCATAGGGCTCAGTATATTTAGAGCTTTACTGTACGTAAAGCTTTACATATCTAGT	2580
D	2520	ACATCATAGGGCTCAGTATATTTAGAGCTTTACTGTACGTAAAGCTTTACATATCTAGT	2579
Q	2581	TAGTCTCACTGTACAAACAAACAAATCCAAATTCGTAACTATATATCAATACTACTA	2640
D	2580	TAGTCTCACTGTACAAACAAACAAATCCAAATTCGTAACTATATATCAATACTACTA	2639
Q	2641	GTATCGATTTAGGCTACGTATACATGCTTTTCGCAAAATTTCTAACTATATACAA	2700
D	2640	GTATCGATTTAGGCTACGTATACATGCTTTTCGCAAAATTTCTAACTATATACAA	2699
Q	2701	CAAACTGTAATGTTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTTGG	2760
D	2700	CAAACTGTAATGTTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTTGG	2759
Q	2761	AGCTACACTCTAGTCCCTTTTCCCAAAATATATCTCTTAACATGCACCGGTTAAAGT	2820
D	2760	AGCTACACTCTAGTCCCTTTTCCCAAAATATATCTCTTAACATGCACCGGTTAAAGT	2819
Q	2821	ATTTAAACCAACAAATTTTAAATTTGTTGTCGAAGGTCACAACTATATATAGAGA	2880
D	2820	ATTTAAACCAACAAATTTTAAATTTGTTGTCGAAGGTCACAACTATATATAGAGA	2879
Q	2881	CAGCATCGTTTATACAAATATGTTGATGTATTTGGAATCAAAATTAATAATCGAATTA	2940
D	2880	CAGCATCGTTTATACAAATATGTTGATGTATTTGGAATCAAAATTAATAATCGAATTA	2939
Q	2941	GGCAGTCACTGGTTTATATGTTTGAAGATTAAGAAATTAATAATCAAAAGATA	3000
D	2940	GGCAGTCACTGGTTTATATGTTTGAAGATTAAGAAATTAATAATCAAAAGATA	2999
Q	3001	CAGAGCTATATATAGTGGGCTCATTTAGAGCCGTGACCAAAAGTTTGTGTATATTTCTAC	3060
D	3000	CAGAGCTATATATAGTGGGCTCATTTAGAGCCGTGACCAAAAGTTTGTGTATATTTCTAC	3059
Q	3061	GGTGGCTCATTAAGAAATTTTGAATTTTCTTCACTCCCTTTATGAACCTTCTGTATAGTTT	3120
D	3060	GGTGGCTCATTAAGAAATTTTGAATTTTCTTCACTCCCTTTATGAACCTTCTGTATAGTTT	3119
Q	3121	TGTGGATTAATATATTTGTATTTGTTATTTTGTCTTAATATGATACGTAAATTC	3180
D	3120	TGTGGATTAATATATTTGTATTTTGTCTTAATATTTTGTCTTAATATGATACGTAAATTC	3179
Q	3181	CGATTAAGAAAGACTCTCTTTTATTTATTTGATTTATTAACCTTTGTTTGGAAATGACT	3240
D	3180	CGATTAAGAAAGACTCTCTTTTATTTATTTGATTTTATTAACCTTTGTTTGGAAATGACT	3239
Q	3241	CATACACAAGGTTAAAGTTGATGTATCCAAATTTTCAAAAATGTTTGCAGAGTGCCTTC	3300
D	3240	CATACACAAGGTTAAAGTTGATGTATCCAAATTTTCAAAAATGTTTGCAGAGTGCCTTC	3299
Q	3301	GAGTGTCTTACCACTCGTACCACTCGTATGGGTTTATTTATTTAGTTTCTTCTT	3360
D	3300	GAGTGTCTTACCACTCGTACCACTCGTATGGGTTTATTTATTTAGTTTCTTCTT	3359
Q	3361	TTTCCAAATGCTTTATATATTTGAACCACTGAAATTTCTTTTAAATTAAGTTAAGAT	3420
D	3360	TTTCCAAATGCTTTATATATTTGAACCACTGAAATTTCTTTTAAATTAAGTTAAGAT	3419
Q	3421	CTTGAATTTTCTGTGATTTTAAACCAAGTTTTCATTTCTTTAGCACAABAAAAA	3479
D	3420	CTTGAATTTTCTGTGATTTTAAACCAAGTTTTCATTTCTTTAGCACAABAAAAA	3479
Q	3481	AAAAGTTTCAATTTATTAAGATCTAAATTTTGTAGTTCAAGATTATATGATGCT	3540
D	3480	AAAAGTTTCAATTTATTAAGATCTAAATTTTGTAGTTCAAGATTATATGATGCT	3539
Q	3541	GAAAGTTTATGAATGATGCAAGTTTGCAACAGATGTCGATGATACATATCAAAA	3600
D	3540	GAAAGTTTATGAATGATGCAAGTTTGCAACAGATGTCGATGATACATATCAAAA	3599
Q	3601	CATGCATCAAAATTAATATTCGCTTAGCAGAGAAACGATTTGAATTAACAGAACAT	3660
D	3600	CATGCATCAAAATTAATATTCGCTTAGCAGAGAAACGATTTGAATTAACAGAACAT	3659
Q	3661	CGTTAACCACTTAAATCTTGAATATTTTGTAGTATATTTTCTGTAAAGAGAGG	3720
D	3660	CGTTAACCACTTAAATCTTGAATATTTTGTAGTATATTTTCTGTAAAGAGAGG	3719
Q	3721	TATCATATCTTACAAAAAAACCTCATTTCAGATTAATAATGTGTCCAAATGTTACCA	3780
D	3720	TATCATATCTTACAAAAAAACCTCATTTCAGATTAATAATGTGTCCAAATGTTACCA	3779
Q	3781	AGTATGTTTTTGTGTCATCAGTTGATTTGTAATCGTCTCTTAAGCATATAGTTCTTAAG	3840
D	3780	AGTATGTTTTTGTGTCATCAGTTGATTTGTAATCGTCTCTTAAGCATATAGTTCTTAAG	3839
Q	3841	TTTTAAATGTTTCAAAAGCTTTACAAAATTAATAATTAATATAGTGCATTTGTAGGG	3900
D	3840	TTTTAAATGTTTCAAAAGCTTTACAAAATTAATAATTAATATAGTGCATTTGTAGGG	3899
Q	3901	CTTAAAGCGAAAAATTAATAATTAATAAGTAAAGAAACGCTTCTCAATTAAGAAC	3960
D	3900	CTTAAAGCGAAAAATTAATAATTAATAAGTAAAGAAACGCTTCTCAATTAAGAAC	3959
Q	3961	AGATCCCAACGATTTCAAAACAGCAATTTGTGCTTGTCTTCTCTTATTAATATC	4020
D	3960	AGATCCCAACGATTTCAAAACAGCAATTTGTGCTTGTCTTCTCTTATTAATATC	4019
Q	4021	CTTCAAAAAACCTCTCTATATCTCTCTTAAGCCCCCTTCTTGTCTTCTACCGCAA	4080
D	4020	CTTCAAAAAACCTCTCTATATCTCTCTTAAGCCCCCTTCTTGTCTTCTACCGCAA	4079
Q	4081	CAAAAGAAAAACAAAGTTTGAAGAAATGAGTGTCTGTTGTGTAAACCAATATGGGCT	4140
D	4080	CAAAAGAAAAACAAAGTTTGAAGAAATGAGTGTGTCTGTTGTGTAAACCAATATGGGCT	4139
Q	4141	TTTACCTTACTACTTTCGAGAGATTTATTAAGAAAGAAAGATGAATATTAAGAAAGA	4200
D	4140	TTTACCTTACTACTTTCGAGAGATTTATTAAGAAAGAAAGATGAATATTAAGAAAGA	4199
Q	4201	AGAGAAACAGAAACCAAAAAAGAAAC	4228
D	4200	AGAGAAACAGAAACCAAAAAAGAAAC	4227

RESULT 4
ADG88432
ID ADG88432 standard; DNA; 4228 BP.
XX
AC ADG88432;
XX
DT 11-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana aintegumenta (ANT) promoter DNA.
XX
KW plant; genetic engineering; cell proliferation; aintegumenta; ANT;
KW transgenic; transgenic plant; organ mass alteration; fertility;
KW asexual reproduction; de.
XX
OS Arabidopsis thaliana.
XX
PN US2003159180-A1.
XX
PD 21-AUG-2003.
XX
PF 28-JAN-2002; 2002US-00059911.
XX
PR 28-JAN-2002; 2002US-00059911.
XX
PA (REGC) UNIV CALIFORNIA OFFICE TECHNOLOGY.
XX
PI Flecher RL, Mizukami Y,
XX
DR WPI; 2003-787370/74.
XX
PT Increasing cell proliferation in a plant by introducing into the plant an
PT expression cassette containing a plant promoter operably linked to a
PT nucleic acid encoding a modified ANT polypeptide and selecting plants
PT with increased mass.
XX
PS Disclosure, SEQ ID NO 3; 51pp; English.
XX
CC The present invention relates to plant genetic engineering. The invention
CC particularly relates to a method of increasing cell proliferation in a
CC plant. The method involves introducing into the plant an expression
CC cassette containing a plant promoter operably linked to a nucleic acid
CC encoding a modified aintegumenta (ANT) polypeptide comprising an ANT AP2
CC domain and selecting plants the with increased size or mass. The
CC invention is useful to generate transgenic plants. The method is useful
CC for increasing cell proliferation in a plant for altering organ mass,
CC controlling fertility or enhancing asexual reproduction. The present
CC sequence is Arabidopsis thaliana ANT promoter DNA.
XX
SQ Sequence 4228 BP; 1488 A; 651 C; 643 G; 1446 T; 0 U; 0 Other;
Query Match 93.1%; Score 3936; DB 10; Length 4228;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 1 GTGACCTCTAGGCTCACTGGCTTAATGACACTACTATAGGAGCTCGAGATCTTTA 60
DB 1 GTGACCTCTAGGCTCACTGGCTTAATGACACTACTATAGGAGCTCGAGATCTTTA 60
QY 61 GTTAGAAAAAATTCTTTGAGCTGTGTGTGTGTTTAAGTTCAATTAACTAGTC 120
DB 61 GTTAGAAAAAATTCTTTGAGCTGTGTGTGTGTTTAAGTTCAATTAACTAGTC 120
QY 121 ACATGATATATCAATATATATATGAAATTGAAATTATCATTTAATAGTTAGAT 180
DB 121 ACATGATATATCAATATATATATGAAATTGAAATTATCATTTAATAGTTAGAT 180
QY 181 TAATATATATACGCTGACATTAACCAACCAATGTTTCTGCTTTATGATAGTTCTATAT 240
DB 181 TAATATATATACGCTGACATTAACCAACCAATGTTTCTGCTTTATGATAGTTCTATAT 240
QY 241 GTTGCACTGATTTATAGTACTATATATAAACTGGGTTTATTTAAATCCGATAC 300

DB 241 GTTGCACTGATTTATAGTACTATATATAAACTGGGTTTATTTAAATCCGATAC 300
QY 301 AAAAGTGACCAAAACGAGATCCATGGTTTGTGTTTACTTTGTTGTTAAACGATATAT 360
DB 301 AAAAGTGACCAAAACGAGATCCATGGTTTGTGTTTACTTTGTTGTTAAACGATATAT 360
QY 361 ATGATTTATGAAAGTTAAATCTTTTACTTAATTTAATAATTTGAAAAACAACCTTAA 420
DB 361 ATGATTTATGAAAGTTAAATCTTTTACTTAATTTAATAATTTGAAAAACAACCTTAA 420
QY 421 ATATGTTAGAGTGTCTTCACTGCTCACTGTTCAAGATATATCTCGTTATATCTTGA 480
DB 421 ATATGTTAGAGTGTCTTCACTGCTCACTGTTCAAGATATATCTCGTTATATCTTGA 480
QY 481 CTAGAAAGTTATATATCAATTAACAGTGAATATTTTAAAGACCGTATCAATCAATGAT 540
DB 481 CTAGAAAGTTATATATCAATTAACAGTGAATATTTTAAAGACCGTATCAATCAATGAT 540
QY 541 CGATCAAAATACAAATTTATATGAGCTAGAAATCCAGATGAGATGACTCTAGCAAGATA 600
DB 541 CGATCAAAATACAAATTTATATGAGCTAGAAATCCAGATGAGATGACTCTAGCAAGATA 600
QY 601 TACACAGCTAAGAAATTTGTCAAGAGAGTGAAGAAATATGATTTCAATCATTTAAAGAA 660
DB 601 TACACAGCTAAGAAATTTGTCAAGAGAGTGAAGAAATATGATTTCAATCATTTAAAGAA 660
QY 661 TATGATTTTCACTAGCTAGATTTGATATTTACATTAACGATATGATATATATTTT 720
DB 661 TATGATTTTCACTAGCTAGATTTGATATTTACATTAACGATATGATATATATTTT 720
QY 721 TGTGTTTGTGTTTACCGATATATAGAAATGTTGTGTTTAAATATGTTGTTTACTTA 780
DB 721 TGTGTTTGTGTTTACCGATATATAGAAATGTTGTGTTTAAATATGTTGTTTACTTA 780
QY 781 AACTCGTTTATGTTAATCTATATATATGTTTCCGATGTTAAATGTTAACTGTTAA 840
DB 781 AACTCGTTTATGTTAATCTATATATGTTTCCGATGTTAAATGTTAACTGTTAA 840
QY 841 TACAAATTAATGTTAAGCTATGCAATTTAAATAATCAACGGGTATGTAATCTCGAAGAT 900
DB 841 TACAAATTAATGTTAAGCTATGCAATTTAAATAATCAACGGGTATGTAATCTCGAAGAT 900
QY 901 TATGTTAAGCTTACAAATTTTCTTTTATGATTAAGTTGAGTGAACAAATTTATGTTA 960
DB 901 TATGTTAAGCTTACAAATTTTCTTTTATGATTAAGTTGAGTGAACAAATTTATGTTA 960
QY 961 CTTGCAAGGGGTATTAAGGTCACTGATGATGAGATCAGCATGATGACCAAGAGTGTGTC 1020
DB 961 CTTGCAAGGGGTATTAAGGTCACTGATGATGAGATCAGCATGATGACCAAGAGTGTGTC 1020
QY 1021 TCTGTCTTAAAGATATCTTACAGCTGTCTTCCCTGTGATGATGAGAAATTTGAATGATGA 1080
DB 1021 TCTGTCTTAAAGATATCTTACAGCTGTCTTCCCTGTGATGATGAGAAATTTGAATGATGA 1080
QY 1081 GAGATCCCATCTACCGTTTACCGTTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTT 1140
DB 1081 GAGATCCCATCTACCGTTTACCGTTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTT 1140
QY 1141 TTTTCTTATATGTTGTTTGAATATTTTCTTCAAGTGAAGATGTTAATCAAAAACT 1200
DB 1141 TTTTCTTATATGTTGTTTGAATATTTTCTTCAAGTGAAGATGTTAATCAAAAACT 1200
QY 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATCTATTGTCGAAAGACATTAATGAC 1260
DB 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATCTATTGTCGAAAGACATTAATGAC 1260
QY 1261 ACTAAATTTGGAATATTTAAATATGTTATATATGTTGTTGGAATTTTAAATCAATACCAA 1320
DB 1261 ACTAAATTTGGAATATTTAAATATGTTATATATGTTGTTGGAATTTTAAATCAATACCAA 1320
QY 1321 AATCAAGAAAGAGAGAGGACCTCTCGGCTTAAATTTCCCTCTAAAGAACTGCT 1380

D	b	1321	AATCAAGGAAGAGAGAGGGAAGCTCTTCGTCCTTAATGATTTCCCTCTTAACAACCTGCT	1380
Q	y	1381	CCCACTACCTTTTCTTCTTCCAACAAAATCATTCAACGAGAAATCTGTCGTATC	1440
D	b	1381	CCCACTACCTTTTCTTCTTCCAACAAAATCATTCAACGAGAAATCTGTCGTATC	1440
Q	y	1441	ACTTCATGCAAAATTAAACTBAATTTTGGTAATTTTGTCAAGTCTTGCTGTTTAAG	1500
D	b	1441	ACTTCATGCAAAATTAAACTBAATTTTGGTAATTTTGTCAAGTCTTGCTGTTTAAG	1500
Q	y	1501	TGCAATTATGSGTATACCTATATGAGGATATACATCCAGCTAATCAATTAATGAT	1560
D	b	1501	TGCAATTATGSGTATACCTATATGAGGATATACATCCAGCTAATCAATTAATGAT	1560
Q	y	1561	CTCCTCTGCTTATCAATAAATTAACAACAATTAGCTAATCAAGCTAATAATTAACA	1620
D	b	1561	CTCCTCTGCTTATCAATAAATTAACAACAATTAGCTAATCAAGCTAATAATTAACA	1620
Q	y	1621	CATTCTCTTATCAATTTTATATGATTAATAAACAACGACTATAGCTACAGATT	1680
D	b	1621	CATTCTCTTATCAATTTTATATGATTAATAAACAACGACTATAGCTACAGATT	1680
Q	y	1681	GGATTTAAGGATATATGCGCTTCAAGTGAAGAAATTTTGTATGATTAACCTGCTG	1740
D	b	1681	GGATTTAAGGATATATGCGCTTCAAGTGAAGAAATTTTGTATGATTAACCTGCTG	1740
Q	y	1741	GGAATAAAATCAGACCTAATATGCTCATTTAAGAGATTAATGAATTTAAATGCTTTAATCA	1800
D	b	1741	GGAATAAAATCAGACCTAATATGCTCATTTAAGAGATTAATGAATTTAAATGCTTTAATCA	1800
Q	y	1801	TTAAATTAAGTTTTGCTTTTAAGGTTACACCGCTTAATTCATCATTAAGAGAAAT	1860
D	b	1801	TTAAATTAAGTTTTGCTTTTAAGGTTACACCGCTTAATTCATCATTAAGAGAAAT	1860
Q	y	1861	ATTACCTTGAATCCAAAATTCCTTTTAAACAATAGAATAATTTTCAGCATTT	1920
D	b	1861	ATTACCTTGAATCCAAAATTCCTTTTAAACAATAGAATAATTTTCAGCATTT	1920
Q	y	1921	TTAATAAAGGGTACATTTATTTGGGTCAATAAATATGTTCCAGCTAAGTTGGAGGT	1980
D	b	1921	TTAATAAAGGGTACATTTATTTGGGTCAATAAATATGTTCCAGCTAAGTTGGAGGT	1980
Q	y	1981	TTAAACAATGATTTTTTGTGATTTAAAAACAATAAATTTTCTAGTAATTAACAATT	2040
D	b	1981	TTAAACAATGATTTTTTGTGATTTAAAAACAATAAATTTTCTAGTAATTAACAATT	2040
Q	y	2041	TTTAAACGTCATCCAGATTGTAATTAAGTGAACAATCTGAAAAAATTTTTTTTCTTG	2100
D	b	2041	TTTAAACGTCATCCAGATTGTAATTAAGTGAACAATCTGAAAAAATTTTTTTTCTTG	2100
Q	y	2101	AATCTGTGTTAAATTCCTCTGCTGCGCATATCTGAGGCAATTTGACCAACGATACATA	2160
D	b	2101	AATCTGTGTTAAATTCCTCTGCTGCGCATATCTGAGGCAATTTGACCAACGATACATA	2160
Q	y	2161	TTGAAGCAAAATATCCACAGAGATGATAGGTTAGATCCACATTCATCATCTTTTGT	2220
D	b	2161	TTGAAGCAAAATATCCACAGAGATGATAGGTTAGATCCACATTCATCATCTTTTGT	2220
Q	y	2221	CTTTGTTATTTATGAAAAAACAATATTTATCAGAAAAAAAGCTTTCTCTCTAGTGTA	2280
D	b	2221	CTTTGTTATTTATGAAAAAACAATATTTATCAGAAAAAAAGCTTTCTCTCTAGTGTA	2280
Q	y	2281	TAAAGTATAGTAAATTAACAAATTTAATCTAGTATGATTAATTAATTAATTAATTAAT	2340
D	b	2281	TAAAGTATAGTAAATTAACAAATTTAATCTAGTATGATTAATTAATTAATTAATTAAT	2340
Q	y	2341	ACCATCTTCAACATTAATATGATTCATTTTTTTTTTAACTAACTCACTCACTA	2400
D	b	2341	ACCATCTTCAACATTAATATGATTCATTTTTTTTTTAACTAACTCACTCACTA	2400
Q	y	2401	AAAAATGCAAAAGAGATATATTAATTAAGTCAAAAGTAAATTAAGATGATGGTGAT	2460
D	b	2401	AAAAATGCAAAAGAGATATATTAATTAAGTCAAAAGTAAATTAAGATGATGGTGAT	2460

QY	2461	TCCTCAGCAAAA	CGGCGCCGCGTAGAGGAGTGTCTTAATCTCACTTACAGCTGGGTGGCGAG	2522
Db	2461	TCCTCAGCAAAA	CGGCGCCGCGTAGAGGAGTGTCTTAATCTCACTTACAGCTGGGTGGCGAG	2522
QY	2521	ACATCATATGGGACC	TACGTAATATTTGAGCTTACTGTACGTAAAGCTTAAACATATCTAGT	2580
Db	2521	ACATCATATGGGACC	TACGTAATATTTGAGCTTACTGTACGTAAAGCTTAAACATATCTAGT	2580
QY	2581	TAGTTCCTCACTGTACAAACAAACAAATCCAAATTCGTATACATATATACAAATCTACTA	2640	
Db	2581	TAGTTCCTCACTGTACAAACAAACAAATTCAAATTCGTATATATACAAATACTACTA	2640	
QY	2641	GTACTAGATTACGCTACGTATACATCGCTTTTTCGCAAAATTTCTAAATCTATACAA	2700	
Db	2641	GTACTAGATTACGCTACGTATACATCGCTTTTTCGCAAAATTTCTAAATCTATACAA	2700	
QY	2701	CAAACTGGAATGTTGGTTTGTATTTATCTTAAACCAAGTTTGAATTCGCAATTCGG	2766	
Db	2701	CAAACTGGAATGTTGGTTTGTATTTATCTTAAACCAAGTTTGAATTCGCAATTCGG	2766	
QY	2761	AGTACACACTAGTCCCTTTTTCGCCCAAAATATCTCCTTACATCGACCGGTAAAGT	2822	
Db	2761	AGTACACACTAGTCCCTTTTTCGCCCAAAATATCTCCTTACATCGACCGGTAAAGT	2822	
QY	2821	ATTTTAAACCAAAATTTTAAATTTGGTTCGTAAGGTACAAACATGTCCATATATAGAGA	2880	
Db	2821	ATTTTAAACCAAAATTTTAAATTTGGTTCGTAAGGTACAAACATGTCCATATATAGAGA	2880	
QY	2881	CAGCATGTTTATTCAAATTAATGTTGCATGTATTTGGAAATCAAAATTAATTAAGAAATTA	2946	
Db	2881	CAGCATGTTTATTCAAATTAATGTTGCATGTATTTGGAAATCAAAATTAATTAAGAAATTA	2946	
QY	2941	GCGACTCACTGGTTTAAATAGTTTGGAAAGATTAATGAATTAATAA - ATGAATTCAAAGAT	2999	
Db	2940	GCGACTCACTGGTTTAAATAGTTTGGAAAGATTAATGAATTAATAAAGATCAATTCAAAGAT	2999	
QY	3000	ACAGAGCTATATATATGTCGGGTGATTTAGAGCCGTACCAAAAGTTTCGTCTAAATTTCTA	3055	
Db	3000	ACAGAGCTATATATATGTCGGGTGATTTAGAGCCGTACCAAAAGTTTCGTCTAAATTTCTA	3055	
QY	3060	CGGTCCGTATATAGAAATTTTGGACTTTTCTTCACCCCTTTATGAACTTCTGTATAGTT	3119	
Db	3060	CGGTCCGTATATAGAAATTTTGGACTTTTCTTCACCCCTTTATGAACTTCTGTATAGTT	3119	
QY	3120	TTTGGGATTAATATTTTGAATTCGTATATGTTTCTTAATATATATATGATACGTAATTC	3179	
Db	3120	TTTGGGATTAATATATTTGATTCGTATATATTTTGTCTTAAATATATATATGATACGTAATTC	3179	
QY	3180	ACGATTAAGAAAGACTTCCTTTTATTTATTTGATTTAAACTTTTGTTTGGAAATGAC	3239	
Db	3180	ACGATTAAGAAAGACTTCCTTTTATTTATTTGATTTAAACTTTTGTTTGGAAATGAC	3239	
QY	3240	TCATATACAAAGTTAAAGTTTGAATGTATCCAAATTTCAAAAAAGTTTCGAGAGTGCCT	3299	
Db	3240	TCATATACAAAGTTAAAGTTTGAATGTATCCAAATTTCAAAAAAGTTTCGAGAGTGCCT	3299	
QY	3300	CGAGTGTCTTACCAACCAATCGTACCAACTCGATGGGTTTATATATAGGTTTTTTCTTCT	3355	
Db	3300	CGAGTGTCTTACCAACCAATCGTACCAACTCGATGGGTTTATATATAGGTTTTTTCTTCT	3355	
QY	3360	TTTTCCATATCTTTATATATTTGAACCACTCTAAATTTCTTTTAAATATAGTTAAGAA	3419	
Db	3360	TTTTCCATATCTTTATATATTTGAACCACTCTAAATTTCTTTTAAATATAGTTAAGAA	3419	
QY	3420	TCCTTGAATTTCTGTGATTTTAAACCAAGTTTTCATTTCTTGTAGCACAAAAAAAA	3479	
Db	3420	TCCTTGAATTTCTGTGATTTTAAACCAAGTTTTCATTTCTTGTAGCACAAAAAAAA	3479	
QY	3480	AAAAAGTTTTCATTTTAAAGATCTAAATTTTGTGAGTTCAAGGTTTAATATATATGATGC	3539	
Db	3480	AAAAAGTTTTCATTTTAAAGATCTAAATTTTGTGAGTTCAAGGTTTAATATATGATGC	3539	

QY	3540	GGAAAGTTAAGTAAGATTGCAAGTTTGCA	CAGAAAGTGCGATGATACATTACAA	3539
Db	3540	TGAAAGTTAAGTAAGATTGCAAGTTTGCA	CAGAAAGTGCGATGATACATTACAA	3539
QY	3600	ACATGCATCAAAATTAATATTCGTGCTT	AGCAAGAAACGATTAATTAACAGAACAA	3659
Db	3600	ACATGCATCAAAATTAATATTCGTGCTT	AGCAAGAAACGATTAATTAACAGAACAA	3659
QY	3660	TCGTTAACCACTTAAAAATCTTAGAATA	TTTGTGATTAATTTCTGTAAAGAGAG	3719
Db	3660	TCGTTAACCACTTAAAAATCTTAGAATA	TTTGTGATTAATTTCTGTAAAGAGAG	3719
QY	3720	GTAATCATATCTTACAAAATAAACTCAT	TTCAGATAAATAATGTGTGCCAATCGT	3779
Db	3720	GTAATCATATCTTACAAAATAAACTCAT	TTCAGATAAATAATGTGTGCCAATCGT	3779
QY	3780	AAGATGTTTTTGGCTGATCAGTTGTAAT	TGTAACGCTCTCTTAGACATTAATGTTCT	3839
Db	3780	AAGATGTTTTTGGCTGATCAGTTGTAAT	TGTAACGCTCTCTCTTAGACATTAATGTTCT	3839
QY	3840	GTTTTTAAATGTTTTCAAGACTTTACAA	AAAAATAAATAATAGTGAATTTGTAGG	3899
Db	3840	GTTTTTAAATGTTTTCAAGACTTTACAA	AAAAATAAATAATAGTGAATTTGTAGG	3899
QY	3900	GCTAAAGCGAAAAATAAATAATTAATA	ATTAAGTAAGAAAGCTCTTTCTCATTA	3959
Db	3900	GCTAAAGCGAAAAATAAATAATTAATA	ATTAAGTAAGAAAGCTCTTTCTCATTA	3959
QY	3960	CAGATCCCAAGGATTCAAACAGCAAAT	TTTGCTTGCTCTCTCTCTTAATTAATAT	4019
Db	3960	CAGATCCCAAGGATTCAAACAGCAAAT	TTTGCTTGCTCTCTCTCTCTTAATTAATAT	4019
QY	4020	CCTCTCAAAAAACCCCTCTCTAATTCCT	CTTAAGCCCCCTCTCTGTTTCTCTAC	4079
Db	4020	CCTCTCAAAAAACCCCTCTCTAATTCCT	CTTAAGCCCCCTCTCTGTTTCTCTAC	4079
QY	4080	ACAAAGAAAAACAAAGTTTGAGAAAAAT	GTGTGTTCGTTGTGTGAACAATGTTGGG	4139
Db	4080	ACAAAGAAAAACAAAGTTTGAGAAAAAT	GTGTGTTCGTTGTGTGAACAATGTTGGG	4139
QY	4140	TTTTAGCTTACTACTTCGAGAGATTATTA	AGAAAGAAAGTGAAGATACATTATGAAAG	4199
Db	4140	TTTTAGCTTACTACTTCGAGAGATTATTA	AGAAAGAAAGTGAAGATACATTATGAAAG	4199
QY	4200	AAGAGAGCAAAACCAAAAAAGAAAC	4228	
Db	4200	AAGAGAGCAAAACCAAAAAAGAAAC	4228	

XX	RESULT 5
XX	AAA59220
ID	AAA59220 standard; cDNA; 2148 BP.
XX	
AC	AAA59220;
XX	
DT	07-NOV-2000 (first entry)
XX	
DE	cDNA encoding an Arabidopsis aintegumenta (ANT) polypeptide.
XX	
KW	Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility;
KW	asexual reproduction; plant; male sterile plant; female sterile plant;
KW	early flowering; ss.
XX	
OS	Arabidopsis sp.
XX	
FH	Key
FT	Location/Qualifiers
CDS	269..1936
FT	/*tag= a
FT	/product= "aintegumenta polypeptide"
XX	
FN	W0200040694-A2.
XX	
PD	13-JUL-2000.

XX 07-JAN-2000; 2000WO-US000465.
 XX
 XX
 PR 08-JAN-1999; 99US-00227421.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Fischer RL, Mizukami Y;
 XX WPI: 2000-465969/40.
 DR P-PSDB; AAB07724.
 XX
 PT Modulating growth and cell proliferation in a plant used to alter organ
 PT mass, control fertility and enhance asexual reproduction in plants
 PT comprises modulating ANT activity and selecting plants with altered cell
 PT number.
 XX
 XX
 PS Claim 9; Page 40-41; 54pp; English.
 XX
 XX
 CC The present sequence encodes an ainegumenta (ANT) polypeptide. The ANT
 CC gene is expressed and functions not only in developing ovules but also in
 CC various developing organs. Growth and cell proliferation in plant can be
 CC modulated by modulating ANT activity. Modulation of ANT activity is used
 CC to alter organ mass, control fertility and enhance asexual reproduction
 CC in plants. Increased ANT activity can be used to produce male or female
 CC sterile plants. Inhibition of ANT activity can be used to truncate
 CC vegetative growth, resulting in early flowering
 XX
 XX Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;

	Query Match	Best Local Similarity	6.3%: Score 268; DB 3; Length 2148;	100.0%: Pred. No. 1, 1e-97;	Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3961 AGATCCCAACGGATTCAACACGCAAAATTGTGCTTTGCTCTCTCTCTTATTAATATATC				
Db	1 AGATCCCAACGGATTCAACACGCAAAATTGTGCTTTGCTCTCTCTTATTAATATATC				
Qy	4021 CTCTCAAAAACCCCTCTGCTCTATATCTCTCTTAAAGCCCCCTTCCTTGTTCTCTACCGCAA				
Db	61 CTCTCAAAAACCCCTCTGCTCTATATCTCTTAAAGCCCCCTTCCTTGTTCTCTACCGCAA				
Qy	4081 CAAAGAAAAAACAATAATTGAGAAAAATGGTGTGTTGCTGTGTAACAATGATTGGGT				
Db	121 CAAAGAAAAAACAATAATTGAGAAAAATGGTGTGTTGCTGTGTAACAATGATTGGGT				
Qy	4141 TTTAGCTTACTACTCTTGAGAGATTATTAAGAAAGATGAGATACATTATTAAGAGA				
Db	181 TTTAGCTTACTACTCTTGAGAGATTATTAAGAAAGATGAGATACATTATTAAGAGA				
Qy	4201 AGAGAACGAAACCAAAAAAAGAAACC 4228				
Db	241 AGAGAACGAAACCAAAAAAAGAAACC 268				
RESULT 6					
ABX13437					
ID	ABX13437	standard; DNA; 2148 BP.			
XX					
AC	ABX13437;				
XX					
DT	04-JUN-2003	(first entry)			
XX					
DE	A. thaliana AINREBUMENTA DNA corresponding to Genbank U40256.				
XX					
KW	Expression cassette; transgenic; promoter; LOX5; plant; food production;				
KW	animal feed; seed; stress resistance; disease resistance; starch content;				
KW	lipid content; dormancy; fibre content; pharmaceutical production;				
KW	fine chemical production; sterile plant; vitamin; flavouring; perfume;				
KW	dye; cotyledon; embryonic tissue; stress factor; LOX; ds.				
XX					
OS	Arabidopsis thaliana.				
XX					

Db 241 AGAAGCAGAAACCAAAAAAGAAACC 268

RESULT 8
ADG88430
ID ADG88430 standard; cDNA; 2148 BP.
XX
XX ADG88430;
XX
XX 11-MAR-2004 (first entry)
XX
XX Arabidopsis thaliana aintegumenta (ANT) cDNA.
DE
XX plant; genetic engineering; cell proliferation; aintegumenta; ANT;
XX transgenic; transgenic plant; organ mass alteration; fertility;
XX asexual reproduction; gene; ss.
XX
XX Arabidopsis thaliana.
XX
XX
XX Key Location/Qualifiers
XX CDS 269..1936
XX FT /*tag= a
XX FT /product= "Arabidopsis thaliana ANT protein"
XX
XX US2003159180-A1.
XX
XX 21-AUG-2003.
XX
XX 28-JAN-2002; 2002US-00059911.
XX
XX 28-JAN-2002; 2002US-00059911.
XX
XX (REGC) UNIV CALIFORNIA OFFICE TECHNOLOGY.
XX
XX Fischer RL, Mizukami Y;
XX
XX WPI; 2003-787370/74.
XX
XX P-PSDB; ADG88431.
XX
XX Increasing cell proliferation in a plant by introducing into the plant an
XX expression cassette containing a plant promoter operably linked to a
XX nucleic acid encoding a modified ANT polypeptide and selecting plants
XX with increased mass.
XX
XX Example 1; SEQ ID NO 1; s1pp; English.
XX
XX The present invention relates to plant genetic engineering. The invention
XX particularly relates to a method of increasing cell proliferation in a
XX plant. The method involves introducing into the plant an expression
XX cassette containing a plant promoter operably linked to a nucleic acid
XX encoding a modified aintegumenta (ANT) polypeptide comprising an ANT AP2
XX domain and selecting plants the with increased size or mass. The
XX invention is useful to generate transgenic plants. The method is useful
XX for increasing cell proliferation in a plant for altering organ mass,
XX controlling fertility or enhancing asexual reproduction. The present
XX sequence is Arabidopsis thaliana ANT cDNA.
XX
XX Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
SQ

Query Match 6.3%; Score 268; DB 10; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3961 AGATCCCAAGGATTCAAAGCAAAATTTGCTTGTCTCTCTATTATATATATC 4020
Db 1 AGATCCCAAGGATTCAAAGCAAAATTTGCTTGTCTCTCTATTATATATATC 60

Qy 4021 CTCGCAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTTCTTACCGCA 4080
Db 61 CTCGCAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTTCTTACCGCA 120

Qy 4081 CAAAGAAAAAACAATTTGAGAAAAATGATGTTCTGTGTATACATATATGGGT 4140

Db 121 CAAAGAAAAAACAAGTTTGAGAAAAATGATGTTCTGTGTATACATATATGGGT 180

Qy 4141 TTTTGCTTACTTCTGAGAGATTTATAGAAAGAGTGAAATCATTTATAGAA 4200
Db 181 TTTTGCTTACTTCTGAGAGATTTATAGAAAGAGTGAAATCATTTATAGAA 240

Qy 4201 AGAAGCAGAAACCAAAAAAGAAACC 4228
Db 241 AGAAGCAGAAACCAAAAAAGAAACC 268

RESULT 9
AEA17180
ID AEA17180 standard; cDNA; 2148 BP.
XX
XX AEA17180;
XX
XX 25-AUG-2005 (first entry)
XX
XX A. thaliana aintegumenta (ANT) cDNA, seq id 1.
XX
XX plant engineering; growth; cell proliferation; organ mass; fertility;
XX asexual reproduction; aintegumenta; ANT; plant; gene; ss.
XX
XX Arabidopsis thaliana.
XX
XX
XX Key Location/Qualifiers
XX CDS 269..1936
XX FT /*tag= a
XX FT /product= "aintegumenta protein"
XX
XX US2005132445-A1.
XX
XX 16-JUN-2005.
XX
XX 18-JUL-2003; 2003US-00623477.
XX
XX 07-JAN-2000; 2000US-00479855.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Fischer RL, Mizukami Y;
XX
XX WPI; 2005-424635/43.
XX
XX P-PSDB; AEA17181.
XX
XX Modulating growth and cell proliferation in a plant, useful in plant
XX genetic engineering, comprises modulating aintegumenta (ANT) gene
XX activity and selecting plants with altered cell number.
XX
XX Claim 9; SEQ ID NO 1; 27pp; English.
XX
XX The invention relates to modulating growth and cell proliferation in a
XX plant comprising modulating aintegumenta (ANT) gene activity and
XX selecting plants with altered cell number. Further disclosed is a method
XX for directing expression of a heterologous nucleic acid in meristematic
XX cells of a plant. The method is useful in plant genetic engineering,
XX specifically for altering organ mass, controlling fertility and enhancing
XX asexual reproduction in plants. The current sequence represents A.
XX thaliana ANT cDNA.
XX
XX Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
SQ

Query Match 6.3%; Score 268; DB 14; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3961 AGATCCCAAGGATTCAAAGCAAAATTTGCTTGTCTCTCTATTATATATATC 4020
Db 1 AGATCCCAAGGATTCAAAGCAAAATTTGCTTGTCTCTCTATTATATATATC 60

Qy 4021 CTCGCAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTTCTTACCGCA 4080

Db	61	CTCTCAAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCCTGTTCTCTACCGCA	120
Qy	4081	CAAGAAAAAACAAGATTGAGAAAAATGCTGTCTGTTGTATACCAATGATTGGGT	4140
Db	121	CAAGAAAAAACAAGATTGAGAAAAATGCTGTCTGTTGTATACCAATGATTGGGT	180
Qy	4141	TTTAGCTTACATCTTCGAGAGTTTAAAGAAAGAGTGAAAGTACATTATAGAAAG	4200
Db	181	TTTAGCTTACATCTTCGAGAGTTTAAAGAAAGAGTGAAAGTACATTATAGAAAG	240
Qy	4201	AGAGAAAGCAAAACCAAAAAAGAAACC	4228
Db	241	AGAGAAAGCAAAACCAAAAAAGAAACC	268
RESULT 10			
ADMA42796	ID	ADMA42796 standard; DNA; 1421 BP.	
XX	AC	ADMA42796;	
XX	D7	03-JUN-2004 (first entry)	
XX	DE	DNA encoding a murine odourant receptor Sl9 Segid 40.	
XX	KW	murine; mouse; db; gene; chemical sensor system; taste; smell;	
KW	KW	artificial sensory organ; olfactory stimulation; food industry;	
KW	KW	hygiene inspection; environmental examination; disease diagnosis;	
XX	XX	carvone.	
OS	MS	Mus musculus.	
XX	PN	WO2003100057-A1.	
XX	PD	04-DEC-2003.	
XX	PF	28-MAY-2003; 2003WO-JP006719.	
XX	PR	28-MAY-2002; 2002JP-00154239.	
XX	PR	13-JUN-2002; 2002JP-00172412.	
XX	PR	14-JAN-2003; 2003JP-00005175.	
XX	PA	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.	
XX	PI	Sato T, Hirono J, Hamana H, Miyake M, Yoshikawa T, Miyake J;	
XX	DR	WPI: 2004-023356/02.	
XX	DR	P-PSDB; ADMA42797.	
XX	PT	Chemical sensor systems based on chemical receptors introduced into cells	
XX	PT	for immobilization onto support to form chip as component of sensor,	
XX	PT	useful in detecting stimuli e.g. taste and smell applicable in food	
XX	XX	industry.	
XX	XX	Claim 7; SEQ ID NO 40; 521bp; Japanese.	
XX	PS	This invention relates to a novel chemical sensor system method.	
XX	CC	Specifically, it refers to an isolated nucleic acid molecule that encodes	
XX	CC	a receptor protein, which binds to chemicals that can stimulate the sense	
XX	CC	of taste or smell for example. The present invention describes the	
XX	CC	manufacture of a chip that acts as a support to immobilise transfected	
XX	CC	cells expressing the receptor gene, such that this chip can be employed	
XX	CC	as a component of the chemical sensor model. Furthermore, this chip is	
XX	CC	usable as an artificial sensory organ where the chemical receptor	
XX	CC	contains an olfactory receptor the sensor can react to olfactory	
XX	CC	stimulation. Accordingly, these sensors are useful in the food industry	
XX	CC	for analysing freshness of meat, fruit and vegetables, hygiene	
XX	CC	inspection, environmental examination and disease diagnosis. Furthermore,	
XX	CC	such systems are automatable for high throughput applications under	
XX	CC	various conditions, even for differentiating optical isomers of R(-)-	
XX	CC	carvone from S(+)-carvone easily. This polynucleotide sequence is DNA	
XX	CC	encoding a murine odourant receptor of the invention.	

5Q	Sequence	1421 BP; 341 A; 368 C; 278 G; 434 T; 0 U; 0 Other;
	Query Match	1.3%; Score 55; DB 12; Length 1421;
	Best Local Similarity	100.0%; Pred. No. 7.0e-12;
	Matches	55; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1	GTCGACTCTTAGGCTTCACTGGCCTTAATACGACTCACTTAGAGGCTGAGATC 55
DB	387	GTCGACTCTTAGGCTTCACTGGCCTTAATACGACTCACTTAGAGGCTGAGATC 441
RESULT 11		
ID	ADY55721	standard; DNA; 1421 BP.
XX	ADY55721;	
XX	ADY55721;	
XX	19-MAY-2005	(first entry)
XX	Mouse odorant receptor Sl9 gene.	
DE		
XX	biocomputer; drug screening; diagnosis; food; cosmetics; agriculture;	
KW	analysis; fibronectin; gene; ds.	
XX		
XX	Mus musculus.	
OS		
XX	Key	Location/Qualifiers
FH	CDS	291..1310
FT		/*tag= a
FT		/product= "Mouse odorant receptor Sl9"
XX		
PN	W02005021744-A1.	
PD		
XX	10-MAR-2005.	
PF	25-JUN-2004; 2004MO-JP009404.	
XX		
XX	25-JUN-2003; 2003JP-00181915.	
XX	07-AUG-2003; 2003JP-00289469.	
PA	(NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.	
XX		
XX	Miyake M, Yoshikawa T, Miyake J;	
FL		
DR	WPI; 2005-262218/27.	
XX	P-PSDB; ADY55722.	
PT		
XX	Performing data production and presenting cell information under a	
PT	similar environment as digital cells, useful e.g. in drug development,	
PT	comprises profiling the actual status of cells.	
XX		
PS	Example 13; SEQ ID NO 19; 517bp; Japanese.	
XX		
CC	The invention relates to a novel method for producing profile data that	
CC	relates to cell information in an identical environment. The method	
CC	comprises placing several cells on a support in the same environment, and	
CC	monitoring the biological factors on or in the cells or their aggregate	
CC	chronologically to generate profile data of the cells. The methods and	
CC	systems are useful for performing data production by profiling actual	
CC	status of cells, and for presenting time-lapse and/or real-time cell	
CC	information at a cellular level under a similar environment as well as	
CC	digital cells in the form of a library of databases with cell	
CC	information, which are particularly useful in drug development, disease	
CC	diagnosis and management, as well as in fields including food technology,	
CC	cosmetics, agriculture, environmental sciences, in silico computational	
CC	biological studies, cell analysis and biotechnology. The methods and	
CC	systems are capable of providing information with controllability,	
CC	specificity and most importantly directly even in complex systems. This	
CC	polynucleotide sequence represents the DNA encoding a mouse odorant	
CC	receptor Sl9 protein used in the method for producing a digital cell	
CC	profile of the invention.	
XX		
XX	Sequence 1421 BP; 341 A; 368 C; 278 G; 434 T; 0 U; 0 Other;	

Query Match 1.3%; Score 55; DB 14; Length 1421;
Best Local Similarity 100.0%; Pred. No. 7.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 GTGACTCTAGGCGCTCACTGAGCTAATACGACTCACTATAGGAGGCTCGAGATC 55
DB 387 GTGACTCTAGGCGCTCACTGAGCTAATACGACTCACTATAGGAGGCTCGAGATC 441

RESULT 12
ID ABB56275
AC ABB56275;
DT 20-OCT-2005 (first entry)
DE Event sequencer related DNA SEQ ID NO 19.
KW analyte detection; ds; gene.
OS Unidentified.
PN MO2005073890-A1.
PD 11-AUG-2005.
PF 27-JAN-2005; 2005WO-JP001151.
PR 30-JAN-2004; 2004JP-00024923.
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX Miyake M, Yoshikawa T, Miyake J;
XX WPI; 2005-571425/58.
XX DR P-PSDB; ABB56276.
XX DR
XX PT Event sequencer extracts portion of timer series data with peculiar
XX PT behavior associated with index of system, as event timing, to generate
XX PT event descriptor described by event timing.
XX PS Disclosure; SEQ ID NO 19; 281pp; Japanese.
XX CC The invention relates to an event sequencer that acquires time-series
XX CC data on an index derived from a system and provides a peculiar behavior
XX CC associated with the index. A portion of time series data having the
XX CC peculiar behavior is extracted as an even timing and an event descriptor
XX CC described by the event timing is generated. The sequencer is useful for
XX CC analysis of the state of a system. The sequencer performs meaningful
XX CC analysis of a system state using specific index effectively. The present
XX CC sequence represents an event sequencer related DNA.
XX SQ Sequence 1421 BP; 341 A; 368 C; 278 G; 434 T; 0 U; 0 Other;

Query Match 1.3%; Score 55; DB 14; Length 1421;
Best Local Similarity 100.0%; Pred. No. 7.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 GTGACTCTAGGCGCTCACTGAGCTAATACGACTCACTATAGGAGGCTCGAGATC 55
DB 387 GTGACTCTAGGCGCTCACTGAGCTAATACGACTCACTATAGGAGGCTCGAGATC 441

RESULT 13
ID AAT30737
AC AAT30737;
DT 20-OCT-1996 (first entry)

DE Rat cryptdin 2 gene.
XX Cryptdin 2; antibiotic; antimicrobial; defensin; inflammation;
XX antiinflammatory; inflammatory bowel disease; pancreatitis; cancer;
XX tumour; ileitis; ds.
XX Rattus sp.
XX OS
XX Key Location/Qualifiers
XX FT exon 1..1345
XX FT /tag= a
XX FT /codon start= 1174..1176
XX FT /note="exon 1 codes for the 5' untranslated region and
XX FT cryptdin-1 prepro sequence"
XX FT 1345..1930
XX FT /tag= b
XX FT 1931..2408
XX FT /tag= c
XX FT /note="exon 2 codes for cryptdin-2 and 3' untranslated
XX FT region"

XX PN MO9616075-A1.
XX PD 30-MAY-1996.
XX PP 05-OCT-1995; 95WO-US013328.
XX PR 18-NOV-1994; 94US-00342268.
XX PA (REGC) UNIV CALIFORNIA.
XX PA (SHRI-) SHRINER'S HOSPITAL FOR CRIPPLED CHILDREN.
XX PI Selected ME, Ouellette AJ;
XX PI
XX DR WPI; 1996-268527/27.
XX DR P-PSDB; AAR98787, AAR98792.
XX FT New isolated cryptdin peptide(s) - which have antimicrobial activity,
XX FT used partic. in the detection and treatment of inflammatory pathologies.
XX PS Claim 31; Page 64-65; 103pp; English.
XX CC The rat cryptdin-2 gene (T30737) codes for the precursor (R98787) of
XX CC cryptdin-2 (R98792), an antimicrobial peptide that exhibits activity
XX CC against a broad range of intestinal and opportunistic pathogens. Rat
XX CC cryptdin-1, -2, and -3 genes (see also T30736 and T30738) were isolated
XX CC from a Sprague-Dawley genomic library cloned in EMBL3. The cryptdin-2
XX CC gene, or corresponding cDNA (see also T30734), can be used to produce
XX CC large amounts of cryptdin-2 for use in treating inflammatory pathologies
XX CC of the intestine
XX SQ Sequence 2408 BP; 640 A; 531 C; 557 G; 680 T; 0 U; 0 Other;

Query Match 1.3%; Score 55; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 7.5e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 GTGACTCTAGGCGCTCACTGAGCTAATACGACTCACTATAGGAGGCTCGAGATC 55
DB 666 GTGACTCTAGGCGCTCACTGAGCTAATACGACTCACTATAGGAGGCTCGAGATC 720

RESULT 14
ID ABB81284
AC ABB81284;
DT 22-AUG-2002 (first entry)
DE Beet promoter polynucleotide SEQ ID NO 4.
XX Beet; promoter; carbohydrate metabolism; invertase inhibitor;
XX KM

KW	fructosyl transferase; levan sucrase; nitrogen transporter protein;
KV	pathogen resistance; plant; transgenic; ds.
XX	Beta vulgaris.
OS	
XX	
FH	Key
FT	Promoter
FT	Location/Qualifiers 1..2998
FT	TATA_signal
FT	/tag= a
FT	2877..2883
FT	/tag= c
FT	2928..3049
FT	/tag= b
XX	
PN	EP1207204-A1.
PD	
PD	22-MAY-2002.
PF	16-NOV-2000; 2000EP-00124989.
PR	16-NOV-2000; 2000EP-00124989.
PA	(KWS-) KWS SAAT AG.
PI	Hehl R., Kloos D., Stahl DJ.
PI	WPI; 2002-437465/47.
PT	New tissue-specific promoters from Beta vulgaris, useful e.g. for altering carbohydrate metabolism, express transgenes selectively in roots or aerial parts.
PS	Claim 1; Page 30-31; 57pp; German.
XX	
CC	The invention relates to a promoter (A) that is: (i) any of the sequences ABBN1281-ABN81284; (ii) the complement of (i); or (iii) a sequence that hybridises to (ii). (A) are used, specifically in Beta vulgaris, to control expression of transgenes, particularly to alter carbohydrate metabolism; reduce loss of storage substances; express invertase inhibitor; fructosyl transferase, levan sucrase or genes that encode transport proteins for nitrogen compounds, or increase resistance to, or tolerance of, pathogens. (A) provide tissue-specific transgene expression, either in roots or above-ground parts, so avoid pleiotropic effects, e.g. when expressing invertase inhibitor
SQ	Sequence 3049 BP; 783 A; 699 C; 876 G; 691 T; 0 U; 0 Other;
Query Match	1.3%; Score 55; DB 6; Length 3049;
Best Local Similarity	100.0%; Pred. No. 7,4e-12;
Matches	55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy	1 GTGCACTTAGAGCCTCACTGGCTTAATACGACTCTATTAGGAGCTCGAGATC 55 DB 2656 GTGCAGCTTAGGCCCTCACTGGCTTAATACGACTCTATTAGGAGCTCGAGATC 2710
RESULT 15	
ID	ABZ82143 standard; DNA; 3869 BP.
XX	
AC	ABZ82143;
DT	17-JUN-2003 (first entry)
XX	
DE	Arabidopsis 9-cis-epoxycarotenoid dioxygenase NCED nucleic acid.
XX	
KM	NCED; AtNCED; 9-cis-epoxycarotenoid dioxygenase; enzyme; salt tolerance;
XX	stress resistance; plant; transgenic plant; gene; ds.
OS	Arabidopsis thaliana.
XX	
FH	Key
FT	Location/Qualifiers
FT	1831..3630
FT	/tag= a

```

FT      /product= "AtNCED"
FN      WO2003020015-A2.
PN      13-MAR-2003.
PD      30-AUG-2002; 2002WO-US027701.
PE      30-AUG-2001; 2001US-0316894P.
PR      30-AUG-2001; 2001US-0316894P.
PX      (PURD ) PURDUE RES FOUND.
XX      Ruggiero B, Bressan RA, Hasegawa PM;
XX      WPI; 2003-300807/29.
XX      P-PSDB; ABP72777.
XX      Producing transgenic plants resistant to environmental stress such as
XX      salt, drought, cold, osmotic or pathogen, by using 9-cis-epoxycarotenoid
XX      dioxygenase nucleic acid.
XX      Claim 3; Page 27-30; 125pp; English.
XX      The present sequence is a nucleic acid encoding Arabidopsis thaliana 9-
XX      cis-epoxycarotenoid dioxygenase (NCED). The NCED nucleic acid can be used
XX      in the practice of the invention. The invention provides plants that
XX      exhibit increased salt tolerance or increased stress resistance. These
XX      comprise: a mutant plant having a mutated NCED gene; a plant having a
XX      null mutation in an endogenous NCED gene; a transgenic plant comprising
XX      an isolated NCED nucleic acid (including the present sequence) operably
XX      linked to a promoter functional in a plant cell; a transgenic plant
XX      comprising an isolated nucleic acid that encodes an inhibitory NCED RNA
XX      that inhibits the function of endogenous NCED RNA; and a transgenic plant
XX      where the inhibitory RNA is complementary to the present sequence or
XX      hybridises to endogenous RNA encoding NCED. The plants can develop in the
XX      presence of a concentration of salt that would normally inhibit the
XX      development of the plant. The plants may be dicots (e.g. soybean) or
XX      monocots (e.g. corn, rice, rye, oat or wheat) and can be used to produce
XX      food or feed (all claimed)
XX      Sequence 3869 BP; 1155 A; 845 C; 773 G; 1096 T; 0 U; 0 Other;
SQ
Query Match      1.3%; Score 55; DB 8; Length 3869;
Best Local Similarity 100.0%; Pred. No. 7.2e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 GTGCACCTCTAGGCGCTCACTGAGCCCTAATACGACCTCACTATAGGAGGCTCGAGGATC 55
DB      1 GTGCACCTCTAGGCGCTCACTGAGCCCTAATACGACCTCACTATAGGAGGCTCGAGGATC 55
RESULT 16
AAS02362
ID      AAS02362 standard; DNA; 11630 BP.
XX      AAS02362;
XX      12-SEP-2001 (first entry)
DB      Galactosyl transferase gene targeting vector.
XX      Gal alpha(1,3) galactosyl transferase; gene targeting; transgenic animal;
XX      transplant rejection; immunomodulation; systemic lupus erythematosus;
XX      immune-hemolytic anaemia; collagen intron targeting construct;
XX      rheumatoid arthritis; ds.
XX      Synthetic.
XX      Sus scrofa.
XX      Key location/Qualifiers
XX      primer_bind 235..260
XX      /*tag= a
XX      /note= "PCR primer as displayed in AAS02349"
XX      FT
XX      TT

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```

FT primer_bind complement(4851)
PT /*tag= b
FT /note= "PCR primer as displayed in AAS02350"
FT mlec_feature 4851..4852
FT /*tag= c
FT /note= "Site of insertion of the puromycin/bovine growth
FT primer_bind 4852..4875
FT /*tag= d
FT /note= "PCR primer as displayed in AAS02351"
FT primer_bind complement(6911..6935)
FT /*tag= e
FT /note= "PCR primer as displayed in AAS02352"
XX
XX WO200123541-A2.
XX
XX 05-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US027065.
XX
XX 30-SEP-1999; 99US-0156953P.
XX
XX (ALEX-) ALEXION PHARM INC.
XX
XX Fodor WL, Ramseondar JJ;
XX
XX WPI; 2001-266147/27.
XX
XX Modulating the expression of a eukaryotic gene in a cell, involves
XX PT transfecting the cell with a nucleic acid construct that disrupts at
XX PT least a portion of the DNA sequence of the gene to be modulated.
XX
XX Example 2; Fig 7; 86pp; English.
XX
XX The sequence represents Porcine Gal alpha(1,3) galactosyl transferase
XX CC gene targeting construct. The construct replaces exon 4 with the
XX CC pyrimycin encoding gene. The invention relates to a method for modulating
XX CC the expression of a eukaryotic gene in a cell. The method involves
XX CC transfecting the cell with a nucleic acid construct. The construct
XX CC contains 2 nucleotide sequences which are portions of one or more introns
XX CC of the eukaryotic gene, and a sequence encoding a selectable marker. The
XX CC marker sequence is integrated into the gene sequence, so that expression
XX CC of the marker results in modulation of the expression of the gene. The
XX CC construct is useful for making a transgenic mammal. The construct is
XX CC useful for reducing transplant rejection by harvesting cells, tissue, or
XX CC organs from the offspring of the transgenic mammal, and transplanting the
XX CC harvested cells, tissue, or organs into a patient in need. The knockout
XX CC mammals produced by the method are useful for screening drugs for
XX CC immunomodulation (e.g for systemic lupus erythematosus, rheumatoid
XX CC arthritis and immune-haemolytic anaemia) and for producing proteins of
XX CC interest
XX
XX Sequence 11630 BP; 2956 A; 2688 C; 2693 G; 3290 T; 0 U; 3 Other:
XX
XX Query Match 1.3%; Score 55; DB 4; Length 11630;
XX Best Local Similarity 100.0%; Pred. No. 6,7e-12;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GTGACCTTAGGCGCTCACTGACCTAATACGACTGACTATAGGAGCTCGAGGATC 55
XX Db 1 GTGACCTTAGGCGCTCACTGACCTAATACGACTGACTATAGGAGCTCGAGGATC 55
XX
XX RESULT 17
XX ADO59305/c
XX ID ADO59305 standard; DNA; 16905 BP.
XX
XX ADO59305;
XX
XX 26-AUG-2004 (first entry)
XX
XX Mouse kank (mkank) gene - genomic DNA region #2.
XX

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XX mouse; murine; kank; mkank; cancer; gene; ds.
XX
XX Mus musculus.
XX OS
XX WO2004048568-A1.
XX PN
XX 10-JUN-2004.
XX PD
XX
XX 21-NOV-2003; 2003WO-JP014930.
XX PF
XX 22-NOV-2002; 2002JP-00339909.
XX PR
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX PA (INFO-) INFO GENES CO LTD.
XX
XX Kiyama R, Kitajima K;
XX PI
XX WPI; 2004-450380/42.
XX DR
XX
XX Novel mouse kank protein useful for detecting cancer, treating cancer, in
XX PT drug discovery for treating cancer.
XX PS Claim 3; SEQ ID NO 2; 83pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequence of the mouse
XX CC kank (mkank) protein. The DNA and protein sequences of the invention are
XX CC useful in the detection and treatment of cancer. The present DNA sequence
XX CC represents a region of the mouse kank genomic DNA sequence.
XX
XX Sequence 16905 BP; 4333 A; 3945 C; 4066 G; 4561 T; 0 U; 0 Other:
XX
XX Query Match 1.3%; Score 55; DB 12; Length 16905;
XX Best Local Similarity 100.0%; Pred. No. 6,5e-12;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 TCGACCTTAGGCGCTCACTGACCTAATACGACTGACTATAGGAGCTCGAGGATC 56
XX Qy 16905 TCGACCTTAGGCGCTCACTGACCTAATACGACTGACTATAGGAGCTCGAGGATC 16851
XX Db
XX
XX RESULT 18
XX AAS02354
XX ID AAS02354 standard; DNA; 27048 BP.
XX
XX AAS02354;
XX AC
XX 12-SEP-2001 (first entry)
XX DT
XX Porcine Gal alpha(1,3) galactosyl transferase gene introns 3-8.
XX DB
XX Pig; Gal alpha(1,3) galactosyl transferase; intron 3-8; gene targeting;
XX KW transgenic animal; transplant rejection; immunomodulation;
XX KW systemic lupus erythematosus; immune-haemolytic anaemia;
XX KW rheumatoid arthritis; ds.
XX
XX Sub scrofa.
XX
XX Key
XX FT intron 1..4851
XX FT /*tag= a
XX FT /number= 3
XX FT primer_bind 10..23
XX FT /*tag= b
XX FT complement(3998..4020)
XX FT primer_bind /*tag= c
XX FT 4852..4937
XX FT /*tag= d
XX FT /number= 4
XX FT /note= "The exon sequence is represented by dashes in the
XX FT sequence presented in figure 1 in the specification and
XX FT have been replaced with N's to maintain the sequence
XX FT numbering"
XX FT intron 4938..11715
XX

```

PT /*tag= d
PT /number= 4
PT /note= "This sequence is specifically claimed in claim
PT 14"
PT primer_bind
PT 11521. .11537
PT /*tag= e
PT complement(11688. .11716)
PT /*tag= f
PT 11716. .11752
PT /*tag= g
PT /number= 5
PT /note= "The exon sequence is represented by dashes in the
PT sequence presented in figure 1 in the specification and
PT have been replaced with N's to maintain the sequence
PT numbering"
PT 11753. .13747
PT /*tag= h
PT /number= 5
PT 13748. .13810
PT /*tag= i
PT /number= 6
PT /note= "The exon sequence is represented by dashes in the
PT sequence presented in figure 1 in the specification and
PT have been replaced with N's to maintain the sequence
PT numbering"
PT 13811. .14358
PT /*tag= j
PT /number= 6
PT 14359. .14463
PT /*tag= k
PT /number= 7
PT /note= "The exon sequence is represented by dashes in the
PT sequence presented in figure 1 in the specification and
PT have been replaced with N's to maintain the sequence
PT numbering"
PT 14464. .21627
PT /*tag= l
PT /number= 7
PT /note= "This sequence is specifically claimed in claim
PT 16"
PT 21628. .21705
PT /*tag= m
PT /number= 8
PT /note= "The exon sequence is represented by dashes in the
PT sequence presented in figure 1 in the specification and
PT have been replaced with N's to maintain the sequence
PT numbering"
PT 21706. .27048
PT /*tag= n
PT /number= 8
PT /note= "This sequence is specifically claimed in claim
PT 42"
XX WO200123541-A2.
XX PN
XX PD
XX 05-APR-2001.
XX PP 02-OCT-2000; 2000WO-US027065.
XX PR 30-SEP-1999; 99US-0156953P.
XX PA (ALEX-) ALEXION PHARM INC.
XX PI Fodor WL, Ramsoondar JJ;
XX DR WPI; 2001-266147/27.
XX XX
PT Modulating the expression of a eukaryotic gene in a cell, involves
PT transfecting the cell with a nucleic acid construct that disrupts at
PT least a portion of the DNA sequence of the gene to be modulated.
XX XX
PS Example 1; Fig 1; 86pp; English.
XX

CC The sequence represents Porcine Gal alpha(1,3) galactosyl transferase
CC Intron 3-8, a gene used to make a gene targeting construct of the
CC invention. The invention relates to a method for modulating the
CC expression of a eukaryotic gene in a cell. The method involves
CC transfecting the cell with a nucleic acid construct. The construct
CC contains 2 nucleotide sequences which are portions of one or more introns
CC of the eukaryotic gene, and a sequence encoding a selectable marker. The
CC marker sequence is integrated into the gene sequence, so that expression
CC of the marker results in modulation of the expression of the gene. The
CC construct is useful for making a transgenic mammal. The construct is
CC useful for reducing transplant rejection by harvesting cells, tissue, or
CC organs from the offspring of the transgenic mammal, and transplanting the
CC harvested cells, tissue, or organs into a patient in need. The knockout
CC mammals produced by the method are useful for screening drugs for
CC immunomodulation (e.g. for systemic lupus erythematosus, rheumatoid
CC arthritis and immune-haemolytic anaemia) and for producing proteins of
CC interest
XX SQ Sequence 27048 BP; 6964 A; 5958 C; 6323 G; 7365 T; 0 U; 438 Other;
XX
XX Query Match 1.3%; Score 55; DB 4; Length 27048;
XX Best Local Similarity 100.0%; Pred.No. 6.3e-12; Indels 0; Gaps 0;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCGACTTAGGCTCAGCTGCTTAATACGACTCAGCTATAGGAGCTCGAGATC 55
Db 1 GTCGACTTAGGCTCAGCTCAGCTGCTTAATACGACTCAGCTATAGGAGCTCGAGATC 55
RESULT 19
AAS023355
ID AAS02355 standard; DNA; 4026 BP.
AC AAS02355;
XX 12-SEP-2001 (first entry)
XX DE Porcine Gal alpha(1,3) galactosyl transferase gene intron 3, 5' sequence.
XX KW Pig; Gal alpha(1,3) galactosyl transferase; intron 3; gene targeting;
XX KW transgenic animal; transplant rejection; immunomodulation;
XX KW systemic lupus erythematosus; immune-haemolytic anaemia;
XX KW rheumatoid arthritis; ds.
XX OS Sus scrofa.
XX FH Key Location/Qualifiers
FT primer_bind 1..23
FT /*tag= a
FT /note= "PCR primer as displayed in AAS02338"
FT primer_bind complement(3999. .4026)
FT /*tag= b
FT /note= "PCR primer as displayed in AAS02339"
XX WO200123541-A2.
XX PN
XX PD
XX 05-APR-2001.
XX PP 02-OCT-2000; 2000WO-US027065.
XX PR 30-SEP-1999; 99US-0156953P.
XX PA (ALEX-) ALEXION PHARM INC.
XX PI Fodor WL, Ramsoondar JJ;
XX DR WPI; 2001-266147/27.
XX XX
PT Modulating the expression of a eukaryotic gene in a cell, involves
PT transfecting the cell with a nucleic acid construct that disrupts at
PT least a portion of the DNA sequence of the gene to be modulated.
XX XX
PS Example 1; Fig 3A; 86pp; English.
XX

PF 18-NOV-1997; 97MO-BP006472.
 XX
 PR 18-NOV-1996; 96EB-00203213.
 XX
 PA (MOGE-) MOGEN INT NV.
 XX
 PI Ohl SA, Van Der Lee FM, Goddijn OJM, Klap J, Sijmons PC;
 XX WPI; 1998-312484/27.
 DR
 XX New Arabidopsis thaliana DNA promoter - useful for, e.g. generating plant
 PT reduced susceptibility to plant parasitic nematodes.
 XX
 PS Claim 1; Page 22-24; 47pp; English.
 XX
 CC This DNA fragment obtainable from Arabidopsis thaliana is capable of
 CC promoting root knot and cyst nematode-inducible transcription of an
 CC associated DNA sequence when reintroduced into a plant. The promoterless
 CC GUS construct binary vector PMO553 was mobilised by triparental mating
 CC to Agrobacterium tumefaciens MOG101 and the resulting strain was used for
 CC Arabidopsis root transformation. Line PMO553H25 was identified as a line
 CC which showed strong GUS expression inside syncytia and giant cells
 CC induced by the cyst nematode Heterodera schachtli and the root knot
 CC nematode Meloidogyne incognita, respectively. Promoter tags from line
 CC PMO553H25 were sequenced. The claimed DNA fragment is nematode feeding
 CC site-specific. Also claimed are: (1) a portion or variant of the above
 CC sequence capable of promoting root knot and cyst nematode inducible
 CC transcription of an associated DNA sequence comprising a DNA fragment as above
 CC plus a DNA sequence which is not naturally under its transcriptional
 CC control, and which causes the production of a plant cell-disruptive
 CC substance, preferably barnase; (3) a replicon comprising the chimeric DNA
 CC sequence of (2), or the above DNA and at least 1 restriction endonuclease
 CC recognition site; (4) a microorganism containing the replicon of (3); (5)
 CC a plant cell having incorporated into its genome the chimeric DNA of (2);
 CC (6) a plant system of a plant consisting of the cells of (5); (7) a plant
 CC consisting of the cells of (5), preferably a dicotyledonous plant,
 CC especially a potato plant; (8) a plant grafted onto the root system of
 CC (6); (9) a part of a plant, selected from seeds, flowers, tubers, roots,
 CC leaves, fruits, pollen and wood, obtained from the plant of (7) or (8),
 CC and (10) a crop consisting of the plants of (7) or (8). The DNA fragment
 CC can be used to identify subfragments capable of promoting transcription
 CC of an associated DNA sequence in a plant. It can also be used for making
 CC hybrid regulatory DNA sequences. The chimeric DNA sequence of (2) can be
 CC used for transforming plants (all claimed). The DNA sequence can be used
 CC to reduce the susceptibility of a plant to parasitic nematodes. (Updated
 CC on 17-Oct-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 3484 BP; 1143 A; 583 C; 625 G; 1133 T; 0 U; 0 Other;
 Query Match 0.7%; Score 28; DB 2; Length 3484;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 CTATATGAGACTCACTATAGGAGCTCGA 50
 Db 698 CTATATGAGACTCACTATAGGAGCTCGA 725
 RESULT 22
 AAT94303
 ID AAT94303 standard; DNA; 1205 BP.
 XX
 AC AAT94303;
 XX
 DT 18-MAR-1998 (first entry)
 XX
 DE EGM3 gene promoter.
 XX
 KW Promoter; eukaryotic gene regulation; insecticidal toxin production;
 KM sterility induction; root nematode control; amplify; modulator gene;
 KM EGM3 gene; ss.
 XX

OS Eucalyptus grandis.
 XX
 PN WO9730162-A1.
 XX
 PD 21-AUG-1997.
 XX
 PF 19-FEB-1997; 97MO-AU000089.
 XX
 PR 19-FEB-1996; 96AU-00008161.
 XX
 PA (FORB-) FORBIO RES PTY LTD.
 XX
 PI Teasdale RD, Mouradov A, Southern SG, Sawbridge TI;
 XX WPI; 1997-425037/39.
 DR
 XX
 XX
 PT Regulating eukaryotic gene by expressing modulator gene and gene that
 PT regulates the modulator - with two of these genes controlled by inducible
 PT or developmental promoters, particularly used in plants to impart
 PT reversible sterility, nematode or insect resistance, to regulate pigment
 PT production etc.
 XX
 PS Disclosure; Fig 13; 87pp; English.
 XX
 CC This sequence represents a promoter used in the method of the invention.
 CC The method of the invention is for regulating a eukaryotic gene by
 CC transforming a cell with a construct. The construct expresses a modulator
 CC gene product that regulates the eukaryotic gene or its product, and a
 CC further gene product that regulates the modulator gene or its product.
 CC Two of the promoters controlling the eukaryotic gene, modulator and
 CC further genes are inducible or developmental promoters from the same or
 CC complementary tissues. The process provides highly specific expression of
 CC the eukaryotic gene in target organs, especially of plants but possibly
 CC also in yeasts and animals. Typical applications include induction of
 CC sterility (which may be reversible); control of root nematodes;
 CC production of pigments, dyes, insecticidal toxins, fragrances etc. A
 CC transformation cassette with the 3 genes under the control of the
 CC specified promoters, provides expression of the eukaryotic gene in target
 CC tissues with increased specificity and reduced promoter leakage
 CC
 XX
 SQ Sequence 1205 BP; 421 A; 218 C; 213 G; 353 T; 0 U; 0 Other;
 Query Match 0.6%; Score 27; DB 2; Length 1205;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 TATATGAGACTCACTATAGGAGCTCGA 50
 Db 72 TATATGAGACTCACTATAGGAGCTCGA 98
 RESULT 23
 AAA51053/C
 ID AAA51053 standard; DNA; 6975 BP.
 XX
 AC AAA51053;
 XX
 DT 09-OCT-2000 (first entry)
 XX
 DE Plasmid pMH40-delta.
 XX
 KW S-adenosyl-L-methionine synthetase; SAMS; probe; promoter; embryo;
 KM constitutive; tissue-specific; development-specific;
 KM herbicide resistance; pathogen resistance; pMH40-delta; ss.
 XX
 OS Synthetic.
 XX
 PN WO200037662-A2.
 XX
 XX
 PD 29-JUN-2000.
 XX
 PF 17-DEC-1999; 99WO-US030180.
 XX

PR 21-DEC-1998; 98US-0113045P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Palco SC, LI Z;
XX
XX WPI; 2000-442682/38.
XX
XX S-adenosyl-L-methionine synthetase promoter for expressing target
PT heterologous herbicide-resistance or pathogen-resistance nucleic acid
PT fragments in plants, especially soybean.
XX
XX Example 5; Page 45-47; 50pp; English.
XX
XX The S-adenosyl-L-methionine synthetase (SAMS) promoter (see AA051042) was
CC inserted into plasmid pM40-delta, which contains a 35S promoter::GUS::3'
CC Nos DNA fragment, to form plasmid pS11. The SAMS promoter is active in
CC seedlings and callus and over-expression of a gene in embryo stage can be
CC achieved at an early developing stage using the SAMS promoter. The SAMS
CC promoter may be used as an alternative to cauliflower mosaic virus 35S
CC promoter to drive expression of selectable marker genes. Plant cells
CC transformed with the SAMS constitutive promoter are useful for increasing
CC or decreasing the expression of heterologous nucleic acid fragments in a
CC plant, preferably corn, rice, wheat, barley, palm, Arabidopsis, soybean,
CC oil seed Brassica, peanut, sunflower, safflower, cotton, tobacco, tomato,
CC potato or cocoa. Target heterologous nucleic acid fragments include
CC herbicide resistance or pathogen resistance nucleic acid fragments
XX
SQ Sequence 6975 BP; 1890 A; 1694 C; 1699 G; 1691 T; 0 U; 1 Other;

Query Match 0.6%; Score 27; DB 3; Length 6975;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTATACGACTCACTATAGGAGCTCG 49
DB 4123 CTATACGACTCACTATAGGAGCTCG 4097
|||||

RESULT 24
AAC55633/c
ID AAC55633 standard; DNA; 7038 BP.
XX
XX AAC55633;
XX
XX
DT 11-JAN-2001 (first entry)
XX
XX 2-hybrid vector pMAB5 nucleotide sequence.
DE
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; ds.
XX
XX Bacteriophage lambda.
OS Synthetic.
XX
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005432.
XX
XX 02-MAR-1999; 99US-0122389P.
XX 23-MAR-1999; 99US-0126049P.
XX 28-MAY-1999; 99US-0136744P.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT

PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX
XX
XX Disclosure; Fig 98; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 7038 BP; 2000 A; 1596 C; 1526 G; 1916 T; 0 U; 0 Other;

Query Match 0.6%; Score 27; DB 3; Length 7038;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TAATAGACTCACTATAGGAGCTCGA 50
DB 6005 TAATAGACTCACTATAGGAGCTCGA 5979
|||||

RESULT 25
AAC55630/c
ID AAC55630 standard; DNA; 6815 BP.
XX
XX AAC55630;
XX
XX
DT 11-JAN-2001 (first entry)
XX
XX Destination vector pDEST33 nucleotide sequence.
DE
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; ds.
XX
XX Bacteriophage lambda.
OS Synthetic.
XX
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005432.
XX
XX 02-MAR-1999; 99US-0122389P.
XX 23-MAR-1999; 99US-0126049P.
XX 28-MAY-1999; 99US-0136744P.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT

PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides.
 XX
 PS Disclosure; Fig 95; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombinational sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombinational site and a second att
 CC recombinational site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombinational sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombinational site and a second nucleic acid molecule
 CC comprising a second recombinational site that interacts with the mutated
 CC att recombinational site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 8815 BP; 2513 A; 1954 C; 1943 G; 2405 T; 0 U; 0 Other;
 XX
 Query Match 0.6%; Score 27; DB 3; Length 8815;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 TTAATAGCACTCACTATTAGGAGCTCGA 50
 Db 7782 TTAATAGCACTCACTATTAGGAGCTCGA 7756
 XX
 RESULT 26
 AEA62089/c
 ID AEA62089 standard; cDNA; 11240 BP.
 XX
 AC AEA62089;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Replication competent hepatitis C virus polynucleotide.
 XX
 KW Hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;
 KW gastrointestinal disease; drug screening; gene; ss.
 XX
 OS Hepatitis C virus.
 OS Human immunodeficiency virus 1.
 OS Hepatitis delta virus.
 OS Encephalomyocarditis virus.
 OS Chimeric.
 OS
 XX
 FH Key Location/Qualifiers
 FH 5'UTR 1..341
 FT /*tag= a
 FT 342..1457
 FT /*tag= b
 FT /*product= "Tat2Neo"
 FT 1458..2076
 FT /*tag= c
 FT /*function= "IRES"
 FT 2077..8037
 FT /*tag= d
 FT /*product= "HCV polypeptide"
 FT 8038..8259
 FT /*tag= e
 FT misc_feature 8260..8345

FT /*tag= f
 FT /function= "Ribozyme"
 XX
 PN WO2005053516-A2.
 XX
 PD 16-JUN-2005.
 XX
 PF 01-DEC-2004; 2004WO-US040120.
 XX
 PR 01-DEC-2003; 2003US-0525989P.
 XX
 PA (TEXA) UNITV TEXAS.
 XX
 PI Lemon SM, Yi M;
 XX
 DR WPI; 2005-418069/42.
 DR P-PADB; AEA62092.
 XX
 PT New replication competent polynucleotide comprising a 5' non-translated
 PT region (NTR), a 3' NTR, and a first coding sequence present between the
 PT 5' NTR and 3' NTR and encoding a hepatitis C virus polypeptide, useful in
 PT drug discovery.
 XX
 PS Disclosure; SEQ ID NO 13; 102pp; English.
 XX
 CC The present invention provides replication competent polynucleotides that
 CC include a 5' non-translated region (NTR), a 3' NTR and a coding sequence
 CC encoding a hepatitis C virus (HCV) polypeptide that comprises an Ile
 CC residue at about amino acid 2204, and an adaptive mutation selected from
 CC Arg at about amino acid 1067, Arg at about amino acid 1691, Val at about
 CC amino acid 2080, Ile at about amino acid 1655, Arg at about amino acid
 CC 2040, and Arg at about amino acid 1188, or a combination of these. The
 CC polypeptide may include the cleavage products core E1, E2, P7, NS2, NS3,
 CC NS4A, NS4B, NS5A and NS5B. The polynucleotide may further comprise a
 CC second coding sequence encoding a marker or transactivator, or a
 CC nucleotide sequence having cis-acting ribozyme activity located 3' of the
 CC 3' NTR. Also provided are: a method for making the replication component
 CC polynucleotide; a method for using the replication component
 CC polynucleotide to identify a compound that inhibits replication of the
 CC replication competent nucleotide; a method for selecting a replication
 CC competent polynucleotide; and a method for detecting a replication
 CC competent polynucleotide. The present sequence is that of a replication
 CC competent polynucleotide of the invention comprising a 5' NTR, a tat2Neo
 CC sequence, an encephalomyocarditis virus IRES, a coding sequence for HCV
 CC polypeptide, and the hepatitis delta virus ribozyme.
 XX
 SQ Sequence 11240 BP; 2431 A; 3214 C; 3038 G; 2557 T; 0 U; 0 Other;
 XX
 Query Match 0.6%; Score 27; DB 14; Length 11240;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 CTAATAGCACTCACTATTAGGAGCTCG 49
 Db 8390 CTAATAGCACTCACTATTAGGAGCTCG 8364
 XX
 RESULT 27
 ADU81180
 ID ADU81180 standard; cDNA; 21178 BP.
 XX
 AC ADU81180;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Thale cress diacylglycerol acyltransferase, DGAT, cDNA #2.
 XX
 KW diacylglycerol acyltransferase; DGAT; plant breeding; crop improvement;
 KW fatty acid biosynthesis; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO2004101793-A1.

```

XX 25-NOV-2004.
PD
XX
XX 14-MAY-2004; 2004WO-AU000635.
PF
XX
XX 16-MAY-2003; 2003AU-00902413.
PR
XX
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA
XX (AGRE-) AGRESEARCH LTD.
PI
XX Bryan GT, Burling MF, Roberts NJ, Trollope AJ, Woodfield DR;
DR WPI; 2004-821891/81.
XX
XX New nucleic acid from a ryegrass (Lolium) or fescue (Festuca) species
PT encoding a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
PT polypeptide, useful as a genetic marker or for modifying fatty acid
PT biosynthesis in a plant.
XX
XX Example 2; SEQ ID NO 43; 188bp; English.
XX
XX The invention relates to a new substantially purified or isolated nucleic
CC acid or its fragment from a ryegrass (Lolium) or fescue (Festuca) species
CC encodes a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
CC polypeptide or its fragment or variant. The nucleic acid or nucleic acid
CC fragment and/or its nucleotide sequence information or single nucleotide
CC polymorphism of perennial ryegrass Lolium perenne is useful as a
CC molecular genetic marker or for modifying fatty acid biosynthesis in a
CC plant. The present sequence represents a plant diacylglycerol
CC acyltransferase, DGAT, cDNA.
XX
XX Sequence 21178 BP; 5350 A; 5440 C; 5462 G; 4926 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 27; DB 13; Length 21178;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCG 49
Db 10500 CTATACGACTCACTATAGGAGCTCG 10526
RESULT 28
ADU81181
XX ADU81181 standard; DNA; 22635 BP.
XX
XX ADU81181;
AC
XX
XX 10-FEB-2005 (first entry)
DT
XX
XX Thale cress diacylglycerol acyltransferase, DGAT, DNA #2.
DE
XX
XX diacylglycerol acyltransferase; DGAT; plant breeding; crop improvement;
KM fatty acid biosynthesis; db.
XX
XX Arabidopsis thaliana.
OS
XX
XX WO2004101793-A1.
PN
XX
XX 25-NOV-2004.
PD
XX
XX 14-MAY-2004; 2004WO-AU000635.
PF
XX
XX 16-MAY-2003; 2003AU-00902413.
PR
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA
XX (AGRE-) AGRESEARCH LTD.
PI
XX Bryan GT, Burling MF, Roberts NJ, Trollope AJ, Woodfield DR;
DR WPI; 2004-821891/81.
XX
XX New nucleic acid from a ryegrass (Lolium) or fescue (Festuca) species
PT

```

```

PT encoding a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
PT polypeptide, useful as a genetic marker or for modifying fatty acid
PT biosynthesis in a plant.
XX
XX Example 2; SEQ ID NO 44; 188bp; English.
XX
XX The invention relates to a new substantially purified or isolated nucleic
CC acid or its fragment from a ryegrass (Lolium) or fescue (Festuca) species
CC encodes a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
CC polypeptide or its fragment or variant. The nucleic acid or nucleic acid
CC fragment and/or its nucleotide sequence information or single nucleotide
CC polymorphism of perennial ryegrass Lolium perenne is useful as a
CC molecular genetic marker or for modifying fatty acid biosynthesis in a
CC plant. The present sequence represents a plant diacylglycerol
CC acyltransferase, DGAT, cDNA.
XX
XX Sequence 22635 BP; 5760 A; 5684 C; 5710 G; 5481 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 27; DB 13; Length 22635;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCG 49
Db 11957 CTATACGACTCACTATAGGAGCTCG 11983
RESULT 29
AAC60777
XX AAC60777 standard; DNA; 38 BP.
XX
XX AAC60777;
AC
XX
XX 06-FEB-2001 (first entry)
DT
XX
XX Candidate oncogene ZNF217 reverse PCR primer SEQ ID NO:6.
DE
XX
XX Vitamin D 24 hydroxylase; vitamin D receptor; CYP24; VDR; ZNF24;
KM oncogene; breast cancer; chromosome 20; 20q13.2; PCR primer;
KM 25-hydroxyvitamin D3 24-hydroxylase enzyme; cytostatic; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200060109-A1.
PN
XX
XX 12-OCT-2000.
PD
XX
XX 06-MAR-2000; 2000WO-US005972.
PF
XX
XX 02-APR-1999; 99US-00285292.
PR
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Albersson DG, Pinkel D, Collins C, Gray JW, Ystra B;
PI
XX
XX WPI; 2000-656233/63.
DR
XX
XX Detecting a predisposition to or a progression of cancer especially
PT breast cancer in humans comprises detecting levels of CYP24 in a
PT biological sample.
XX
XX Example 1; Page 53; 73pp; English.
XX
XX The present invention describes a method for detecting (I) a
CC predisposition to cancer in an animal. The method comprises detecting the
CC level of CYP24 (25-hydroxyvitamin D3 24-hydroxylase enzyme) in a
CC biological sample from the animal and comparing it with a control sample
CC taken from a normal, cancer-free tissue, where an increased level of
CC CYP24 in the biological sample compared to the control sample indicates a
CC predisposition to cancer in the animal. (I) is useful for detecting a
CC predisposition to cancer in humans, non-human primates, canines, felines,
CC murines, bovines, equines, porcines and lagomorphs. An example from the
CC present invention describes the identification of CYP24 as a driver

```

CC oncogene for amplification at chromosome band 20q13.2; the present
CC sequence represents a PCR primer for the candidate oncogene ZNF217 which
CC is used in this example
XX

Sequence 38 BP; 14 A; 8 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 26; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAAATAGCACTCACTATAGGAGCTCG 49
Db 1 TAAATAGCACTCACTATAGGAGCTCG 26

RESULT 30
AAK8214
XX AAK8214 standard; DNA; 40 BP.
XX
AC AAK8214;
XX
XX 10-SEP-1999 (first entry)
XX
XX Oligonucleotide primer 2.
XX
XX Ribozyme; modification; inhibitor; gene expression; gene therapy; primer;
XX retrovirus; probe; nuclease resistant ribonucleic acid; antisense; tRNA;
XX transgenic plant; acylation; aminoacyl-tRNA synthetase; ss.
XX
XX Synthetic.
XX
XX DE19801153-A1.
XX
XX 15-JUL-1999.
XX
XX 14-JAN-1998; 98DE-01001153.
XX
XX 14-JAN-1998; 98DE-01001153.
XX
XX (JENNN/) JENNE A.
XX
XX WPI; 1999-396161/34.
XX
XX Selection of a ribozymes useful for, e.g. inhibiting gene expression and
XX improving nuclease resistance.
XX
XX Example 1; Page 7; 22pp; German.
XX
XX This invention describes a novel method to select a ribozyme that can
XX covalently modify the 2'-OH group of ribonucleic acids in trans. The
XX ribozyme can be used to inhibit gene expression (e.g. in gene therapy) or
XX to fight retroviruses in vitro or in vivo. The ribozyme, DNA encoding it
XX or a vector containing the DNA, can be used as a sequence specific gene
XX probe. They can also be used for manufacture of nuclease resistant
XX ribonucleic acids (especially antisense oligonucleotides) or to produce
XX transgenic plants. The ribozyme can be used to acylate the 3' end of
XX tRNA. In other words, it can be used as an aminoacyl-tRNA synthetase.
XX This sequence represents a primer used in the method of the invention
XX
XX Sequence 40 BP; 10 A; 12 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 26; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGCACTCACTATAGGAGCTC 48
Db 2 CTAATAGCACTCACTATAGGAGCTC 27

RESULT 31
AEB00576
ID AEB00576 standard; DNA; 43 BP.

XX
XX AEB00576;
AC
XX 25-AUG-2005 (first entry)
XX
XX
XX Drosophila kinase CG7125/T7 promoter reverse PCR primer.
XX
XX Mitosis; kinase; gene silencing; RNA interference; cell cycle;
XX proliferation; ss; PCR; primer; T7 promoter; cancer; cytostatic;
XX psoriasis; antipsoriatic; glomerulonephritis; nephrotic; gene therapy.
XX
XX Drosophila melanogaster.
OS
XX Enterobacteria phage T7.
XX
XX WO2005056802-A2.
XX
XX
XX 23-JUN-2005.
XX
XX 13-DEC-2004; 2004WO-GB005218.
XX
XX 12-DEC-2003; 2003GB-00028928.
XX
XX (CANC-) CANCER RES TECHNOLOGY LTD.
XX
XX Glover DM, Bettencourt-Dias M, Giet R, Sinka R, Carpenter L;
XX WPI; 2005-488189/49.
XX
XX The invention relates to modulating proliferation in a cell or population
XX of cells comprising contacting the cell or population of cells with an
XX agent capable of modulating expression or activity of a target kinase or
XX a regulator of the target kinases listed in table 1 the specification.
XX The modulating agent is a nucleic acid chosen from an anti-sense RNA or
XX DNA, a triple helix-forming molecule, RNAi, siRNA or a ribozyme. The
XX target kinase is a homolog of a Drosophila kinase which, when its
XX expression is modulated by a dsRNA interference molecule, is shown to
XX arrest the cell cycle. Also included are screening for a modulator of
XX cell proliferation, determining the effect of a candidate substance on
XX proliferation of a cell or population of cells, preparing a
XX pharmaceutical composition for the treatment of a proliferative disorder,
XX treating a proliferative disorder in a subject, diagnosing a
XX proliferative disorder, identifying a kinase which is abnormally
XX expressed in a proliferative disorder, a vector (comprising a coding
XX sequence for a kinase (or a regulator of target kinases) listed in the
XX specification operably linked to transcriptional regulatory sequences for
XX use in a method of gene therapy) and a pharmaceutical composition
XX comprising the above vector and a pharmaceutical carrier. The methods and
XX composition (including the vector or nucleic acid or the modulator of
XX expression or activity of the target kinases) are useful for treating
XX proliferative disorders or for manufacturing a medicament for the
XX treatment of proliferative disorders, such as cancer, psoriasis or
XX glomerulonephritis. These may also be used for diagnosing such disorders.
XX The present sequence is a PCR primer that amplifies a region of a
XX Drosophila kinase (which, when its expression is modulated by a dsRNA
XX interference molecule, is shown to arrest the cell cycle). The primer
XX adds a T7 promoter sequence for in-vitro transcription.
XX
XX Sequence 43 BP; 8 A; 12 C; 9 G; 14 T; 0 U; 0 Other;

Query Match 0.6%; Score 26; DB 14; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGCACTCACTATAGGAGCTC 48
Db 5 CTAATAGCACTCACTATAGGAGCTC 30

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RESULT 32
AA236342
ID AAT36342 standard; RNA; 239 BP.
XX
AC AAT36342;
XX
XX 24-OCT-1997 (first entry)
XX
DE Human immunodeficiency virus 1 tat ligand, tat7.
XX
XX Human immunodeficiency virus type 1; HIV 1; reverse transcriptase;
KM high affinity ligand; AIDS; treatment; diagnosis; inhibition;
KM acquired immune deficiency syndrome; rev; tat; pol; ss.
XX
OS Synthetic.
XX
XX MO9703085-A1.
XX
XX 30-JAN-1997.
XX
XX 10-JUL-1996; 96MO-US011473.
XX
XX 11-JUL-1995; 95US-0000872P.
XX
XX 30-AUG-1995; 95US-00521515.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Gold L, Lochrie M, Chen H, Tuerk C;
PI WPI; 1997-118979/11.
XX
XX Identification of feline immunodeficiency virus reverse transcriptase
PT nucleic acid ligands - for treatment and diagnosis of viral infection.
XX also treatment of intracellularly mediated diseases.
XX
XX Example 3; Page 57; 71pp; English.
XX
XX Intracellularly mediated conditions such as cancer involving dominant ras
CC mutations or infectious diseases including AIDS can be treated by
CC administering oligonucleotides (i.e. nucleic acid ligands) which can
CC enter the cell and attenuate the condition. In a specific example, RNA
CC ligands to HIV-1 tat, rev and reverse transcriptase were generated by the
CC SILEX combinatorial method. Fusion of the SILEX ligands to the initiator
CC met RNA used for expressing the ligands in CEMs cell lines either had
CC little effect on their affinity (tat7 and rev30A, see AAT36342 and
CC AAT36343, respectively) or reduced it significantly (rtw17, see AAT36344)
XX
XX Sequence 239 BP; 65 A; 61 C; 68 G; 0 T; 45 U; 0 Other;
SQ
Query Match 0.6%; Score 26; DB 2; Length 239;
Best Local Similarity 76.9%; Pred. No. 4.3;
Matches 20; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATATGCACTCACTATAGGAGCTC 48
DB 94 CUAUACGACUCACUAUAGGAGGACUC 119

```

```

XX
XX Zea mays.
XX
XX Key Location/Qualifiers
XX Key 1931..3136
XX CDS /*tag= a
XX
XX MO9964579-A2.
XX
XX 16-DEC-1999.
XX
XX 09-JUN-1999; 99MO-US012884.
XX
XX 11-JUN-1998; 98US-0088987P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Shen JB;
XX
XX WPI; 2000-097535/08.
XX
XX New maize oleosin promoter, used for producing transgenic plants with
XX altered fatty acid composition of the oil, used e.g. in animal feeds.
XX
XX Claim 22; Page 104-106; 108pp; English.
XX
XX This is the nucleotide sequence of corn fad2-1 DNA in plasmid pBN257. The
XX fad2-1 gene codes for corn delta-12 desaturase. A full-length or a
XX portion of the coding region of fad2-1, in antisense or sense
XX orientation, may be used to suppress either fad2-1 or fad2-2 (see
XX AA235178), thereby producing a high oleic acid phenotype in transgenic
XX corn. The invention generally relates to the preparation and use of
XX nucleic acid fragments comprising all, or substantially all, of a corn
XX oleosin promoter (see AA235165-77), a stearyl-ACP desaturase (see
XX AA23284-85) and a delta-12 desaturase, which can be used individually or
XX in combination to modify the lipid profile of corn. Also claimed are
XX seeds of such plants, oil obtained from the grain of such plants, animal
XX feed, use of the oil in food, feed, and cooking oil or industrial
XX applications
XX
XX Sequence 6337 BP; 1486 A; 1655 C; 1569 G; 1627 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 26; DB 3; Length 6337;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATATGCACTCACTATAGGAGCTC 48
DB 6312 CTATATGCACTCACTATAGGAGCTC 6337

```

```

RESULT 33
AA235182
ID AA235182 standard; CDNA; 6337 BP.
XX
XX AA235182;
XX
XX 13-MAR-2000 (first entry)
XX
XX Corn delta-12 desaturase fad2-1 gene in plasmid pBN257.
XX
XX Corn; maize; transgenic plant; lipid; food; feedstuff; vegetable oil;
KM seed oil; oleic acid; fatty acid desaturase; delta-12 desaturase; fad2-1;
KM pBN257; ss.

```

```

RESULT 34
AAD64515
ID AAD64515 standard; DNA; 6337 BP.
XX
XX AAD64515;
XX
XX 12-FEB-2004 (first entry)
XX
XX Plasmid pBN257 DNA.
XX
XX Corn oleosin promoter; food; industry; animal feed; cooking; plant; corn;
KM delta-12 desaturase; fad2-1; cyclic; circular; ds.
XX
XX Zea mays.
XX
XX US2003140372-A1.
XX
XX 24-JUL-2003.
XX
XX 19-AUG-2002; 2002US-00223646.
XX
XX 07-JUN-1999; 99US-00326285.

```

XX (SHEN/) SHEN J B.
 XX Shen JB;
 XX WPI; 2003-851762/79.
 XX New nucleic acid fragment comprising a corn oleosin promoter, or encoding
 PT a corn delta-9-steroyl-ACP desaturase, useful for producing corn plant
 PT that produces oil useful in food, animal feed, cooking and industrial
 PT applications.
 XX Claim 22; SEQ ID NO 58; 80pp; English.
 XX The present invention relates to an isolated nucleic acid fragment
 CC comprising a corn oleosin promoter. The invention is useful for producing
 CC corn plant that produces oil useful in food, animal feed, cooking and
 CC industrial applications. The present sequence is plasmid pBN257 DNA
 CC containing fad2-1 (delta-12 desaturase) gene
 XX
 XX Sequence 6337 BP; 1486 A; 1655 C; 1569 G; 1627 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 26; DB 10; Length 6337;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 23 CTAATACGACTCACTATAGGAGCTC 48
 Db 6312 CTAATACGACTCACTATAGGAGCTC 6337
 RESULT 35
 ACN45188/c
 ID ACN45188 standard; DNA; 96499 BP.
 XX ACN45188;
 AC
 XX 18-NOV-2004 (first entry)
 DT
 XX Mouse genomic sequence MCG9393.
 DE
 XX Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
 XX
 XX Mus musculus.
 OS
 XX MO2003073826-A2.
 PN
 XX 12-SEP-2003.
 PD
 XX 28-FEB-2003; 2003WO-US006235.
 PF
 XX 01-MAR-2002; 2002US-00087192.
 PR
 XX (SAGR-) SAGRES DISCOVERY.
 PA
 XX Morris DW;
 PI
 XX WPI; 2003-328604/31.
 DR
 XX Recombiant nucleic acid useful for diagnosis and treatment of carcinoma
 PT comprises a nucleotide sequence.
 PT
 XX Claim 1; SEQ ID NO 2011; 0pp; English.
 PS
 XX The present invention relates to novel DNA and protein sequences which
 CC are associated with carcinomas. The sequences are useful for: (i) for
 CC screening drug candidates; (ii) for screening of bioactive agent capable
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a bioclip;
 CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for

CC determining Carcinoma Associated (CA) gene copy number. In addition, the
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
 CC carcinoma including lymphoma. The present sequence is one such CA coding
 CC sequence. Note: This patent is an equivalent to basic patent
 CC US2002182586A1, for which no sequence data was published
 XX
 XX Sequence 96499 BP; 25733 A; 19192 C; 19812 G; 28608 T; 0 U; 3154 Other;
 SQ
 Query Match 0.6%; Score 26; DB 11; Length 96499;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3914 ATAAATATAAATAAGTAAAGAAA 3939
 Db 1233 ATAAATATAAATAAGTAAAGAAA 1208
 RESULT 36
 ABD33362/c
 ID ABD33362 standard; DNA; 301477 BP.
 XX ABD33362;
 AC
 XX 18-NOV-2004 (first entry)
 DT
 XX Human cancer-associated (CA) gene HD07-066.
 DE
 XX Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
 KW db; cancer; cytostatic.
 XX
 XX Homo sapiens.
 OS
 XX MO2004058146-A2.
 PN
 XX 15-JUL-2004.
 PD
 XX 15-DEC-2003; 2003WO-US040081.
 PF
 XX 17-DEC-2002; 2002US-00322281.
 PR
 XX (SAGR-) SAGRES DISCOVERY INC.
 PA
 XX Morris DW, Malandro MS;
 PI
 XX WPI; 2004-499109/47.
 DR
 XX Novel human cancer associated protein encoded within open reading frame
 PT of cancer associated gene, useful as targets for diagnosing cancer.
 PT
 XX Claim 16; SEQ ID NO 456; 182pp; English.
 PS
 XX The invention relates to cancer-associated proteins (CAP) and the cancer-
 CC associated (CA) nucleic acids encoding them. The invention also relates
 CC to a method for treating cancers involving administering to a patient an
 CC inhibitor of CAP, and a method of screening for anticancer activity in a
 CC potential drug involving providing a cell that expresses a CA gene,
 CC contacting a tissue sample derived from a cancer cell with an anticancer
 CC drug candidate and monitoring the effect of the anticancer drug candidate
 CC on expression of the CA gene. The CAP proteins are useful for detecting
 CC cancer associated with expression of a CAP protein in a test cell sample
 CC and for screening for a bioactive agent capable of modulating the
 CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
 CC cancer, involving determining the expression of a CA nucleic acid in a
 CC tissue. This sequence represents a human CA gene of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 301477 BP; 82572 A; 54594 C; 57306 G; 97116 T; 0 U; 9889 Other;
 SQ
 Query Match 0.6%; Score 26; DB 13; Length 301477;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAATATAAATAAATATAAAGTAAA 3935
 |||||||
 DB 105296 AAAAATATAAATATAAAGTAAA 105271

RESULT 37
 ADC64226
 ID ADC64226 standard; DNA; 45 BP.
 AC ADC64226;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Identification of gene function method-related PCR primer #2.
 XX
 CC gene function identification; host cell; PCR; primer; ss.
 KW
 XX Unidentified.
 OS
 XX JP2002306183-A.
 PN
 XX 22-OCT-2002.
 PD
 XX 01-JUN-2001; 2001JP-00166101.
 PF
 XX 02-JUN-2000; 2000JP-00165414.
 PR
 XX (MITU) MITSUBISHI CHEM CORP.
 PA
 XX WPI; 2003-397234/38.
 DR
 XX
 PT Identification of gene function by introducing it into a vertebrate cell
 and observing changes in the cell.
 PT
 XX Example 3; SEQ ID NO 2; 12pp; Japanese.
 PS
 XX The invention comprises a method for identifying the function of a target
 CC gene - the method involves introducing the sequence into a host cell and
 CC then analysing the change in character of the cell. The method is used
 CC for identifying the function of a target gene. The present DNA sequence
 CC represents a PCR primer that was used in an example of the invention.
 CC
 SQ Sequence 45 BP; 14 A; 10 C; 9 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGCCTAATACGACTCACTATAGCG 43
 |||||||
 DB 15 TGGCCTAATACGACTCACTATAGCG 39

RESULT 38
 AAV45614
 ID AAV45614 standard; DNA; 47 BP.
 XX
 AC AAV45614;
 XX
 DT 04-MAR-1999 (first entry)
 XX
 DE Primer for Mycobacterium identification.
 XX
 CC PCR primer; probe; acid-fast bacteria; human type tubercular bacillus;
 KW Mycobacterium; detection; identification; ss.
 XX
 OS Synthetic.
 XX Mycobacterium sp.
 XX
 PN JP10323189-A.
 PD 08-DEC-1998.

XX
 PE 23-MAY-1997; 97JP-00133553.
 XX
 PR 23-MAY-1997; 97JP-00133553.
 XX
 PA (TOYM) TOYOBO KK.
 XX
 DR WPI; 1999-088863/08.
 XX
 CC Novel oligonucleotides - useful for the detection and identification of
 PT acid-fast bacteria.
 PS
 XX Claim 5; Page 13; 15pp; Japanese.
 XX
 CC This sequence represents an oligonucleotide of the invention. The
 CC oligonucleotides of the invention are probes and primers used for the
 CC detection of acid-fast bacteria, human type tubercular bacillus, and
 CC specifically for the identification of Mycobacterium intracellulare,
 CC and M. kansasii. The oligonucleotides allow the simple and rapid
 CC detection and identification of acid-fast bacteria
 CC
 SQ Sequence 47 BP; 11 A; 13 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAGCT 47
 |||||||
 DB 5 CTAATACGACTCACTATAGGAGCT 29

RESULT 39
 AAZ44303
 ID AAZ44303 standard; DNA; 47 BP.
 XX
 AC AAZ44303;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE M. tuberculosis 16S rRNA detecting primer 1.
 DE
 XX 16S rRNA; primer; nucleic acid amplification; signal; sensitivity; ss.
 KW
 XX Mycobacterium tuberculosis.
 OS
 XX JP11318473-A.
 PN
 XX 24-NOV-1999.
 PD
 XX 27-JAN-1999; 99JP-00018434.
 PE
 XX 17-MAR-1998; 98JP-00066988.
 PR
 XX (TOYM) TOYOBO KK.
 PA
 XX WPI; 2000-100772/09.
 DR
 XX
 PT A reagent for nucleic acid amplification and a sequence-specific nucleic
 PT acid amplification - used to inhibit nonspecific reactions to improve
 PT sensitivity and signal.
 PT
 XX Disclosure; Page 9; 10pp; Japanese.
 PS
 XX This invention describes a novel reagent for nucleic acid amplification
 CC containing at least one substance selected from BDTA, methylotriacetic
 CC acid, uramidilactic acid, trans-1,2-cyclohexanediaminetetraacetic acid,
 CC diethylenetriaminopentaacetic acid, ethylene glycol bis(2-aminoethyl)
 CC ether diaminetetraacetic acid and triethylenetetraaminohexaacetic acid.
 CC The method can be used to inhibit nonspecific reactions to improve
 CC sensitivity and signal. AAZ44303-244306 represent primers used in the
 CC method of the invention
 CC

SQ Sequence 47 BP; 11 A; 13 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 3; Length 47;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATATGAGCTCACTATAGGAGCT 47
 |||||
 DB 5 CTATATGAGCTCACTATAGGAGCT 29

RESULT 40
 AAF77539
 ID AAF77539 standard; DNA; 47 BP.
 AC AAF77539;
 XX
 XX 23-MAY-2001 (first entry)
 XX
 DE M tuberculosis 16S rRNA gene PCR primer #1.
 XX
 XX Immunological measuring method; antibody; disease diagnosis;
 KW autoimmune disease; cancer; infection; PCR primer; ss.
 XX
 XX Mycobacterium tuberculosis.
 OS
 PN JP2001013139-A.
 XX
 XX 19-JAN-2001.
 PD
 XX 28-JUN-1999; 99JP-00182063.
 PF
 XX 28-JUN-1999; 99JP-00182063.
 PR
 XX (TOYM) TOYOBO KK.
 PA
 XX WPI; 2001-248305/26.
 DR
 XX Immunological chemical component measurement for disease diagnosis;
 PT involves detecting amount of standard nucleic acid in antigen mixed
 PT sample through reaction between nucleic acid and sample at constant
 PT temperature.
 XX
 XX PS Disclosure; Page 5; 6pp; Japanese.
 XX
 CC The present invention describes a method of immunological measuring,
 CC involving reacting an antibody or antigens in a biological sample and
 CC measuring the amount of nucleic acid in the antibody/antigen mixed sample
 CC to recognize the target components of sample. This is useful in the
 CC diagnosis of infections due to bacteria, viruses and parasites. It is
 CC also useful for detecting human leukocyte antigen, hormones,
 CC abnormalities in hormones, cancer, and bacteriotoxin in foodstuff
 CC
 XX
 SQ Sequence 47 BP; 11 A; 13 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 4; Length 47;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATATGAGCTCACTATAGGAGCT 47
 |||||
 DB 5 CTATATGAGCTCACTATAGGAGCT 29

RESULT 41
 AAQ52391
 ID AAQ52391 standard; DNA; 48 BP.
 AC AAQ52391;
 XX
 XX 25-MAR-2003 (revised)
 DT 13-JUN-1994 (first entry)
 XX

DE PCR primer for amplifying template RNA used in selection process.
 XX
 XX ligand; identification; target; selection; amplification; partition;
 KW detection; binding; affinity; herpes simplex virus; HSV; DNA polymerase;
 KW ss.
 XX
 XX Synthetic.
 OS
 PN US5270163-A.
 XX
 XX 14-DEC-1993.
 PD
 XX 17-AUG-1992; 92US-00931473.
 PF
 XX 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 XX
 XX (UYRE-) UNIV RES CORP.
 PA
 XX
 PI Tuerk C, Gold L;
 XX
 XX WPI; 1993-404920/50.
 DR
 XX Identifying nucleic acids which bind target ligands - by partitioning
 PT increased affinity nucleic acids from candidate mixt. and amplifying
 PT these nucleic acids.
 XX
 XX Example 11; Col 52; 129pp; English.
 PS
 XX
 XX A method (SELEX) for identifying nucleic acid ligands which bind target
 CC ligands comprises, contacting a candidate mixture with the target ligand
 CC so that nucleic acids with an increased affinity for the target can be
 CC partitioned from the remainder of the candidate mixture; partitioning the
 CC increased affinity nucleic acids from the remainder of the candidate
 CC mixture and amplifying them. Preferably this procedure is repeated
 CC numerous times to yield a desired level of ligand enrichment. Two primers
 CC (AAQ52390, AAQ52391) were used to amplify the template RNA (AAQ52392)
 CC from which the ligands specific for herpes simplex virus were
 CC synthesised. (updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATATGAGCTCACTATAGGAGCTC 48
 |||||
 DB 9 TATATGAGCTCACTATAGGAGCTC 33

RESULT 42
 AAQ62710
 ID AAQ62710 standard; DNA; 48 BP.
 AC AAQ62710;
 XX
 XX 25-MAR-2003 (revised)
 DT 20-JAN-1995 (first entry)
 XX
 XX Primer for amplification of antibody fragment.
 DE
 XX Amplification; primer; immunoglobulin; light chain; heavy chain; IgG;
 KW gamma; ss.
 KW
 XX Synthetic.
 OS
 PN WO9411507-A2.
 XX
 XX 26-MAY-1994.
 PD
 XX 19-NOV-1993; 93WO-US011295.
 PF
 XX

```

PR 19-NOV-1992; 92US-00978835.
XX
XX (GING/) GINGERAS T R.
PA (KLIN/) KLINMAN N R M D.
PA (STIL/) STILLMAN C A.
PA (LINT/) LINTON P.
PA (DECK/) DECKER D J.
PA (BIER/) BIERER M C.
XX
PI GINGERAS TR, KlInman NRMd, Stillman CA, Linton P, Decker DJ;
PI Biery MC;
XX
XX WPI, 1994-183508/22.
XX
XX Obtaining RNA encoding light- or heavy-chain of antibody having desired
PT specificity - comprising in vitro spleen fragment culture and isothermal
PT self-sustained sequence replication, also recombinant prodn. of the
PT antibody.
XX
XX Disclosure; Fig 2; 66pp; English.
XX
XX This primer was used for the amplification of the coding region of the
CC constant light chain region (CL) of an antibody. It may be used in 3SR
CC reactions (isothermal self sustained sequence replication) It hybridises
CC to the sense strand. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 48 BP; 15 A; 7 C; 14 G; 12 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 TAATACGACTCCTATAGGAGCTC 48
Db 5 TAATACGACTCCTATAGGAGCTC 29
RESULT 43
AA063026
ID AA063026 standard; DNA; 48 BP.
AC
XX AA063026;
XX
XX 25-MAR-2003 (revised)
DT 07-NOV-1994 (first entry)
DE Primer used in SELEX procedure for production of bFGF ligands.
XX
XX Thrombin; coagulation; adhesion; blood clot; clot formation; ligand;
KM binding; SELEX; human immunodeficiency virus; HIV; rev protein;
KM tat protein; basic fibroblast growth factor; bFGF; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Key 10.25
FT Promoter /*tag= A
FT /label= T7 promoter.
XX
XX WO9408050-A1.
XX
XX 14-APR-1994.
XX
XX 28-SEP-1993; 93WO-US009296.
XX
XX 29-SEP-1992; 92US-00953694.
PR 21-OCT-1992; 92US-00964624.
PR 06-NOV-1992; 92US-00973333.
PR 22-APR-1993; 93US-00061691.
XX
XX (NEXA-) NEXAGEN INC.
XX
XX Gold LM, Tuerk C, Tasset D, Janjic N;
PI

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```

XX
XX WPI, 1994-135610/16.
DR
XX
XX Producing target specific nucleic acid ligands - by selection for high
PT affinity then structure determination, esp directed against HIV proteins,
PT thrombin or basic fibroblast growth factor.
XX
XX Example 5; Page 106; 208pp; English.
XX
XX Three oligonucleotides (AA063025-Q63027) were used together in a variable
CC template SELEX procedure (Experiment A) to produce ligands for basic
CC fibroblast growth factor (bFGF). This is a primer used in the procedure.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 TAATACGACTCCTATAGGAGCTC 48
Db 9 TAATACGACTCCTATAGGAGCTC 33
RESULT 44
AA063022
ID AA063022 standard; DNA; 48 BP.
AC
XX AA063022;
XX
XX 25-MAR-2003 (revised)
DT 07-NOV-1994 (first entry)
DE Primer used in SELEX procedure for production of HIV tat ligands.
XX
XX Thrombin; coagulation; adhesion; blood clot; clot formation; ligand;
KM binding; SELEX; human immunodeficiency virus; HIV; rev protein;
KM tat protein; ss.
XX
OS Synthetic.
XX
XX WO9408050-A1.
XX
XX 14-APR-1994.
XX
XX 28-SEP-1993; 93WO-US009296.
XX
XX 29-SEP-1992; 92US-00953694.
PR 21-OCT-1992; 92US-00964624.
PR 06-NOV-1992; 92US-00973333.
PR 22-APR-1993; 93US-00061691.
XX
XX (NEXA-) NEXAGEN INC.
XX
XX Gold LM, Tuerk C, Tasset D, Janjic N;
PI
XX WPI, 1994-135610/16.
XX
XX Producing target specific nucleic acid ligands - by selection for high
PT affinity then structure determination, esp directed against HIV proteins,
PT thrombin or basic fibroblast growth factor.
XX
XX Example 3; Page 91; 208pp; English.
XX
XX Three oligonucleotides (AA063022-Q63024) were used together in a variable
CC template SELEX procedure to produce ligands for the HIV tat protein. This
CC is the 5' primer used in the procedure. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 25; DB 2; Length 48;

```

Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCACTATAGGAGCTC 48
Db 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 45

AAT06077 standard; DNA; 48 BP.

AC AAT06077;

DT 12-AUG-1997 (first entry)

DE Substance P ligand library 5' PCR primer.

XX ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KM Systematic Evolution of Ligands by EXponential enrichment; primer; ss;
KM polymerase chain reaction; structure; mimicry; substance P; tachykinin;
KM neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
KM diabetic retinopathy.

XX Synthetic.

Key Location/Qualifiers
FT promoter 10..25
FT /tag= a
FT /note= "T7 promoter sequence"

PN MO9530775-A1.

PD 16-NOV-1995.

PF 03-MAY-1995; 95WO-US005600.

PP 06-MAY-1994; 94US-00238863.

PR 24-MAY-1994; 94US-00248632.

PR 09-SEP-1994; 94US-00303362.

PR 21-DEC-1994; 94US-00361795.

XX (UYRE-) UNIV RES CORP.

XX Gold L, Nieuwlandt D, Wecker M, Schneider DJ, Feigon J, Allen P;
PI Sullenger BA, Doudna JA;

XX WPI; 1995-404132/51.

PT Systematic evolution of ligands by exponential enrichment - for
PT identifying nucleic acid ligands used in the treatment of, e.g. type B
PT insulin resistance and HIV.

XX Example 6; Fig 8; 209pp; English.

XX The invention relates to a novel method of isolating ligands that bind to
XX target proteins e.g. antibodies or receptors, which bind other proteins
XX or ligands. The method, designated Systematic Evolution of Ligands by
XX exponential enrichment (SELEX), comprises generating a library of random
XX oligonucleotide sequences, about 40-60 nucleotides in length, and binding
XX these sequences to the target proteins. After removal of unbound
XX material, the remaining bound nucleotide sequences are amplified e.g. by
XX PCR, and the newly amplified material is bound again with the target
XX protein. This cycle continues until a sufficiently pure oligonucleotide
XX sequence is isolated. The method allows the isolation of oligonucleotide
XX sequences which structurally mimic the target protein's ligand. The
XX primers AAT06077-8 were used to generate a random oligonucleotide library
XX of length 60 nucleotides to isolate ligands (AAT06081-130) which bind the
XX tachykinin-family neuropeptide Substance P. The ligands can be used to
XX block the activity of Substance P and is useful in the treatment of e.g.
XX rheumatoid arthritis, atherosclerosis, diabetic retinopathy or cancer
XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCACTATAGGAGCTC 48
Db 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 46

AAT73197 standard; DNA; 48 BP.

AC AAT73197;

DT 26-AUG-1997 (first entry)

DE HIV-1 integrase ligand binding library 3' PCR primer.

XX ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KM Systematic Evolution of Ligands by EXponential enrichment; autoimmunity;
KM polymerase chain reaction; structure; mimicry; integrase; primer; ss;
KM human immunodeficiency virus.

XX Synthetic.

Key Location/Qualifiers
FT promoter 8..33
FT /tag= a
FT /note= "T7 promoter sequence"

PN MO9530775-A1.

PD 16-NOV-1995.

PF 03-MAY-1995; 95WO-US005600.

PP 06-MAY-1994; 94US-00238863.

PR 24-MAY-1994; 94US-00248632.

PR 09-SEP-1994; 94US-00303362.

PR 21-DEC-1994; 94US-00361795.

XX (UYRE-) UNIV RES CORP.

XX Gold L, Nieuwlandt D, Wecker M, Schneider DJ, Feigon J, Allen P;
PI Sullenger BA, Doudna JA;

XX WPI; 1995-404132/51.

PT Systematic evolution of ligands by exponential enrichment - for
PT identifying nucleic acid ligands used in the treatment of, e.g. type B
PT insulin resistance and HIV.

XX Example 13; Page 98; 209pp; English.

XX The invention relates to a novel method of isolating ligands that bind to
XX target proteins e.g. antibodies or receptors, which bind other proteins
XX or ligands. The method, designated Systematic Evolution of Ligands by
XX exponential enrichment (SELEX), comprises generating a library of random
XX oligonucleotide sequences, about 40-60 nucleotides in length, and binding
XX these sequences to the target proteins. After removal of unbound
XX material, the remaining bound nucleotide sequences are amplified e.g. by
XX PCR, and the newly amplified material is bound again with the target
XX protein. This cycle continues until a sufficiently pure oligonucleotide
XX sequence is isolated. The method allows the isolation of oligonucleotide
XX sequences which structurally mimic the target protein's ligand. The
XX primers AAT73197-8 were used to generate a random sequence (AAT73196)
XX containing a 30 nucleotide random sequence for generating a random
XX oligonucleotide library to isolate ligands (AAT06139-93) which bind the
XX human immunodeficiency virus type 1 (HIV-1) integrase protein. The
XX ligands can be used to inhibit integrase activity and thus be used to
XX treat HIV-1 infections

```
XX SQ Sequence 48 BP, 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCCTATAGGAGCTC 48
    |||||
DB 9 TAATACGACTCCTATAGGAGCTC 33

RESULT 47
AAQ8306
ID AAQ8306 standard; DNA; 48 BP.
XX
AC AAQ8306;
XX
DT 07-AUG-1996 (first entry)
XX
DE SELEX primer 1 molecule for isolation of bFGF ligands (experiment A).
XX
KM Family 1; family 2; ligand; thrombin;
KM systematic evolution of ligands by exponential enrichment; SELEX;
KM heparin; selection; region of homology; inhibitor; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT promoter 10..25
FT /*tag= a
FT /note= "T7 promoter"
XX
XX WO9521853-A1.
XX
XX 17-AUG-1995.
XX
XX 06-FEB-1995; 95WO-US001458.
XX
XX 10-FEB-1994; 94US-00195005.
XX
XX 28-MAR-1994; 94US-00219012.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Janjic N, Gold L, Taeset D;
XX
XX WPI; 1995-233073/38.
XX
XX Identification of ligands to basic fibroblast growth factor and thrombin
XX - which can be modified for increased in vivo stability.
XX
XX Example 2; Page 69; 236pp; English.
XX
XX The sequences given in AAQ8306-07 are primers which were used in the
XX isolation of ligands to thrombin. The ligands were isolated using
XX systematic evolution of ligands by exponential enrichment (SELEX). DNA
XX templates such as the one in AAQ8305, containing a region of 30 random
XX nucleotides flanked by constant sequence regions, were synthesized. The
XX random region was generated by utilizing an equimolar mixture of the four
XX nucleotides during oligonucleotide synthesis. The constant regions were
XX designed to contain PCR primer annealing sites, allowing cDNA synthesis
XX and containing a T7 RNA promoter region. An initial pool of RNA molecules
XX was prepared by in vitro transcription of the double stranded DNA
XX template. Transcription mixtures were incubated at 37 deg.C for 2-3 hours
XX which resulted in a typical amplification of 10-100 fold. Selection of
XX the high affinity ligands was done by incubating with bFGF for 10 mins a
XX buffer solution at 37 deg. C then separating the protein-RNA complexes by
XX filtration. After 10 rounds of selection, no additional improvement in
XX binding was seen. The experiment was repeated using the sequences given
XX in AAQ8308-10, using heparin as a competitor for binding of randomised
XX RNA to bFGF. The isolated ligands fell into two families, family 1 having
XX a consensus sequence of CTAACGAGG and family two having the consensus
XX sequence given in AAQ8434
```

```
XX SQ Sequence 48 BP, 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCCTATAGGAGCTC 48
    |||||
DB 9 TAATACGACTCCTATAGGAGCTC 33

RESULT 48
AAQ89173
ID AAQ89173 standard; RNA; 48 BP.
XX
AC AAQ89173;
XX
DT 25-MAR-2003 (revised)
XX
DT 16-JAN-1996 (first entry)
XX
DE VEGF RNA binding ligand amplification primer (1).
XX
XX Nucleic acid; ligand; thrombin; elastase; theophylline; caffeine;
XX pharmaceutical; diagnosis; vascular endothelial growth factor; VEGF;
XX gene therapy; RNA; DNA; ss.
XX
XX Synthetic.
XX
XX WO9507364-A1.
XX
XX 16-MAR-1995.
XX
XX 08-SEP-1994; 94WO-US010306.
XX
XX 08-SEP-1993; 93US-00117991.
XX
XX 07-OCT-1993; 93US-00134028.
XX
XX 22-FEB-1994; 94US-00195507.
XX
XX 25-APR-1994; 94US-00233012.
XX
XX 28-APR-1994; 94US-00234997.
XX
XX (NEXA-) NEXAGEN INC.
XX
XX Gold L, Pieken W, Taeset D, Janjic N, Kirschenheuter GP;
XX Polisky B, Jayasena S, Biessecker G, Smith D, Jenison RD;
XX
XX WPI; 1995-123436/16.
XX
XX Identifying nucleic acid ligands for target molecules - by partitioning
XX increased affinity nucleic acids from a candidate mixt. and amplifying.
XX
XX Example 12; Fig 26; 251pp; English.
XX
XX The sequences given in AAQ89173-74 are primers which were used to amplify
XX the target sequence given in AAQ89172. The amplified sequences represent
XX vascular endothelial growth factor (VEGF) RNA ligands (see also AAQ88982-
XX AAQ89965). The amplified ligand sequences were identified using the
XX method of the invention. This method comprises contacting a candidate
XX mixture with the target molecule (i.e. VEGF) where the nucleic acids
XX which have an increased affinity to the target relative to the candidate
XX mixture can be partitioned from the remainder of the candidate mixture.
XX The increased affinity nucleic acids are partitioned from the remainder
XX of a candidate mixture and the isolated nucleic acids are amplified to
XX yield a ligand-enriched mixture of nucleic acids, in which the nucleic
XX acid ligands can be identified. The isolated ligands may be used as
XX pharmaceuticals, diagnostic agents and in gene therapy. The ligands may
XX be RNA or DNA molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 48 BP, 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 24 TATACGACTACTATAGGAGCTC 48
 DB 9 TATACGACTACTATAGGAGCTC 33

RESULT 49

AAQ89176
 ID AAQ89176 standard; RNA; 48 BP.

AC AAQ89176;

DT 25-MAR-2003 (revised)

DT 16-JUN-1996 (first entry)

DE VEGF RNA binding ligand amplification primer, 5G1.

XX Nucleic acid; ligand; thrombin; elastase; theophylline; caffeine;

KM pharmaceutical; diagnosis; vascular endothelial growth factor; VEGF;

KM gene therapy; RNA; DNA; ss.

XX Synthetic.

OS WO9507364-A1.

PN 16-MAR-1995.

PD 08-SEP-1994; 94MO-US010306.

PF 08-SEP-1994; 94US-00117991.

XX 07-OCT-1993; 93US-00134028.

PR 22-FEB-1994; 94US-00199507.

PR 25-APR-1994; 94US-00233012.

PR 28-APR-1994; 94US-00234997.

XX (NEKA-) NEXAGEN INC.

XX Gold L, Pleken W, Tasset D, Janjic N, Kirschenhuter GP;

PI Polisky B, Jayasena S, Biesecker G, Smith D, Jentson RD;

XX WPI; 1995-123436/16.

XX Identifying nucleic acid ligands for target molecules - by partitioning

PT increased affinity nucleic acids from a candidate mixt. and amplifying.

XX Example 12; Fig 46; 251p; English.

XX The sequences given in AAQ89176-77 are primers which were used to amplify

CC the target sequence given in AAQ89175. The amplified sequences represent

CC vascular endothelial growth factor (VEGF) RNA ligands (see also AAQ8982-

CC AAQ89065). The amplified ligand sequences were identified using the

CC method of the invention. This method comprises contacting a candidate

CC mixture with the target molecule (i.e. VEGF) where the nucleic acids

CC which have an increased affinity to the target relative to the candidate

CC mixture can be partitioned from the remainder of the candidate mixture.

CC The increased affinity nucleic acids are partitioned from the remainder

CC of the candidate mixture and the isolated nucleic acids are amplified to

CC yield a ligand-enriched mixture of nucleic acids, in which the nucleic

CC acid ligands can be identified. The isolated ligands may be used as

CC pharmaceutical, diagnostic agents and in gene therapy. The ligands may

CC be RNA or DNA molecules. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

QY Query Match 0.6%; Score 25; DB 2; Length 48;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTACTATAGGAGCTC 48

DB 9 TATACGACTACTATAGGAGCTC 33

RESULT 50

AAT07688
 ID AAT07688 standard; cDNA; 48 BP.

AC AAT07688;

DT 25-MAR-2003 (revised)

DT 15-JUL-1996 (first entry)

DE Amplification primer #2 for SELEX of HSV-1 DNA polymerase.

XX DNA polymerase; gp43; ligand; cell sorting; inhibitor; probe; primer;

KM systematic evolution of ligands by exponential enrichment; SELEX; PCR;

KM bacteriophage coat protein; serine protease; mammalian receptor; amplify;

KM mammalian hormone; mammalian growth factor; ribosomal protein; T7;

XX viral rev protein; polymerase chain reaction; HSV-1; ss.

XX Synthetic.

OS US5475096-A.

PN 12-DEC-1995.

PF 10-JUN-1991; 91US-00714131.

XX 11-JUN-1990; 90US-00536428.

XX (UYRE-) UNITV RES CORP.

XX Tuerk C, Gold L;

PI WPI; 1996-039557/04.

XX Artificial nucleic acid ligands - for selected target proteins.

XX Example 11; Col 49; 133p; English.

XX This sequence represents an amplification primer used as the PCR primer 2

CC in a systematic evolution of ligands by exponential enrichment (SELEX)

CC reaction on HSV-1 DNA polymerase. This sequence amplifies a portion of

CC the T7 RNA polymerase promoter. The primer represented by AAT07687 is

CC also used in this reaction. In a SELEX reaction, a target molecule (such

CC as T7 RNA polymerase) is contacted with a mixture of random nucleic acids

CC under conditions favourable for binding. Unbound nucleic acids are then

CC separated from those bound to the target, and the nucleic acid-target

CC pairs are dissociated. The dissociated nucleic acids are amplified (using

CC a primer such as this) to give a ligand enriched mixture. These steps are

CC repeated until the specific ligand is obtained. This procedure can also

CC be carried out for ligands for bacteriophage coat proteins, serine

CC proteases, mammalian receptors, mammalian hormones, mammalian growth

CC factors, ribosomal proteins, DNA polymerases and viral rev proteins. The

CC ligands identified (such as the sequences represented by AAT07653-T07660)

CC may be used in assays, diagnostic procedures, or cell sorting as an

CC inhibitor of the target molecule function. It may also be used as a probe

CC or sequestering agent, and also possess catalytic activity. (Updated on

XX 25-MAR-2003 to correct PF field.)

XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

QY Query Match 0.6%; Score 25; DB 2; Length 48;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTACTATAGGAGCTC 48

DB 9 TATACGACTACTATAGGAGCTC 33

RESULT 51

AAT84603
 ID AAT84603 standard; DNA; 48 BP.

XX AAT84603;

XX 25-MAR-2003 (revised)
 DT 17-DEC-1997 (first entry)
 XX
 XX RNA ligand to HIV-1 nucleocapsid 3' PCR primer.
 DE
 XX
 XX Human immunodeficiency virus type 1; HIV-1; nucleocapsid; RNA ligand;
 KM inhibitor; SELEX; therapy; diagnosis; primer; PCR;
 KM polymerase chain reaction; ss.
 XX
 XX Synthetic.
 OS
 XX US5654151-A.
 PN
 XX 05-AUG-1997.
 PD
 XX 07-JUN-1995; 95US-00477530.
 PF
 XX 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 PR 17-AUG-1992; 92US-00931473.
 PR 21-OCT-1992; 92US-00964624.
 PR 08-SEP-1993; 93US-00117991.
 PR 21-DEC-1994; 94US-00361795.
 PR 19-MAY-1995; 95US-00447172.
 XX
 XX (NEXS-) NEXSTAR PHARM INC.
 PA
 XX Gold L, Allen PN;
 PI
 XX WPI; 1997-401842/37.
 DR
 XX
 XX Identifying nucleic acid ligands specific for viral nucleocapsid by the
 PT SELEX method - particularly to identify high affinity ligands for human
 PT immunodeficiency virus nucleocapsid, potentially useful as diagnostic and
 PT therapeutic agents.
 PS
 XX Example 1; Col 21-22; 17pp; English.
 XX
 XX This sequence comprises a 3' PCR primer for a random pool of 10 power 14
 CC DNA oligomers (see AAT84602). It includes a 5' HindIII site and a T7
 CC promoter sequence. A 5' primer (AAT84604) is also provided. Oligomers in
 CC the random pool have 5' and 3' proximal ends of fixed sequence to allow
 CC PCR amplification, while the central region consists of 30 randomized
 CC positions. They are used in a SELEX (Systematic Evolution of Ligands by
 CC Exponential enrichment) method to select RNA ligands (see AAT84605-26) to
 CC HIV-1 nucleocapsid. The method involves contacting the oligomers with HIV
 CC -1 nucleocapsid, partitioning nucleic acids of relatively high affinity
 CC and specificity, and amplifying these nucleic acids. The isolated RNA
 CC ligands are inhibitors of HIV-1 nucleocapsid and are potentially useful
 CC as diagnostic and therapeutic agents. (Updated on 25-MAR-2003 to correct
 CC PF field.)
 CC
 XX
 SO Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 24 TAATACGACTCAGCTATAGGAGCTC 48
 Db 9 TAATACGACTCAGCTATAGGAGCTC 33
 RESULT 52
 AAT79124
 ID AAT79124 standard; DNA; 48 BP.
 XX
 XX AAT79124;
 AC
 XX
 XX 25-MAR-2003 (revised)
 DT 07-OCT-1997 (first entry)
 XX

DE 3' primer for SELEX template for HIV-1 nucleocapsid ligands.
 XX
 XX Human immunodeficiency virus; HIV; nucleocapsid; SELEX; infection;
 KM inhibit; ss.
 KM
 XX
 XX Synthetic.
 OS
 XX US5635615-A.
 PN
 XX 03-JUN-1997.
 PD
 XX 07-JUN-1995; 95US-00477530.
 PF
 XX 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 PR 17-AUG-1992; 92US-00931473.
 PR 21-OCT-1992; 92US-00964624.
 PR 08-SEP-1993; 93US-00117991.
 PR 21-DEC-1994; 94US-00361795.
 PR 19-MAY-1995; 95US-00447172.
 XX
 XX (NEXS-) NEXSTAR PHARM INC.
 PA
 XX Gold L, Allen P;
 PI
 XX WPI; 1997-309884/28.
 DR
 XX
 XX Nucleic acids that are HIV-1 nucleocapsid ligands - for treatment of
 PT diagnosis or HIV-1 infection.
 PT
 XX
 XX Example 1; Col 19-20; 17pp; English.
 PS
 XX
 XX AAT79124 and AAT79125 are PCR primers used for the amplification of a
 CC SELEX template molecule having a stretch of 40 randomized nucleotides.
 CC The template was used for the production of nucleic acid (especially RNA)
 CC ligands for the nucleocapsid of human immunodeficiency virus type 1 (HIV-
 CC 1). The ligands bind the nucleocapsid and inhibit its function; they can
 CC be used in the treatment and diagnosis of HIV-1 infection. (Updated on 25
 CC -MAR-2003 to correct PF field.)
 CC
 XX
 SO Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 24 TAATACGACTCAGCTATAGGAGCTC 48
 Db 9 TAATACGACTCAGCTATAGGAGCTC 33
 RESULT 53
 AAT87307
 ID AAT87307 standard; DNA; 48 BP.
 XX
 XX AAT87307;
 AC
 XX
 XX 24-NOV-1997 (first entry)
 DT
 XX
 XX SELEX PCR primer 2 for hTNF-alpha ligand amplification.
 DE
 XX
 XX high affinity ligand; cytokine; interferon-gamma; IFN-gamma; RANTES;
 KM interleukin-4; IL-4; tumour necrosis factor-alpha; TNF-alpha;
 KM Systematic Evolution of Ligands by Exponential enrichment; SELEX;
 KM diagnosis; inflammatory response; septic shock; arthritis;
 KM graft-vs-host reaction; primer; PCR; amplify; ss.
 XX
 XX Synthetic.
 OS
 XX WO9640717-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX

PF 04-JUN-1996; 96MO-US009537.
 XX
 PR 07-JUN-1995; 95US-00477527.
 PR 07-JUN-1995; 95US-00481710.
 XX
 PA (NEXS-) NEXSTAR PHARM INC.
 PI
 XX Tasseet D, Pagratia N, Jayasena S, Gold L;
 XX WPI; 1997-087049/08.
 DR
 XX
 PT Identification of nucleic acid ligands that bind cytokine(s) - by
 PT partitioning the ligands from a nucleic acid mixture, using SELEX
 PT techniques.
 XX
 PS Example 7; Page 73; 175pp; English.
 XX
 CC AAT87306-07 are primers used to begin a new round of SELEX (Systematic
 CC Evolution of Ligands by Exponential enrichment) used to evolve high
 CC affinity ligands to human tumour necrosis factor (hTNF)-alpha (using
 CC AAT87305 as a template). Nucleic acid (NA) ligands to a cytokine can be
 CC identified using SELEX. A candidate mixture of NA's are contacted with a
 CC cytokine where the NA's having an increased affinity to the cytokine
 CC relative to the candidate mixture may be partitioned from the rest of the
 CC mixture. The NA's with increased affinity are amplified to yield a
 CC mixture of NA's enriched for the NA sequences and relatively higher
 CC affinity and selectivity for binding to the cytokine. The NA ligands are
 CC useful in diagnostic and therapeutic applications especially to prevent
 CC or treat diseases or medical conditions in human patients, e.g.
 CC associated with excessive cytokine production such as inflammatory
 CC responses mediated by IFN-gamma or interleukin-4, septic shock, arthritis
 CC or graft-vs-host reactions mediated by hTNF-alpha
 XX
 SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
 DB 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 54

AAV00777
 ID AAV00777 standard; DNA; 48 BP.

AC AAV00777;

DT 25-MAR-1998 (first entry)

DE PCR primer #2 for isolating SELEX ligands to HSV-1 DNA polymerase.

XX Systematic evolution of ligands by exponential enrichment; SELEX;
 KM binding affinity; diagnosis; inhibitor; probe; catalytic; template;
 KM herpes simplex virus type 1; HSV1; DNA polymerase; ss.

XX Synthetic.

OS Herpes simplex virus type 1.

PN US5670637-A.

PD 23-SEP-1997.

PF 27-MAR-1995; 95US-00412110.

PR 11-JUN-1990; 90US-00536428.

PR 10-JUN-1991; 91US-00714131.

XX (NEXS-) NEXSTAR PHARM INC.

PA Tuerk C, Gold L;

XX
 PI

XX WPI; 1997-479527/44.
 DR
 XX
 PT Nucleic acid ligands for binding proteins - obtained by systematic
 PT evolution of ligands by exponential enrichment procedures.
 XX
 PS Example 11; Col 49; 133pp; English.

CC This primer was used to primer cDNA synthesis for generating the template
 CC AAV00778 for use in a SELEX method to isolate nucleic acid ligands that
 CC bind the herpes simplex virus type 1 DNA polymerase. The ligands are
 CC isolated by the systematic evolution of ligands by exponential enrichment
 CC (SELEX) method of the invention. This method is especially used to
 CC isolate novel non-naturally occurring nucleic acid ligands having a
 CC specific binding affinity for a target molecule, where the target
 CC molecule is a protein and the nucleic acid ligand is not a nucleic acid
 CC known to bind the target molecule. The nucleic acid ligands can be used,
 CC e.g. in assay methods, diagnostic procedures, cell sorting, as inhibitors
 CC of target molecule function, as probes, as sequestering agents, for
 CC therapy or as catalysts

SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
 DB 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 55

AAV14558
 ID AAV14558 standard; cDNA; 48 BP.

AC AAV14558;

DT 21-MAY-1998 (first entry)

DE Primer for HSV-1 DNA polymerase.

XX High affinity RNA ligand motif; polymer binding; cell sorting; inhibitor;
 KM sequestering agent; HSV-1 DNA polymerase; PCR primer; amplify; ss.

XX Synthetic.

OS Herpes simplex virus unknown type.

PN US5696249-A.

PD 09-DEC-1997.

PF 24-MAR-1995; 95US-00409442.

PR 11-JUN-1990; 90US-00536428.

PR 10-JUN-1991; 91US-00714131.

XX (NEXS-) NEXSTAR PHARM INC.

PA Tuerk C, Gold L;

DR WPI; 1998-041356/04.

PT Synthetic nucleic acid ligands - that bind to target molecules other than
 PT nucleic acids.

PS Example 11; Col 48; 137pp; English.

CC This sequence represents a primer for the herpes simplex virus 1 (HSV-1)
 CC DNA polymerase. The amplified sequence is used to identify ligands of the
 CC invention. The ligands are non-naturally occurring nucleic acid ligand
 CC with specific binding affinity for a target molecule, where: the target
 CC molecule is not a polynucleotide that binds to the ligand by Watson-Crick

CC base pairing or triple helix binding; the ligand is not a nucleic acid
 CC having the known physiological function of being bound by the target
 CC molecule; and the ligand is obtained by: (a) contacting the target
 CC molecule with a candidate mixture of nucleic acids, each having a region
 CC of randomised sequence; (b) separating the nucleic acids having the
 CC highest affinity for the target; and (c) amplifying the separated nucleic
 CC acids. Ligands as above that bind to natural or synthetic polymers, e.g.
 CC proteins, polysaccharides, glycoproteins, hormones, receptors, cell
 CC surfaces, drugs, metabolites, cofactors, transition-state analogues or
 CC toxins, may be useful in assays, diagnostic procedures or cell sorting,
 CC as inhibitors of target molecule function, as probes, as sequestering
 CC agents, etc., or may have catalytic activity

XX
 SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCCTATAGGAGCTC 48
 |||||
 9 TAATACGACTCCTATAGGAGCTC 33

Db

RESULT 56
 AAV79637
 ID AAV79637 standard; DNA; 48 BP.
 XX
 AC AAV79637;
 XX
 DT 24-FEB-1999 (first entry)
 XX
 DE HSV-1 DNA polymerase cDNA amplifying primer 1.
 XX
 KM Target molecule; detection; measuring; high-affinity; ligand; SELEX;
 KM systematic evolution of ligands by exponential enrichment; assay;
 KM diagnostic; cell sorting; metabolite; HSV-1; DNA polymerase; RNA ligand;
 KM PCR primer; ss.
 XX
 OS Synthetic.
 OS Herpes simplex virus unknown type.
 XX
 PN US6843653-A.
 XX
 PD 01-DEC-1998.
 XX
 PF 06-JUN-1995; 95US-00469609.
 XX
 PR 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 XX
 PA (NEXS-) NEXSTAR PHARM INC.
 XX
 PI Tuerk C, Gold L;
 XX
 DR WPI; 1999-044566/04.
 XX
 PT Detection of target molecule - by detecting binding of nucleic acid
 PT ligand.
 XX
 PS Example 11; Col 48; 138bp; English.
 XX
 CC The invention provides methods for detecting the presence or absence of a
 CC target molecule in a sample and measuring the amount of a target molecule
 CC using high-affinity nucleic acid ligands. The nucleic acid ligands are
 CC identified by the method of the invention referred to as the systemic
 CC evolution of ligands by exponential enrichment (SELEX). The nucleic acid
 CC products are useful in assay methods, diagnostic procedures, cell
 CC sorting, as inhibitors of target molecule function etc. The methods are
 CC used to detect or determine the amount of a protein, small molecule,
 CC controlled substance or metabolite in a biological sample. The present
 CC sequence represents a primer used for amplifying the cDNA encoding a
 CC Herpes simplex virus (HSV-1) DNA polymerase. This is used in the isolation

CC of RNA ligands for HSV-1 DNA polymerase by the method of the invention

XX
 SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCCTATAGGAGCTC 48
 |||||
 9 TAATACGACTCCTATAGGAGCTC 33

Db

RESULT 57
 AAA92737
 ID AAA92737 standard; DNA; 48 BP.
 XX
 AC AAA92737;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE HSV-1 DNA polymerase PCR primer # 2.
 XX
 KM Nucleic acid ligand; assay method; diagnostic procedure; cell sorting;
 KM inhibitor; probe; sequestering agent; PCR primer; ss.
 XX
 OS Herpes simplex virus unknown type.
 XX
 PN US6110900-A.
 XX
 PD 29-AUG-2000.
 XX
 PF 27-AUG-1998; 98US-00143190.
 XX
 PR 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 PR 24-MAR-1995; 95US-00409442.
 PR 27-MAR-1995; 95US-00412110.
 PR 25-APR-1995; 95US-00428964.
 PR 06-JUN-1995; 95US-00469609.
 XX
 PA (NEXS-) NEXSTAR PHARM INC.
 XX
 PI Gold L, Tuerk C;
 XX
 DR WPI; 2000-571430/53.
 XX
 PT Diagnostic composition comprising a nucleic acid ligand useful in binding
 PT reaction e.g. assay methods, diagnostic procedures, cell sorting,
 PT inhibitors of target molecule function, as probes, as sequestering
 PT agents.
 XX
 PS Example 10; Col 49; 138bp; English.
 XX
 CC The present invention relates to a diagnostic composition comprising a
 CC nucleic acid ligand. The present sequence is a PCR primer for
 CC bacteriophage T7 RNA polymerase. The ligands of the present invention are
 CC identified from a candidate mixture of nucleic acids by contacting the
 CC candidate mixture with the target molecule; partitioning increased
 CC affinity nucleic acids from the remainder of the candidate mixture; and
 CC amplifying the increased affinity nucleic acids to yield a ligand.
 CC enriched mixture of nucleic acids. The ligands of the present invention
 CC are useful for detecting a target molecule in a sample, and also in any
 CC binding reaction such as assay methods, diagnostic procedures, cell
 CC sorting, inhibitors of target molecule function, as probes, and as
 CC sequestering agents. The present sequence was used in the isolation of
 CC ligands of the present invention

XX
 SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 3; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
 |||||
 Db 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 58
 AAF70540
 ID AAF70540 standard; DNA; 48 BP.
 XX
 AC AAF70540;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE SELEX experiment oligonucleotide #2.
 XX
 KW Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;
 KM atherosclerosis; angioplasty; stability; ss.
 XX
 OS Unidentified.
 XX
 PN US6177557-B1.
 XX
 PD 23-JAN-2001.
 XX
 PF 05-AUG-1996; 96US-00687421.
 XX
 PR 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 PR 06-NOV-1992; 92US-00973333.
 PR 10-FEB-1994; 94US-00195005.
 PR 28-MAR-1994; 94US-00219012.
 XX
 PA (NEXS-) NEXSTAR PHARM INC.
 XX
 PI Janjic N, Gold L, Tasset D;
 XX
 XX WPI; 2001-158583/16.
 DR
 XX
 PT Novel nucleic acid ligands to basic fibroblast growth factor that are
 PT useful as inhibitors of basic fibroblast growth factors and 2'-amino
 PT modified RNA ligands, exhibit increased in vivo stability.
 XX
 PS Example 19; Col 36; 153pp; English.
 XX
 CC The present invention relates to a purified and isolated non-naturally
 CC occurring DNA ligands to basic fibroblast growth factor (bFGF). The
 CC ligands are useful as part of gene therapy treatments and for diagnosing
 CC pathogenesis of vascular diseases including initiation and progression of
 CC atherosclerosis, acute coronary syndromes, vein graft disease and
 CC restenosis following coronary angioplasty. The ligands have improved
 CC stability in vivo
 CC
 XX
 SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
 XX

Query Match 0.6%; Score 25; DB 4; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
 |||||
 Db 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 59
 AAD44075
 ID AAD44075 standard; DNA; 48 BP.
 XX
 AC AAD44075;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 XX PCR primer #1a used to illustrate the method of the invention.
 DE

XX
 KM Target compound; detector molecule; food; environmental; effluent sample;
 KM water; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN US2002051974-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 24-NOV-1999; 99US-00449204.
 XX
 PR 30-NOV-1998; 98US-0110259P.
 XX
 PA (DODG/) DODGE A H.
 PA (MENG/) MENG Y G.
 PA (SIMS/) SIMS P W.
 PA (SINI/) SINICROPI D V.
 PA (WILL/) WILLIAMS P M.
 PA (WONG/) WONG W L.
 XX
 PI Dodge AH, Meng YG, Sims PW, Sinicropi DV, Williams PM, Wong WL;
 XX
 DR WPI; 2002-453890/48.
 XX
 PT Method for quantitating or detecting the presence of a target compound in
 PT a sample using a nucleic acid detector molecule useful for detecting
 PT target compounds in clinical diagnosis.
 XX
 PS Example 1; Page 13; 37pp; English.
 XX
 CC The invention relates to a method for quantitating or detecting the
 CC presence of a target compound in a sample comprising a nucleic acid
 CC detector molecule, amplification and quantitation of detection of the
 CC detector molecule. The methods are useful for the detection of target
 CC compounds in clinical diagnosis of physiological conditions in the same
 CC way as ELISA, immuno-PCR and ELONA. The methods may also be used to
 CC detect the presence of a target compound in food, environmental, water
 CC and effluent samples. The present sequence is a PCR primer used to
 CC illustrate the method of the invention
 CC
 XX
 SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
 XX

Query Match 0.6%; Score 25; DB 6; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
 |||||
 Db 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 60
 ABK61113
 ID ABK61113 standard; DNA; 48 BP.
 XX
 AC ABK61113;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE SELEX process primer sequence #3.
 XX
 KW SELEX; systematic evolution of ligands by exponential enrichment; ss;
 KM endocrine; hormone reaction modifier; primer.
 XX
 OS Synthetic.
 XX
 PN US6331398-B1.
 XX
 PD 18-DEC-2001.
 XX
 PF 10-FEB-2000; 2000US-00502344.
 XX

PR 11-JUN-1990; 90US-00536428.
PR 25-APR-1995; 95US-00428964.
PR 06-JUN-1995; 95US-00469609.
PR 27-AUG-1998; 98US-00143190.
PA (GILE-) GILEAD SCI INC.
XX
XX
PI Gold L, Tuerk C;
XX
XX WPI; 2002-113091/15.
DR
XX
XX
PT Identifying a function-modifying nucleic acid ligand, useful in
PT diagnostic assays and inhibiting biological function of a target
PT molecule, comprises contacting with target molecule and evaluating
PT whether the ligand modifies the target.
XX
XX
PS Example 11; Col 47; 137pp; English.
XX
XX The invention relates to nucleic acid ligands which bind specifically to
CC a desired target compound or molecule. A function-modifying nucleic acid
CC ligand can be identified by contacting a candidate nucleic acid ligand
CC with the target molecule and evaluating whether the ligand modifies the
CC function of the target molecule. The nucleic acid ligands each have a
CC unique sequence and the property of binding specifically to a desired
CC target compound or molecule. The method, also known as the SELEX method
CC (systematic evolution of ligands by exponential enrichment), can be used
CC to detect proteins which are not known to bind nucleic acids as part of
CC their biological function, meaning that the ligands can be employed in a
CC manner similar to conventional antibody- based diagnostics. The ligands
CC identified are useful as diagnostic assay reagents and have therapeutic
CC uses as sequestering agents, drug delivery vehicles and modifiers of
CC hormone reactions. This sequence represents a primer used in the scope of
CC the invention
XX
SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 24 TAATACGACTCACTATAGGAGCTC 48
Db 9 TAATACGACTCACTATAGGAGCTC 33
XX
RESULT 61
ADP67501
XX ADF67501 standard; DNA; 48 BP.
XX
AC ADF67501;
XX
DT 12-FEB-2004 (first entry)
XX
DE SELEX cDNA synthesis PCR primer 2.
XX
XX
XX ss; SELEX; systematic evolution of ligands by exponential enrichment;
KM ligand; diagnostic agent; cell sorting; inhibitor; probe;
KM sequestering agent.
XX
XX
OS Synthetic.
XX
XX US2003157487-A1.
PN
XX
PD 21-AUG-2003.
XX
PF 18-OCT-2001; 2001US-00037986.
XX
XX
PR 11-JUN-1990; 90US-00536428.
PR 10-JUN-1991; 91US-00714131.
PR 24-MAR-1995; 95US-00409442.
PR 27-MAR-1995; 95US-00412110.
PR 25-APR-1995; 95US-00428964.
PR 06-JUN-1995; 95US-00469609.
PR 27-AUG-1998; 98US-00143190.
PR 10-FEB-2000; 2000US-00469609.

PR 27-AUG-1998; 98US-00143190.
PR 10-FEB-2000; 2000US-00502344.
XX
XX (GOLD/) GOLD L.
PA (TUERK/) TUERK C.
XX
XX
PI Gold L, Tuerk C;
XX
XX WPI; 2003-897816/82.
DR
XX
XX
PT Composition useful as a diagnostic agent for detecting the presence or
PT absence of a target molecule in a sample comprises nucleic acid ligands.
XX
XX
PS Example 11; SEQ ID NO 37; 138pp; English.
XX
XX The invention relates to a composition comprising nucleic acid ligands,
CC typically an RNA molecule selected using the technique of SELEX
CC (systematic evolution of ligands by exponential enrichment). The
CC composition is used as a diagnostic agent for detecting the presence or
CC absence of target molecules (e.g. natural and synthetic polymers
CC including proteins, polysaccharides, glycoproteins, hormones, receptors
CC and cell surfases), and small molecules in a sample, as a diagnostic
CC agent to measure the amount of a target molecule in a sample, in assay
CC methods, cell sorting, as inhibitors of target molecule function, as
CC probes and sequestering agents. The nucleic acids have capacity for
CC forming a variety of two and three dimensional structures and chemical
CC versatility available within their monomers to act as ligands with
CC virtually any chemical compound, whether monomeric or polymeric. The
CC nucleic acids possess unique sequences, which help the nucleic acids to
CC specifically bind to a desired target compound or molecule. The present
CC sequence is an oligonucleotide used in the construction of a SELEX
CC library or starting sequence.
XX
XX
SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.6%; Score 25; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 24 TAATACGACTCACTATAGGAGCTC 48
Db 9 TAATACGACTCACTATAGGAGCTC 33
XX
RESULT 62
ADG39049
XX ADG39049 standard; DNA; 48 BP.
XX
AC ADG39049;
XX
DT 26-FEB-2004 (first entry)
XX
DE cDNA primer #3.
XX
XX
XX ss; SELEX; systematic evolution of ligands by exponential enrichment;
KM cell sorting; unique sequence specificity; unique binding specificity;
KM PCR; primer.
XX
XX
OS Synthetic.
XX
XX US2003198989-A1.
PN
XX
PD 23-OCT-2003.
XX
PF 03-APR-2003; 2003US-00408085.
XX
XX
PR 11-JUN-1990; 90US-00536428.
PR 24-MAR-1995; 95US-00409442.
PR 27-MAR-1995; 95US-00412110.
PR 25-APR-1995; 95US-00428964.
PR 06-JUN-1995; 95US-00469609.
PR 27-AUG-1998; 98US-00143190.
PR 10-FEB-2000; 2000US-00502344.

```
PR 18-OCT-2001; 2001US-00037986.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Gold L, Tuerk C;
XX
XX WPI; 2004-059537/06.
XX
PT Diagnostic composition useful for detecting the presence or absence of a
PT target molecule comprises a nucleic acid ligand.
XX
PS Example 11; SEQ ID NO 37; 149bp; English.
XX
CC The invention relates to a diagnostic composition which comprises a
CC nucleic acid ligand. The invention is useful for detecting the presence
CC or absence of a target molecule and as diagnostic reagent to measure the
CC amount of target molecule in a sample; in assay method, diagnostic
CC procedures, cell sorting, as inhibitors of target molecule function, as
CC probes and as sequencing agent. The nucleic acids in the composition
CC have unique sequences and binding specificities; capacity for forming a
CC variety of 2- or 3-dimensional structures; chemical versatility within
CC their monomers; and broad range of functions of the nucleic acid ligands.
CC The composition has ability of binding specifically to a desired target
CC molecule or compound facilitating qualitative and quantitative detection.
CC The present sequence is used in the exemplification of the invention.
XX
SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 12; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
DB 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 63
ABL88785
ID ABL88785 standard; DNA; 59 BP.
XX
XX ABL88785;
XX
DT 22-MAY-2002 (first entry)
XX
DE HIV-1 reverse transcriptase primer 3' ET21-T7 SEQ ID NO:7.
XX
XX Binding molecule; HIV-1; human immunodeficiency virus type 1;
XX reverse transcriptase; binding group; PCR primer; ss.
XX
XX Human immunodeficiency virus 1.
XX Synthetic.
XX
XX EP1174518-A1.
XX
XX 23-JAN-2002.
XX
XX 20-JUL-2000; 2000EP-00202611.
XX
XX 20-JUL-2000; 2000EP-00202611.
XX
XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
XX Loukachov VV, Van Gemen B, Goudsmit J;
XX
XX WPI; 2002-156696/21.
XX
XX Collection of binding groups for determining or typing samples,
XX especially clinical samples, has groups capable to identify essentially
XX all members of the family of nucleic acids of relatively high
XX significance.
XX
XX Example 5; Page 6; 166pp; English.
```

```
XX
XX The present invention describes a collection of binding groups for a
XX family of nucleic acids comprising members of relative high and relative
XX low significance, where the binding groups are selected to be capable to
XX identify, alone or in combination, essentially all members of the family
XX of nucleic acids of relatively high significance. The collection of
XX binding groups is useful for typing of nucleic acid in a clinical sample,
XX by contacting the nucleic acid with the collection and determining
XX whether one or more binding groups bound to the nucleic acid of the
XX sample. This method is useful for determining whether the sample
XX comprises at least a part of a member of relatively high significance of
XX a family of nucleic acids. The collection of binding groups is useful for
XX diagnosing the severity of a disease caused by a pathogen containing a
XX member of a family of nucleic acids. ABL88779 to ABL89321 represent
XX oligonucleotide sequences used in the exemplification of the present
XX invention
XX
SQ Sequence 59 BP; 15 A; 12 C; 12 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATACGACTCACTATAGGAGCT 47
DB 5 CTATACGACTCACTATAGGAGCT 29

RESULT 64
ABL41041
ID ABL41041 standard; DNA; 59 BP.
XX
XX ABL41041;
XX
DT 12-AUG-2002 (first entry)
XX
XX GUS mRNA UTR fragment amplifying primer 7.
XX
XX Translation; untranslated region; UTR; pathogen; virus; GUS; PCR; primer;
XX ss.
XX Synthetic.
XX
XX JP2002095483-A.
XX
XX 02-APR-2002.
XX
XX 25-SEP-2000; 2000JP-00291084.
XX
XX 25-SEP-2000; 2000JP-00291084.
XX
XX (TOYT ) TOYOTA JIDOSHA KK.
XX (KONP-) KONPON KENKYUSHO KK.
XX
XX WPI; 2002-439991/47.
XX
XX Screening potential translational control factors of mRNA, useful for
XX preventative research on pathogenic viruses, involves introducing random
XX oligonucleotide sequences into an untranslated region.
XX
XX Example 1; Page 7; 16pp; Japanese.
XX
XX The invention relates to a method of screening potential translational
XX control factors of mRNA. The method involves synthesizing an mRNA
XX containing a cap structure and a poly(A) chain sequence in which a random
XX oligonucleotide sequence which is a candidate for translational control
XX factor is introduced in the 5'- untranslated region (UTR) and the mRNA in
XX which the translation efficiency is changed compared to the untreated is
XX selected. The method can be used for preventive researches on pathogenic
XX viruses. Sequences ABL41035-42 represent primers used for amplifying the
XX UTRs of GUS mRNA
XX
XX Sequence 59 BP; 26 A; 13 C; 12 G; 8 T; 0 U; 0 Other;
```

```

Query Match      0.6%; Score 25; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      20 GGCTAATAGCACTCACTATAGGGA 44
      |||
DB      4 GGCTAATAGCACTCACTATAGGGA 28

RESULT 65
ABL41037
ID ABL41037 standard; DNA; 63 BP.
XX
AC ABL41037;
XX
DT 12-AUG-2002 (first entry)
XX
DE GUS mRNA UTR fragment amplifying primer 3.
XX
KM Translation; untranslated region; UTR; pathogen; virus; GUS; PCR; primer;
KW ss.
XX
OS Synthetic.
XX
PN JP2002095483-A.
XX
PD 02-APR-2002.
XX
PF 25-SEP-2000; 2000JP-00291084.
XX
PR 25-SEP-2000; 2000JP-00291084.
XX
PA (TOYT ) TOYOTA JIDOSHA KK.
PA (KONP-) KONPON KENKYUSHO KK.
XX
DR WPI; 2002-439991/47.
XX
PT Screening potential translational control factors of mRNA, useful for
PT preventative research on pathogenic viruses, involves introducing random
PT oligonucleotide sequences into an untranslated region.
XX
PS Example 1; Page 7; 16pp; Japanese.
XX
CC The invention relates to a method of screening potential translational
CC control factors of mRNA. The method involves synthesizing an mRNA
CC containing a cap structure and a poly(A) chain sequence in which a random
CC oligonucleotide sequence which is a candidate for translational control
CC factor is introduced in the 5'- untranslated region (UTR) and the mRNA in
CC which the translation efficiency is changed compared to the untreated is
CC selected. The method can be used for preventive researches on pathogenic
CC viruses. Sequences ABL41035-42 represent primers used for amplifying the
CC UTRs of GUS mRNA
XX
SQ Sequence 63 BP; 16 A; 19 C; 13 G; 15 T; 0 U; 0 Other;

Query Match      0.6%; Score 25; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      20 GGCTAATAGCACTCACTATAGGGA 44
      |||
DB      9 GGCTAATAGCACTCACTATAGGGA 33

RESULT 66
ADN14395
ID ADN14395 standard; DNA; 123 BP.
XX
AC ADN14395;
XX
DT 15-JUL-2004 (first entry)
XX

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```

DE PCR primer 1 to construct dsRNA with stabilising hairpin & linker region.
XX
KW ss; RNA complex; immunosuppressive; cytostatic; cancer;
KW systemic lupus erythematosus; Alzheimer's; Huntington's disease;
KW salivary gland carcinoma; melanoma; brain tumour; leukaemia; lymphoma;
KW gene therapy; PCR; primer.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH misc_binding 5..123
FT /*tag= a
FT /bound_molety= "Reverse primer (2)"
FT /note= "Forms double stranded region with nucleotides 123
FT -5"
XX
XX WO2004035765-A2.
XX
PD 29-APR-2004.
XX
XX 20-OCT-2003; 2003WO-US033466.
XX
PF 18-OCT-2002; 2002US-0419532P.
XX
PR 28-OCT-2002; 2002US-0421757P.
XX
PA (NUCL-) NUCLEONICS INC.
XX
PI Pachuk CJ, Satishchandran C, Mccallus DE;
XX
DR WPI; 2004-348454/32.
XX
XX New substantially pure ribonucleic acid (RNA) complex comprising a first
XX strand and a second strand that hybridize to each other, useful for
XX treating cancer, systemic lupus erythematosus, Alzheimer's disease or
XX Huntington's disease.
XX
PS Example 10; Page 126; 204pp; English.
XX
XX This invention relates to double stranded ribonucleic acid (RNA)
XX structures and constructs. Specifically, it comprises first and second
XX RNA strands that hybridize to each other under physiological conditions
XX to form a double-strand region, wherein the double-strand region contains
XX one or more mismatched regions that result in two or more double-stranded
XX segments. Furthermore, the mismatched regions may be cleaved by single-
XX strand ribonuclease enzymes. The present invention describes expression
XX vectors that encode dsRNAs with an intron containing exemplary target
XX genes such as anticlotic resistance genes. Accordingly, using gene
XX therapy, these RNA complexes exhibit immunosuppressive and cytostatic
XX activities and can be used to treat cancer, systemic lupus erythematosus,
XX Alzheimer's and Huntington's disease. The cancer is selected from,
XX amongst others, prostate, breast, ovarian, salivary gland carcinoma,
XX melanoma, brain tumour, leukaemia and lymphoma. This oligonucleotide
XX sequence is a PCR primer given in an exemplification of the invention.
XX
SQ Sequence 123 BP; 32 A; 32 C; 27 G; 32 T; 0 U; 0 Other;

Query Match      0.6%; Score 25; DB 12; Length 123;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 GCTTAATAGCACTCACTATAGGAG 45
      |||
DB      4 GCTTAATAGCACTCACTATAGGAG 28

RESULT 67
AAQ23256
ID AAQ23256 standard; DNA; 136 BP.
XX
AC AAQ23256;
XX
DT 25-MAR-2003 (revised)
DT 31-JUL-1992 (first entry)
XX

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XX DE Plasmid pGENE 8459.
XX XX
XX KM Synthetic ribozyme; virus resistant plants; antiviral agents.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT promoter 1..27
XX FT /tag= a
XX FT /note= "T7 promoter"
XX FT misc_feature 36..73
XX FT /tag= b
XX FT /note= "SFL1 ribozyme RNA coding region"
XX PN JP03219874-A.
XX PD 27-SBP-1991.
XX PF 19-DEC-1989; 89JP-00329831.
XX PR 19-DEC-1989; 89JP-00329831.
XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
XX WPI; 1992-107687/14.
XX DR
XX PT New synthetic ribozyme with hair pin structure - using DNA fragment with
XX PT ribozyme RNA code sequence and 2nd sequence that cleaves transcribed
XX PS ribozyme RNA by self processing.
XX PS Disclosure; Fig 3; 8pp; Japanese.
XX CC The sequence is that of plasmid pGENE 8459 which contains a T7 promoter
XX CC upstream of a Sfl ribozyme and a 3' terminal self-processing ribozyme.
XX CC The plasmid is ligated into pUC19 and can then be used to prepare virus
XX CC resistant plants or new antiviral agents. Its hairpin structure is
XX CC extremely stable against exonucleases in vivo. See also AAQ23255.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 136 BP; 34 A; 31 C; 42 G; 29 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 25; DB 2; Length 136;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 24 TAATACGACTCACTATAGGAGCTC 48
XX DB 11 TAATACGACTCACTATAGGAGCTC 35
XX
XX RESULT 68
XX ADZ13446
XX ID ADZ13446 standard; DNA; 243934 BP.
XX AC ADZ13446;
XX DT 16-JUN-2005 (first entry)
XX DE Human cancer-associated genomic DNA #82.
XX KM Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
XX KM cytostatic; gene; ds.
XX OS Homo sapiens.
XX PN WO2005031001-A2.
XX PD 07-APR-2005.
XX PF 23-SBP-2004; 2004MO-US031617.
XX PR 23-SBP-2003; 2003US-00669920.
XX

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XX PA (CHIR ) CHIRON CORP.
XX PI Morris DM, Malandro MS;
XX DR WPI; 2005-273395/28.
XX PT Nucleic acid array useful for detecting cancer associated nucleic acid,
XX PS comprises two or more nucleic acid probes.
XX PS Disclosure; SEQ ID NO 966; 199pp; English.
XX
XX CC The invention relates to a nucleic acid array for detecting a cancer
XX CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
XX CC The invention also relates to a peptide array comprising two or more
XX CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX CC that binds to a polypeptide, an isolated antibody or its fragment which
XX CC binds to a polypeptide, which is prepared by immunizing a host animal
XX CC with a composition comprising the polypeptide or its antigen binding
XX CC fragment and collecting cells from the host expressing antibodies against
XX CC the antigen or its antigen binding fragment, a composition comprising the
XX CC antibody and a carrier, a method of screening for anticancer activity, a
XX CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
XX CC method of treating cancer and a method of inhibiting expression of a CA
XX CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
XX CC nucleic acids. The antibody is useful for detecting the presence or
XX CC absence of cancer cells in an individual which involves contacting cells
XX CC from the individual with the antibody and detecting a complex of a CA
XX CC protein from the cancer cells and the antibody, where the detection of
XX CC the complex correlates with the presence of cancer cells in the
XX CC individual. The composition is useful for inhibiting growth of cancer
XX CC cells in an individual or for delivering a therapeutic agent to cancer
XX CC cells in an individual. The invention is also useful for diagnosing
XX CC cancer, for treating cancer and for inhibiting expression of a CA gene in
XX CC a cell. This sequence represents human cancer-associated genomic DNA of
XX CC the invention.
XX SQ Sequence 243934 BP; 66213 A; 49129 C; 53448 G; 74301 T; 0 U; 843 Other;
XX
XX Query Match 0.6%; Score 25; DB 14; Length 243934;
XX Best Local Similarity 100.0%; Pred. No. 6.6;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3471 AAAAAAAAAAAGTTTCAATT 3495
XX DB 33789 AAAAAAAAAAAGTTTCAATT 33813
XX
XX RESULT 69
XX AAX00218
XX ID AAX00218 standard; DNA; 29 BP.
XX AC AAX00218;
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-1999 (first entry)
XX DE T7 RNA polymerase promoter sequence.
XX KM Human; platelet 12-LOX; 12-lipoxygenase; tumour; apoptosis; inhibition;
XX KM cancer; chemotherapy; promoter; ss.
XX OS Enterobacteria phage T7.
XX PN US5861268-A.
XX PD 19-JAN-1999.
XX PF 23-MAY-1996; 96US-00652369.
XX PR 23-MAY-1996; 96US-00652369.
XX PA (BIOM-) BIOMIDE INVESTMENT LP.
XX

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XX Tang DG, Horn KV;
 XX WPI; 1999-130388/11.
 XX In vitro method for determining the effectiveness of compound in
 PT producing apoptosis - comprises, providing tumour cells which are known
 PT to produce 12-lipoxygenase, exposing tumour cells compound which inhibits
 PT 12-lipoxygenase, determining apoptosis.
 XX Disclosure; Col 13; 26pp; English.
 XX An in vitro method has been developed for determining the effectiveness
 CC of a compound in producing apoptosis. The method comprises: (a) providing
 CC tumour cells which are known to produce 12-lipoxygenase, using normal
 CC cells as a control; (b) exposing the tumour cells and the normal cells to
 CC a compound (1) which inhibits 12-lipoxygenase which is to be tested in
 CC vitro in a culture medium; and (c) determining if the tumour cells have
 CC undergone apoptosis as a result of exposure to (1), without producing
 CC apoptosis in normal cells. (1) is selected from: a cyclic hydroxamic acid
 CC (1a); an aryl aliphatic acid (1b); nordihydro-guairetic acid (1c); N-
 CC benzyl-N-hydroxy-5-phenylpentanamide (1d); baicalin (1e); and an
 CC antisense segment of DNA which selectively binds to DNA encoding 12-
 CC lipoxygenase (1f). The process is used to determine the effectiveness of
 CC (1) in producing apoptosis, also to induce selective apoptosis of tumour
 CC cells, and to test, detect and compare tumour apoptosis caused by (1).
 CC The process can effectively identify new candidate chemotherapeutic
 CC agents that can be used in the clinical treatment of cancer patients. The
 CC present sequence represents a T7 RNA polymerase promoter sequence from
 CC the present invention. (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 24; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 CCTAATACGACTCCTATAGGAG 45
 Db 5 CCTAATACGACTCCTATAGGAG 28
 RESULT 70
 ABK31899
 ID ABK31899 standard; DNA; 29 BP.
 AC ABK31899;
 XX 29-AUG-2003 (revised)
 DT 23-APR-2002 (first entry)
 XX Bacteriophage T7 DNA sequence relating to *Candida tropicalis* invention.
 DE
 XX CCR4, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A;
 KM CYP52A5B, CYP52A8A, CYP52A8B, CYP52D4A, URA3A; cytochrome P450;
 KM NADPH2 reductase; omega-hydroxylase complex; dicarboxylic acid; ds.
 XX Enterobacteria phage T7.
 OS US6331420-B1.
 XX US6331420-B1.
 PN 18-DEC-2001.
 PD 30-APR-1999; 99US-00302620.
 PF 01-MAY-1998; 98US-0083798P.
 PR 05-OCT-1998; 98US-0103099P.
 PR 10-MAR-1999; 99US-0123555P.
 XX (MILS/) WILSON C R.
 PA (CRAF/) CRAFT D L.
 PA (EIRI/) EIRICH L D.
 PA (ESHO/) ESHOO M.

PA (MADD/) MADDURI K M.
 PA (CORN/) CORNETT C A.
 PA (BREN/) BRENNER A A.
 PA (TANG/) TANG M.
 PA (LOPE/) LOPEZ J C.
 PA (GLEE/) GLEESON M.
 XX Wilson CR, Craft DL, Birch LD, Eshoo M, Madduri KM, Cornett CA;
 PI Brenner AA, Tang M, Loper JC, Gleeson M;
 XX WPI; 2002-138383/18.
 XX Novel isolated nucleic acid encoding cytochrome P450 and NADPH reductase
 PT enzymes of omega-hydroxylase complex of *Candida tropicalis*, useful for
 PT increasing production of dicarboxylic acids.
 XX Disclosure; Col 16; 173pp; English.
 XX The present invention relates to the isolation of *Candida tropicalis*
 CC 20336 novel genes (CPR4, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A,
 CC CYP52A3B, CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B, CYP52D4A and URA3A)
 CC which encode cytochrome P450 and NADPH2 reductase enzymes of the omega-
 CC hydroxylase complex. Also disclosed are vectors containing these genes
 CC and methods of producing these enzymes. The genes and vectors are useful
 CC for increasing production of a dicarboxylic acid by providing a host cell
 CC having a naturally occurring number of the genes of the invention and
 CC increasing in the host cell, the number of genes encoding these enzymes.
 CC The present sequence represents a Bacteriophage T7 DNA sequence of
 CC unknown function. Note: The present sequence is given in the sequence
 CC listing but is not mentioned elsewhere in the specification. (Updated on
 CC 29-AUG-2003 to standardise OS field)
 XX Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 24; DB 6; Length 29;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 CCTAATACGACTCCTATAGGAG 45
 Db 5 CCTAATACGACTCCTATAGGAG 28
 RESULT 71
 ADC44990
 ID ADC44990 standard; DNA; 29 BP.
 AC ADC44990;
 XX 18-DEC-2003 (first entry)
 DT T7 promoter consensus sequence.
 XX
 DE T7 promoter consensus sequence.
 XX T7; promoter; ds; omega oxygenase complex; cytochrome P450 monooxygenase;
 KM CYP; NADPH reductase enzymes; CPR; CPRB; CYP52A1A, CYP52A2A,
 KM CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B;
 KM CYP52D4A; dicarboxylic acid; diester; polymer; thermoplastic;
 KM plasticising agent; lubricant; hydraulic fluid; agricultural chemical;
 KM pharmaceutical; dye; surfactant; adhesive; QC-RT-PCR;
 KM quantitative competitive reverse transcription PCR.
 XX Enterobacteria phage T7.
 OS US2003049821-A1.
 PN 13-MAR-2003.
 PD 03-MAY-2002; 2002US-00138638.
 PF 01-MAY-1998; 98US-0083798P.
 PR 05-OCT-1998; 98US-0103099P.
 PR 10-MAR-1999; 99US-0123555P.
 PR 30-APR-1999; 99US-00302620.

```

PR 12-OCT-2001; 2001US-00976800.
XX (WILS/) WILSON C R.
PA (CRAF/) CRAFT D L.
PA (EIRI/) EIRICH L D.
PA (ESHO/) ESHOO M.
PA (MADD/) MADDURI K M.
PA (CORN/) CORNETT C A.
PA (BREN/) BRENNER A A.
PA (TANG/) TANG M.
PA (LOPE/) LOPER J C.
PA (GLEE/) GLEESON M.
XX Wilson CR, Craft DL, Eirich LD, Eshoo M, Madduri KM, Cornett CA;
PI Brenner AA, Tang M, Loper JC, Gleeson M;
XX WPI; 2003-777150/73.
XX
XX New nucleic acid encoding cytochrome P450 and NADPH reductase enzymes
PT (e.g. CPRA, CPRB or CYP52A1A), useful for producing dicarboxylic acids
PT that may be utilized as industrial intermediates in manufacturing
PT diesters and polymers.
XX
XX Example 11; SEQ ID NO 109; 196pp; English.
XX
XX The invention relates to an isolated nucleic acid selected encoding
CC Candida tropicalis omega oxygenase complex enzymes (CYP) designated CPRA,
CC monooxygenase (CYP) and NADPH reductase enzymes (CPR) designated CPRB,
CC CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A,
CC CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A) or their coding regions. Also
CC included are the CPR/CYP proteins, a vector comprising with the nucleic acid
CC cited above, a host cell transfected or transformed with the above
CC nucleic acid, producing the proteins, discriminating members of a gene
CC family by quantifying the amount of target mRNA in a sample, increasing
CC production of a dicarboxylic acid and increasing the production of the
CC proteins cited above. The host cell is C. tropicalis is specifically
CC H5343 ura-. The nucleic acid is useful for producing dicarboxylic acids
CC that may be utilized as industrial intermediates in the manufacture of
CC diesters and polymers (e.g. as thermoplastics, plasticizing agents,
CC lubricants, hydraulic fluids, agricultural chemicals, pharmaceuticals,
CC dyes, surfactants or adhesives). The present sequence is a T7 promoter
CC consensus sequence incorporated into a quantitative competitive reverse
CC transcription (QC-RT) PCR primer used to assay the levels of CYP, CPR or
CC control FOX mRNA in response to exogenously added substrates.
XX
XX Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 24; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 CCTAATACGACTCATATAGGAG 45
Db 5 CCTAATACGACTCATATAGGAG 28

```

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XX OS Enterobacteria phage T7.
XX US2003049822-A1.
XX
XX 13-MAR-2003.
XX
XX 03-MAY-2002; 2002US-00139031.
XX
XX 01-MAY-1998; 98US-0063798P.
PR 05-OCT-1998; 98US-0103099P.
PR 10-MAR-1999; 99US-0123555P.
PR 30-APR-1999; 99US-00302620.
PR 12-OCT-2001; 2001US-00976800.
XX
XX (WILS/) WILSON C R.
PA (CRAF/) CRAFT D L.
PA (EIRI/) EIRICH L D.
PA (ESHO/) ESHOO M.
PA (MADD/) MADDURI K M.
PA (CORN/) CORNETT C A.
PA (BREN/) BRENNER A A.
PA (TANG/) TANG M.
PA (LOPE/) LOPER J C.
PA (GLEE/) GLEESON M.
XX
XX Wilson CR, Craft DL, Eirich LD, Eshoo M, Madduri KM, Cornett CA;
PI Brenner AA, Tang M, Loper JC, Gleeson M;
XX WPI; 2003-765370/72.
XX
XX New nucleic acid encoding cytochrome P450 and NADPH reductase enzymes
PT (e.g. CPRA, CPRB or CYP52A1A), useful for producing dicarboxylic acids
PT that may be utilized as industrial intermediates in manufacturing
PT diesters and polymers.
XX
XX Example 11; SEQ ID NO 109; 196pp; English.
XX
XX The invention relates to an isolated nucleic acid selected encoding
CC Candida tropicalis omega oxygenase complex enzymes (CYP) designated CPRB,
CC monooxygenase (CYP) and NADPH reductase enzymes (CPR) designated CPRB,
CC CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A,
CC CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A) or their coding regions. Also
CC included are the CPR/CYP proteins, a vector comprising the nucleic acid
CC cited above, a host cell transfected or transformed with the above
CC nucleic acid, producing the proteins, discriminating members of a gene
CC family by quantifying the amount of target mRNA in a sample, increasing
CC production of a dicarboxylic acid and increasing the production of the
CC proteins cited above. The host cell is C. tropicalis is specifically
CC H5343 ura-. The nucleic acid is useful for producing dicarboxylic acids
CC that may be utilized as industrial intermediates in the manufacture of
CC diesters and polymers (e.g. as thermoplastics, plasticizing agents,
CC lubricants, hydraulic fluids, agricultural chemicals, pharmaceuticals,
CC dyes, surfactants or adhesives). The present sequence is a T7 promoter
CC consensus sequence incorporated into a quantitative competitive reverse
CC transcription (QC-RT) PCR primer used to assay the levels of CYP, CPR or
CC control FOX mRNA in response to exogenously added substrates.
XX
XX Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 24; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 CCTAATACGACTCATATAGGAG 45
Db 5 CCTAATACGACTCATATAGGAG 28

```


AC ADE52071;
 XX 29-JAN-2004 (first entry)
 XX T7 promoter consensus sequence.
 DE
 XX
 XX
 KM T7 promoter; ds; cytochrome P450; CYP; NADPH reductase; CPR;
 KM omega-hydroxylase complex; omega-oxidation; long chain fatty acid;
 KM QC-RT PCR; Quantitative competitive reverse transcriptase PCR.
 XX
 OS Enterobacteria phage T7.
 XX
 PN US2003073220-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 03-MAY-2002; 2002US-00138916.
 XX
 PR 01-MAY-1998; 98US-0083798P.
 PR 05-OCT-1998; 98US-0103099P.
 PR 10-MAR-1999; 99US-0123555P.
 PR 30-APR-1999; 99US-00302620.
 PR 12-OCT-2001; 2001US-00976800.
 XX
 PA (WLS/) WILSON C. R.
 PA (CRAF/) CRAFT D. L.
 PA (EIRI/) EIRICH L. D.
 PA (ESHO/) ESHOO M.
 PA (MADD/) MADDURI K. M.
 PA (CORN/) CORNETT C. A.
 PA (BREN/) BRENNER A. A.
 PA (TANG/) TANG M.
 PA (LOPE/) LOPEL J. C.
 PA (GLEB/) GLEESON M.
 XX
 PI Wilson CR, Craft DL, Eirich LD, Eshoo M, Madduri KM, Cornett CA;
 PI Brenner AA, Tang M, Loper JC, Gleeson M;
 XX
 DR WPI; 2003-625522/59.
 XX
 PT New cytochrome P450 and NADPH oxidoreductase, i.e. CPR and CYP, genes and
 PT proteins, useful for discriminating members of a gene family by
 PT quantifying the amount of target mRNA in a sample, or for omega-oxidation
 PT of long chain fatty acids.
 XX
 PS Example 11; SEQ ID NO 109; 194bp; English.
 XX
 CC The invention relates to isolated nucleic acids encoding cytochrome P450
 CC (CYP) and NADPH reductase (CPR) enzymes of the omega-hydroxylase complex
 CC of Candida tropicalis. Also included are the CYP and CPR proteins
 CC (comprising CPR, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B,
 CC CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B, or CYP52D4A), a vector comprising
 CC any one of the nucleic acid sequences cited above, a host cell
 CC transfected or transformed with the nucleic acid, methods of producing
 CC the CPR or CYP proteins, a method for discriminating members of a gene
 CC family by quantifying the amount of target mRNA in a sample and methods
 CC for increasing the production of a dicarboxylic acid, (or the CPR/CYP
 CC proteins). The CPR and CYP genes and proteins are useful for
 CC discriminating members of a gene family by quantifying the amount of
 CC target mRNA in a sample, for increasing production of a dicarboxylic
 CC acid, or for omega-oxidation of long chain fatty acids. The technique of
 CC Quantitative competitive reverse transcriptase PCR (QC-RT PCR) was used
 CC to quantitate the CPR/CYP mRNA in RNA sample. The present sequence is a
 CC T7 promoter consensus sequence incorporated into a QC-RT PCR primer used
 CC in the analysis.
 XX
 SQ Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 24; DB 10; Length 29;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

22 CCTAATCGACTCACTATAGGAG 45

DB 5 CCTAATCGACTCACTATAGGAG 28
 |||
 RESULT 74
 ID ADF72378 standard; DNA; 29 BP.
 XX
 XX ADF72378;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Bacteriophage T7 promoter consensus sequence seq id 109.
 XX
 XX CYP52A2B; cytochrome P450; NADH reductase; dicarboxylic acid production;
 KM organic substrate oxidation; fatty acid oxidation;
 KM gene integration vector; CYP; CPR; bacteriophage T7; promoter; ds.
 XX
 OS Enterobacteria phage T7.
 XX
 PN US2003077795-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 12-OCT-2001; 2001US-00976800.
 XX
 PR 10-MAR-1999; 99US-0123555P.
 XX
 PA (WLS/) WILSON C. R.
 PA (CRAF/) CRAFT D. L.
 PA (EIRI/) EIRICH L. D.
 PA (ESHO/) ESHOO M.
 PA (MADD/) MADDURI K. M.
 PA (CORN/) CORNETT C. A.
 PA (BREN/) BRENNER A. A.
 PA (TANG/) TANG M.
 PA (LOPE/) LOPEL J. C.
 PA (GLEB/) GLEESON M.
 XX
 PI Wilson CR, Craft DL, Eirich LD, Eshoo M, Madduri KM, Cornett CA;
 PI Brenner AA, Tang M, Loper JC, Gleeson M;
 XX
 DR WPI; 2003-810780/76.
 XX
 PT New nucleic acids encoding a CYP52A2B protein useful for increasing the
 PT production of dicarboxylic acid for oxidizing organic substrates such as
 PT fatty acids.
 XX
 PS Example 11; SEQ ID NO 109; 188bp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding a CYP52A2B
 CC protein comprising the fully defined sequence of 522 amino acids, as
 CC given in the specification, and comprising a coding region defined by
 CC nucleotides 1072-2640 of a fully defined sequence of 3755 base pairs, as
 CC given in the specification. The nucleic acids encoding the cytochrome
 CC P450 and NADH reductase enzymes of Candida tropicalis are useful for
 CC increasing the production of dicarboxylic acid for oxidizing organic
 CC substrates such as fatty acids. This sequence represents the
 CC bacteriophage T7 promoter consensus sequence used in the isolation of RNA
 CC for a quantitative competitor reverse transcriptase PCR assay to determine
 CC the level of CYP52A5 RNA in a sample.
 XX
 SQ Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 24; DB 10; Length 29;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

22 CCTAATCGACTCACTATAGGAG 45
 |||
 DB 5 CCTAATCGACTCACTATAGGAG 28

```

RESULT 75
ADFI1818
ID   ADFI1818 standard; DNA; 29 BP.
XX
AC   ADFI1818;
XX
DT   12-FEB-2004 (first entry)
XX
DE   T7 promoter consensus sequence.
XX
KW   CPRA; CPRB; CYP52A1A; CYP52A2A; CYP52A2B; CYP52A3A; CYP52A3B; CYP52A5A;
KM   CYP52A5B; CYP52A8A; CYP52A8B; CYP52D4A; gene family; ds.
XX
OS   Enterobacteria phage T7.
XX
PN   US2003153060-A1.
XX
PD   14-AUG-2003.
XX
PF   03-MAY-2002; 2002US-00139218.
XX
PR   01-MAY-1998; 98US-0083798P.
PR   05-OCT-1998; 98US-0103099P.
PR   10-MAR-1999; 99US-0123555P.
PR   30-APR-1999; 99US-00302620.
PR   12-OCT-2001; 2001US-00976800.
XX
PA   (WILS/) WILSON C R.
PA   (CRAF/) CRAFT D L.
PA   (EIRI/) EIRICH L D.
PA   (ESHOO/) ESHOO M.
PA   (MADD/) MADDURI K M.
PA   (CORN/) CORNETT C A.
PA   (BREN/) BRENNER A A.
PA   (TANG/) TANG M.
PA   (LOPE/) LOPER J C.
PA   (GLEE/) GLEESON M.
XX
PI   Wilson CR, Craft DL, Eirich LD, Eshoo M, Madduri KM, Cornett CA,
PI   Brenner AA, Tang M, Loper JC, Gleeson M;
XX
DR   MPI; 2003-897719/82.
XX
PT   New CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B,
PT   CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A gene, useful for
PT   increasing production of dicarboxylic acid.
XX
PS   Example 11; SEQ ID NO 109; 194bp; English.
XX
CC   The invention relates to a new isolated nucleic acid which encodes a
CC   CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B,
CC   CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A protein. The nucleic acid is
CC   useful for discriminating between members of a gene family by quantifying
CC   the amount of mRNA in a sample. The present sequence represents the T7
CC   promoter consensus sequence.
XX
SQ   Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
Query Match      0.6%; Score 24; DB 10; Length 29;
Best Local Similarity 100.0%; Pred.No. 32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      22 CCTAATCGACTGACTATAGGAG 45
DB      5 CCTAATCGACTGACTATAGGAG 28

```

Search completed: February 27, 2006, 20:48:05
 Job time : 1592 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 20:48:17 ; Search time 10434 Seconds
(without alignments)
18958.768 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtcgacctgagccctcactg.....agaacccaaaaagaacc 4228

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

- EST:*
- 1: gb_sac1.*
 - 2: gb_sac2.*
 - 3: gb_sac3.*
 - 4: gb_hic.*
 - 5: gb_sac4.*
 - 6: gb_sac5.*
 - 7: gb_sac6.*
 - 8: gb_sac7.*
 - 9: gb_g881.*
 - 10: gb_g882.*
 - 11: gb_g883.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	9.9	581	10 BX290871	BX290871 Arabidops
2	278	6.6	652	9 B62389	B62389 T2110TR TA
3	223	5.5	437	9 CC056828	CC056828 SALK_1112
4	193	4.6	234	10 AL936239	AL936239 Arabidops
5	176	4.2	300	11 CR402297	CR402297 Arabidops
6	154	3.6	162	10 AL759737	AL759737 Arabidops
7	140	3.3	276	11 CR402298	CR402298 Arabidops
8	139	3.3	415	9 B2379137	B2379137 SALK_1129
9	135	3.2	2106	4 CNS0A4GJ	BX826641 Arabidops
10	127	3.0	192	10 AL759736	AL759736 Arabidops
11	112	2.6	112	9 CC455690	CC455690 SALK_0857
12	103	2.4	323	9 CC797115	CC797115 SALK_1444
13	91	2.2	92	10 AL769520	AL769520 Arabidops
14	91	2.2	418	10 AL769556	AL769556 Arabidops
15	84	2.0	2315	4 CNS0A2BQ	BX827650 Arabidops
16	80	1.9	92	10 AL754990	AL754990 Arabidops
17	75	1.8	424	3 BP561373	BP561373 Arabidops
18	73	1.7	694	3 BH934314	BH934314 odf65910.
19	71	1.7	268	10 AL756782	AL756782 Arabidops
20	68	1.6	594	6 CB260786	CB260786 65-B9572-
21	65	1.5	110	10 AL769557	AL769557 Arabidops
22	61	1.4	96	10 AL754991	AL754991 Arabidops

23	45	1.1	381	9 BH481919	BH481919 BOGEA30TR
24	45	1.1	673	9 BH676371	BH676371 BOHXY80TR
25	43	1.0	56	9 B2380049	B2380049 SALK_1145
26	32	0.8	335	9 BH451280	BH451280 BOGNW77TR
27	32	0.8	796	9 BH510257	BH510257 BOHKU78TR
28	27	0.6	897	10 CW938563	CW938563 TGB18.3.F
29	27	0.6	901	10 CW938873	CW938873 TGB19.1.C
30	26	0.6	298	2 BP925688	BP925688 CM2-NT015
31	25	0.6	225	2 BE145442	BE145442 IL5-HT019
32	25	0.6	388	10 CE734860	CE734860 L1gr-g88-
33	25	0.6	488	9 AZ088538	AZ088538 RPCI-23-4
34	25	0.6	715	10 AG013324	AG013324 Homo sapi
35	25	0.6	755	10 CNS01002	AL153762 Anopheles
36	25	0.6	793	9 BH510250	BH510250 BOHKU78TF
37	25	0.6	798	10 CW949303	CW949303 TGB33.4.F
38	25	0.6	860	10 AG409273	AG409273 Mus muscu
39	25	0.6	898	10 CW940939	CW940939 TGB22.1.A
40	25	0.6	924	10 AG400158	AG400158 Mus muscu
41	25	0.6	1036	10 CW937215	CW937215 TGB16.1.F
42	24	0.6	161	7 CK121482	CK121482 202020.PI
43	24	0.6	191	9 AQ955990	AQ955990 LERB18TR
44	24	0.6	278	7 CK573161	CK573161 1172 Plas
45	24	0.6	278	8 DR973784	DR973784 CHUT008P1
46	24	0.6	310	9 AQ955989	AQ955989 LERB18TF
47	24	0.6	318	9 BH451271	BH451271 BOGNW77TF
48	24	0.6	320	7 CV263561	CV263561 WS02022.B
49	24	0.6	339	9 CE127892	CE127892 L1gr-g88-
50	24	0.6	349	9 BM163414	BM163414 EST565948
51	24	0.6	350	10 AG229188	AG229188 Lotus cor
52	24	0.6	390	9 B239509	B239509 CH230-456
53	24	0.6	392	3 BM163358	BM163358 EST565881
54	24	0.6	394	9 AQ081838	AQ081838 RPCI11-55
55	24	0.6	399	3 BM163834	BM163834 EST566357
56	24	0.6	399	3 BM966009	BM966009 ko20F03.y
57	24	0.6	418	11 CRO57094	CRO57094 Forward s
58	24	0.6	423	9 AZ301311	AZ301311 UP 315-19
59	24	0.6	429	9 AQ955559	AQ955559 LERB14TF
60	24	0.6	440	3 BM171421	BM171421 EST573944
61	24	0.6	444	9 AQ959560	AQ959560 LERB147TR
62	24	0.6	454	9 AQ028235	AQ028235 CIT-HSP-2
63	24	0.6	469	3 BM166570	BM166570 EST569093
64	24	0.6	478	5 BU303919	BU303919 603737371
65	24	0.6	478	5 BU396654	BU396654 603533803
66	24	0.6	487	2 BP588277	BP588277 UI-R-A1-e
67	24	0.6	511	1 AL720059	AL720059 AL720059
68	24	0.6	523	1 AL720155	AL720155 AL720155
69	24	0.6	525	1 AL715025	AL715025 AL715025
70	24	0.6	529	8 DR576414	DR576414 MS00743.C
71	24	0.6	540	1 AL723652	AL723652 AL723652
72	24	0.6	564	3 BM168186	BM168186 EST570709
73	24	0.6	581	3 B2293554	B2293554 CG0392.r1
74	24	0.6	631	3 BM170115	BM170115 EST572638
75	24	0.6	637	10 CE784932	CE784932 L1gr-g88-
76	24	0.6	668	10 AG366559	AG366559 Mus muscu
77	24	0.6	673	1 AL726822	AL726822 AL726822
78	24	0.6	675	9 AZ393711	AZ393711 IM0156723
79	24	0.6	679	10 AG077514	AG077514 Pan trogl
80	24	0.6	680	9 BH426079	BH426079 BOHIW87TR
81	24	0.6	687	10 AG069432	AG069432 Pan trogl
82	24	0.6	698	9 BH936859	BH936859 ccd82912.
83	24	0.6	699	10 AG120482	AG120482 Pan trogl
84	24	0.6	693	10 AG117960	AG117960 Pan trogl
85	24	0.6	706	6 CA966306	CA966306 CCLX07a27
86	24	0.6	708	1 AL722577	AL722577 AL722577
87	24	0.6	715	10 AG099910	AG099910 Pan trogl
88	24	0.6	718	10 AG106672	AG106672 Pan trogl
89	24	0.6	720	10 AG117860	AG117860 Pan trogl
90	24	0.6	721	3 BM160799	BM160799 EST563322
91	24	0.6	738	10 AG101726	AG101726 Pan trogl
92	24	0.6	740	8 CV908369	CV908369 PDfcd4.36
93	24	0.6	742	1 AL726847	AL726847 AL726847
94	24	0.6	756	10 AG418452	AG418452 Mus muscu
95	24	0.6			

C	96	24	0.6	762	3	BJ348738	BJ348738
	97	24	0.6	775	3	BM159930	BM159930
	98	24	0.6	781	6	CA405371	CA405371
	99	24	0.6	788	11	CR880479	CR880479
	100	24	0.6	808	2	BE300384	BE300384

ALIGNMENTS

RESULT 1
BX290871/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-440605-018216,
genomic survey sequence.
581 bp DNA linear GSS 02-Apr-2004

ACCESSION
BX290871
VERSION
BX290871.1
KEYWORDS
GSS,
Arabidopsis thaliana (chale crees)

SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
AUTHORS
TITLE
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana

JOURNAL
PUBMED
12874060
19 (11), 1441-1442 (2003)

REFERENCE
AUTHORS
Rosso, M.G., Li, Y., Strizhov, N., Reies, B., Dekker, K. and
Weishaar, B.

TITLE
JOURNAL
PUBMED
14756321
An Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

REFERENCE
AUTHORS
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weishaar, B.

TITLE
JOURNAL
PUBMED
14682050
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)

REFERENCE
AUTHORS
4 (bases 1 to 581)
Strizhov, N., Li, Y., Rosso, M.G. and Weishaar, B.

COMMENT
Direct Submission
Submitted (31-MAR-2004) Weishaar, B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T28119. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1. 581
location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-440605-018216"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (Genbank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 417; DB 10; Length 581;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1152	GTGCTGTTGACAAATTTTCTCAGAGTGAGGTGAATCAAGAAAATAATTCGAAA	1211
Db	524	GTGCTGTTGACAAATTTTCTCAGAGTGAGGTGAATCAAGAAAATAATTCGAAA	465
Qy	1212	AGAAAGAAAAAAGCAGAAAACTATTGTGAAAAGACATAATGACACTAAATTGG	1271
Db	464	AGAAAGAAAAAAGCAGAAAACTATTGTGAAAAGACATAATGACACTAAATTGG	405
Qy	1272	ATTATTAAAAATGGTATATATGTTGGTGAATTTATTAATCAATTAACAAATGAGAA	1331
Db	404	ATTATTAAAAATGGTATATATGTTGGTGAATTTATTAATCAATTAACAAATGAGAA	345
Qy	1332	GGAGAGGAGGACCTCTTCGCTTATGATTTCCCTCTTAAACAAGCTCCACTATCT	1391
Db	344	GGAGAGGAGGACCTCTTCGCTTATGATTTCCCTCTTAAACAAGCTCCACTATCT	285
Qy	1392	TTTTTACTTCGAACAATATCATTCACACGAAAAATCTGCTGTGATCATTTTCATGCA	1451
Db	284	TTTTTACTTCGAACAATATCATTCACACGAAAAATCTGCTGTGATCATTTTCATGCA	225
Qy	1452	AAATTAACTAAATTTTGGATTTTGTGCAAGTTCTGCTTTTAAGTCGATTAATTG	1511
Db	224	AAATTAACTAAATTTTGGATTTTGTGCAAGTTCTGCTTTTAAGTCGATTAATTG	165
Qy	1512	GTAATACATATATGTGATATATACATCCAGCTATCAATTAATGATCTCTCT	1568
Db	164	GTAATACATATATGTGATATATACATCCAGCTATCAATTAATGATCTCTCTCT	108

RESULT 2
B62389/c
LOCUS
DEFINITION
T21110TR T21110TR Arabidopsis thaliana genomic clone T21110, genomic
survey sequence.
652 bp DNA linear GSS 21-NOV-1997

ACCESSION
B62389
VERSION
B62389.1
KEYWORDS
GSS,
Arabidopsis thaliana (chale crees)

SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS
1 (bases 1 to 652)
Rounleay, S.D., Field, C.E., Bass, S., Linher, K., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Adams, M.D. and
Venner, J.C.

TITLE
JOURNAL
PUBMED
121110TP
A BAC End Sequence Database for Identifying Minimal Overlaps in
Arabidopsis Genomic Sequencing. Update 3
Unpublished (1997)

COMMENT
Contact: Steve Rounleay
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounleay@tigr.org
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 652.

FEATURES

source

1. 652
location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="T21110"
/sex="hermaphrodite"

ORIGIN /clone.lib="TAMU"
/note="Vector: Belobacit; Site 1: HindIII; Site 2:
HindIII; Produced by Rod Wing"

Query Match 6.6%; Score 278; DB 9; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.7e-107; Indels 0; Gaps 0;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2284 GATATAGATATATACAAATTTTAACTAGTATGATTTTACTATCTTCAAACTTACC 2343
DB 278 GTATATATATATACAAATTTTAACTAGTATGATTTTACTATCTTCAAACTTACC 219
QY 2344 ATCTTCAACATTAATATGATCAATTTTATTTTCTTAAACTTCTCCACTTAAA 2403
DB 218 ATCTTCAACATTAATATGATCAATTTTATTTTCTTAAACTTCTCCACTTAAA 159
QY 2404 AAATGCAAAAGAGATATATTTTAAAGTAAAGTAAAGATGAGTGGATTTCT 2463
DB 158 AAATGCAAAAGAGATATATTTTAAAGTAAAGTAAAGATGAGTGGATTTCT 99
QY 2464 TCAGCAAAAGCGCCGCTAGAGTGTCTTATCTTCACTTACAGCTGGGTTGGCAGACA 2523
DB 98 TCAGCAAAAGCGCCGCTAGAGTGTCTTATCTTCACTTACAGCTGGGTTGGCAGACA 39
QY 2524 TCATAGGGCTTACGTATATTTTACGCTTACTGTACGTA 2561
DB 38 TCATAGGGCTTACGTATATTTTACGCTTACTGTACGTA 1

RESULT 3 437 bp DNA linear GSS 02-APR-2003
CC056828 SALK_111232.51.45.x Arabidopsis thaliana TDNA insertion lines
LOCUS Arabidopsis thaliana genomic clone SALK_111232.51.45.x, genomic
DEFINITION survey sequence.

ACCESSION CC056828.1 GI:29476492
VERSION CC056828.1
KEYWORDS Arabidopsis thaliana (chale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana (chale cress)

REFERENCE 1. Bases 1 to 437
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1. Bases 1 to 437
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shim, P., Zimmerman, J. and Becker, J.R.

REFERENCE 1. Bases 1 to 437
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Becker

JOURNAL TITLE Salik Institute Genomic Analysis Laboratory (SIGNAL)
JOURNAL Arabidopsis Genome
COMMENT The Salik Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: jbecker@salik.edu

FEATURES Class: TDNA
1. 437
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_111232.51.45.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html

ORIGIN 5.5%; Score 233; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.6e-88;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 CAATCTTACCATCTTCAACATTAATATGATCAATTTTATTTTCTTAACTACT 2393
DB 1 CAATCTTACCATCTTCAACATTAATATGATCAATTTTATTTTCTTAACTACT 60
QY 2394 TCCACTTAAATATGCAAAAGAGATATATTTTAAAGTAAAGTAAATGAT 2453
DB 61 TCCACTTAAATATGCAAAAGAGATATATTTTAAAGTAAAGTAAATGAT 120
QY 2454 GGGTATTTCTTCAAGCAAAAGCGCCGCTAGAGTGTCTTATCTTCACTTACAGCTGGGTT 2513
DB 121 GGGTATTTCTTCAAGCAAAAGCGCCGCTAGAGTGTCTTATCTTCACTTACAGCTGGGTT 180
QY 2514 GTGGCAGACATCATAGGCGCTTACGTATTTTACGCTTACTGTAAAGCT 2566
DB 181 GTGGCAGACATCATAGGCGCTTACGTATTTTACGCTTACTGTAAAGCT 233

RESULT 4 234 bp DNA linear GSS 01-APR-2004
AL936239 Arabidopsis thaliana T-DNA flanking sequence GK-047A09-016076,
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-047A09-016076,
DEFINITION genomic survey sequence.

ACCESSION AL936239.1 GI:24367864
VERSION AL936239.1
KEYWORDS Arabidopsis thaliana (chale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana (chale cress)

REFERENCE 1. Bases 1 to 234
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1. Bases 1 to 234
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060

REFERENCE 2. Bases 1 to 234
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321

REFERENCE 3. Bases 1 to 234
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050

JOURNAL TITLE Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
JOURNAL flanking sequence tag-based reverse genetics
COMMENT Submitted (31-MAR-2004) Weisshaar, B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
Biotechniques 35 (6), 1164-1168 (2003)
4 (Bases 1 to 234)
Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar, B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BNC clone
T8119. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES Location/Qualifiers
1. 437
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_111232.51.45.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050

REFERENCE 4 (bases 1 to 162)

AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1..162

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="GK-190B10-014641"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 3.6%; Score 154; DB 10; Length 162;

Best Local Similarity 100.0%; Pred. No. 2.8e-54;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2117 TCTCTGCTGCTACTTTCAGGACATTTGACCAAGCATATATGTAAGCAAAATATC 2116

Db 5 TCTCTGCTGCTACTTTCAGGACATTTGACCAAGCATATATGTAAGCAAAATATC 64

QY 2177 CACCAAGGATGATGAGGTAGATCCACATTCATCTTTGCTTTGATTATGAA 2236

Db 65 CACCAAGGATGATGAGGTAGATCCACATTCATCTTTGCTTTGATTATGAA 124

QY 2237 AACCAATATTTATCAGAAAAAAGTTTCTTC 2270

Db 125 AACCAATATTTATCAGAAAAAAGTTTCTTC 158

RESULT 7

CR402298/c 276 bp DNA linear GSS 02-MAY-2004

LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-853H05-025845,

ACCESSION CR402298

VERSION CR402298.1 GI:46943026

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.

TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

REFERENCE 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

PUBMED 14756321

REFERENCE 3

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050

REFERENCE 4 (bases 1 to 276)

AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

TITLE Direct Submission

JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1..276

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="GK-853H05-025845"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 3.3%; Score 140; DB 11; Length 276;

Best Local Similarity 100.0%; Pred. No. 2.6e-48;

Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2145 CCAACGCTTACATATTGAAAGCAAAATATCCACCGGATGATAGGTTATCCAC 2204

Db 206 CCAACGCTTACATATTGAAAGCAAAATATCCACCGGATGATAGGTTATCCAC 147

QY 2205 ATTCAATATCTTTGCTTTGTTATTATGAAAAAACAATTTATCAGAAAAAAGT 2264

Db 146 ATTCAATATCTTTGCTTTGTTATTATGAAAAAACAATTTATCAGAAAAAAGT 87

QY 2265 TTCTTCTAGTGTATAG 2284

Db 86 TTCTTCTAGTGTATAG 67

RESULT 8

BZ379137 415 bp DNA linear GSS 26-NOV-2002

LOCUS Arabidopsis thaliana T-DNA insertion lines

DEFINITION SALK_112909.37.05.x Arabidopsis thaliana T-DNA insertion lines

ACCESSION BZ379137

VERSION BZ379137.1 GI:25470664

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1

AUTHORS Salik, K., Strizhov, N., Viehoveer, P., Dekker, K.A. and Weisshaar, B.

TITLE Arabidopsis thaliana (thale cress)

JOURNAL Arabidopsis thaliana (thale cress)

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 415)	Spermatophytes: Magnoliophyta; eudicotyledons; core eudicotyledons, rosids; eutroside II; Brassicales; Brassicaceae; Arabidopsis.		
2	Alonso,J.M., Jeske,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Leese,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome	Unpublished (2001)	Contact: Joseph R. Ecker The Salk Institute Genomic Analysis Laboratory (SIGAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel.: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu This is single pass sequence recovered from the left border of TDNA.
3		Class: TDNA tagged.		
4		Location/Qualifiers		
5	1. .415			
6	/organism="Arabidopsis thaliana"			
7	/mol type="genomic DNA"			
8	/ecotype="Col-0"			
9	/db xref="taxon:3702"			
10	/clone="SALK_112909.37.05.x"			
11	/clone_11b="Arabidopsis thaliana TDNA insertion lines"			
12	/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html "			
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100				

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2106)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	The sequences are based on single pass reads. Life technologies (a division of Invitrogen) members carried out full-length libraries construction ; Temple G. Genoscope members carried out sequencing and annotation ; Castelli V., Aury J.M., Jailion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salmoubat M. URVY INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis . Location/Qualifiers
FEATURES	1. 2106
source	/organism="Arabidopsis thaliana"
	/mol_type="mRNA"
	/db_xref="taxon:3702"
	/clone="GSLTFB37ZE02"
	/tissue_type="Flowers and buds"
	/ecotype="Col-0"
	/plasmid="pCMVSPORT_6"
gene	1. 2106
	/gene="At4g37750"
ORIGIN	
Query Match	3.2%; Score 135; DB 4; Length 2106;
Best Local Similarity	100.0%; Prod. No. 3e-46;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	3968 AACGATTCAAAAGCAAAATTGTGCTTTGCTCTTCTCTTATTATATATCTCTCA 4022
Db	1 AACGATTCAAAAGCAAAATTGTGCTTTGCTCTTCTCTTATATATATCTCTCA 60
OY	4028 AAACCTCTCTATATCTCTCTAAAGCCCTCTCTCTTCTCTTCTTCTACCGAAACAAAGA 4087
Db	61 AAACCTCTCTATATCTCTCTAAAGCCCTCTCTCTTCTCTTCTTCTTACCGAAACAAAGA 120
OY	4088 AAAACAAAGTTTGA 4102
Db	121 AAAACAAAGTTTGA 135
RESULT 10	
LOCUS	AL759736 192 bp DNA linear GSS 01-APR-2004
DEFINITION	Arabidopsis thaliana T-DNA Flanking sequence GK-150B10-014640, genomic survey sequence.
ACCESSION	AL759736
VERSION	AL759736.1 GI:21498084
KEYWORDS	GSS.
SOURCE	Arabidopsis thaliana (chale crees)
ORGANISM	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE	1
AUTHORS	Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE	GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)
PMID	12874060
REFERENCE	2
AUTHORS	Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.

TITLE
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

REFERENCE
14756321

AUTHORS
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.

TITLE
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL
Biotechniques 35 (6), 1164-1168 (2003)

REFERENCE
14682050

AUTHORS
Li, Y., Strizhov, N., Rosso, M.G. and Weishaar, B.

TITLE
Direct Submission

JOURNAL
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequences are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
1. .192
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-190B10-014640"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 3.0%; Score 127; DB 10; Length 192;
Best Local Similarity 100.0%; Pred. No. 9.4e-43; Indels 0; Gaps 0;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
2148 ACAGTATACATATGAAAGCAAAATATCCACGAGATAGGTTAGATCCACATT 2207
|||||
Db 56 ACAGTATACATATGAAAGCAAAATATCCACGAGATAGGTTAGATCCACATT 115

Qy
2208 CAATATCTTTTCTCTTTGTTATTTATGAAAAAAATTTATTCAGAAAAAAACGTTTC 2267
|||||
Db 116 CAATATCTTTTCTCTTTGTTATTTATGAAAAAAATTTATTCAGAAAAAAACGTTTC 175

Qy
2268 TTCTCTA 2274
|||||
Db 176 TTCTCTA 182

RESULT 11
CC455690 112 bp DNA linear GSS 30-MAY-2003
LOCUS SALK_085740.55.25.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_085740.55.25.x, genomic survey sequence.

ACCESSION
CC455690

VERSION
CC455690.1 GI:31215945

KEYWORDS
GSS.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 (bases 1 to 112)

AUTHORS
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgil, C., Jeake, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Becker, J.R.

TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL
Unpublished (2001)

COMMENT
Contact: Joseph R. Becker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu
This is single pass sequence recovered from the left border of TDNA.

FEATURES
source
1. .112
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_085740.55.25.x"
/clone_1lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/dna_protocols.html"

ORIGIN
Query Match 2.6%; Score 112; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.5e-36; Indels 0; Gaps 0;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
57 TTTAGTTAGAAAAAATCTTCTTTAGCTGCTGCTGTTTAACTTCAATTAAT 116
|||||
Db 1 TTTAGTTAGAAAAAATCTTCTTTAGCTGCTGCTGTTTAACTTCAATTAAT 60

Qy
117 AGTCACATGATATCAATATATATTTGAAATGGAATTAATTA 168
|||||
Db 61 AGTCACATGATATCAATATATATTTGAAATGGAATTAATTA 112

RESULT 12
CC797115 323 bp DNA linear GSS 01-JUL-2003
LOCUS SALK_144490.54.40.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_144490.54.40.x, genomic survey sequence.

ACCESSION
CC797115

VERSION
CC797115.1 GI:32392338

KEYWORDS
GSS.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 (bases 1 to 323)

AUTHORS
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgil, C., Jeake, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Becker, J.R.

TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL
Unpublished (2001)

COMMENT
Contact: Joseph R. Becker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .323

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_14490.54.40.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 2.4%; Score 103; DB 9; Length 323;

Best Local Similarity 99.4%; Pred. No. 1.6e-32; Mismatches 1; Indels 0; Gaps 0;

Matches 153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2676 CAATTCTAACTAATCTATACAACTGATGTTGTTGTAATTATCTTAA 2735

Db 153 CAATTCTAACTAATCTATACAACTGATGTTGTTGTAATTATCTTAA 212

Qy 2736 CCAAGTTTGAATGTCATGTCGAGCTACCTGTGCTCCCTTTTCCCAATAA 2795

Db 213 CCAAAATTTGAAATGTCATGTCGAGCTACCTGTGCTCCCTTTTCCCAATAA 272

Qy 2796 TCTCCTTACATCGACCGGTTAAAGTATTAAAC 2829

Db 273 TCTCCTTACATCGACCGGTTAAAGTATTAAAC 306

ORIGIN

Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linn-Weig 10, Koeln, 50829, Germany. This sequence has been recovered from the left border of the TDNA. It indicates an insertion within the locus defined by BAC clone 128119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1. .92

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="GK-087A04-011968"

/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: A2537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

Query Match 2.2%; Score 91; DB 10; Length 92;

Best Local Similarity 100.0%; Pred. No. 2.4e-27; Mismatches 0; Indels 0; Gaps 0;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2184 GATGATGAGTTGATGCCAATTCATCTTTGCTTGTATTATGAAAAACAA 2243

Db 2 GATGATGAGTTGATGCCAATTCATCTTTGCTTGTATTATGAAAAACAA 61

Qy 2244 TATTATCAGAAAAAACCCTTCTCTCA 2274

Db 62 TATTATCAGAAAAAACCCTTCTCTCA 92

RESULT 13
AL769520 92 bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-087A04-011968,
genomic survey sequence.
AL769520
AL769520.1 GI:21531722
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weishaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 92)
Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
Direct Submission

RESULT 14
AL769556 418 bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-087D01-012260,
genomic survey sequence.
AL769556
AL769556.1 GI:21531758
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weishaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050
 REFERENCE 4 (bases 1 to 418)
 AUTHORS Strizhov,N., Rosso,M.G., Li,Y. and Weishaar,B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
 source
 1. .418
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-087D01-012260"
 /clone_1b="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pACT161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
 Query Match 2.2%; Score 91; DB 10; Length 418;
 Best Local Similarity 100.0%; Pred. No. 2.1e-27;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2184 GATGATGGGTGATGCCATTCATCTTTGCTTGTATTATGAAAAACAA 2243
 DB 8 GATGATGGGTGATGCCATTCATCTTTGCTTGTATTATGAAAAACAA 67

QY 2244 TATTATCAGAAAAACGTTCTCTCTA 2274
 DB 68 TATTATCAGAAAAACGTTCTCTCTA 98

RESULT 15
 CDS0A2BQ 2315 bp mRNA linear HTC 06-FEB-2004
 LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 DEFINITION GSLTJS902C06 of Adult vegetative tissue of strain col-0 of
 Arabidopsis thaliana (thale cress).
 ACCESSION BX827650.1 GI:42459424
 VERSION BX827650
 KEYWORDS HTC; GSLT cDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 2315)
 CastellI,V., Aury,J.M., Jallion,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2315)
 Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (18-NOV-2003) Genoscope - Centre National de Sequenage :
 JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 PUBMED - Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G, Genoscope members carried out sequencing and annotation : CastellI V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
 UNGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/FullLength
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

FEATURES
 source
 1. .2315
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="GSLTJS902C06"
 /tissue_type="Adult vegetative tissue"
 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"
 1. .2315
 /gene="At4g37750"

ORIGIN
 Query Match 2.0%; Score 84; DB 4; Length 2315;
 Best Local Similarity 100.0%; Pred. No. 1.8e-24;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3999 TCTTCTCTTATTAATATCCCTCAAAACCCCTCTATATCTCCGTAAGCCCC 4058
 DB 1 TCTTCTCTTATTAATATCCCTCAAAACCCCTCTATATCTCCGTAAGCCCC 60

QY 4059 CTTCCCTGTTCTCTACCGCAACA 4082
 DB 61 CTTCCCTGTTCTCTACCGCAACA 84

RESULT 16
 AL754990 92 bp DNA linear GSS 01-APR-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-060D01-013874,
 DEFINITION genomic survey sequence.
 ACCESSION AL754990
 VERSION AL754990.1 GI:21487488
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weishaar,B.
 GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 PUBMED 12874060

REFERENCE 2
 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weishaar,B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 PUBMED 14756321

REFERENCE 3
 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weishaar,B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050
 REFERENCE 4 (bases 1 to 92)

AUTHORS Strizhov,N., Rosso,M.G., Li,Y. and Weishaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
FEATURES
 source
 1..92
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-060D01-013874"
 /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
 Query Match 1.9%; Score 80; DB 10; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.2e-22;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 GGGTTGATCCGCATCATATCTTTGCTTTGTTATTTAGAAACAAATATTTAT 2250
 |||||
 9 GGGTTGATCCGCATCATATCTTTGCTTTGTTATTTAGAAACAAATATTTAT 68
 |||||

QY 2251 CAGGAAAAAAGCTTCTTC 2270
 |||||
 69 CAGGAAAAAAGCTTCTTC 88
 |||||

Db

RESULT 17
 BP561373 424 bp mRNA linear EST 24-NOV-2004
 LOCUS BP561373 RAFL6 Arabidopsis thaliana cDNA clone RAFL06-86-Pl9 5',
 DEFINITION mRNA sequence.
 ACCESSION BP561373 GI:56086434
 VERSION BP561373
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 424)
 Seki,M., Narusaka,M., Kamliya,A., Ishida,J., Satou,M., Sakurai,T., Nakajima,M., Enjuu,A., Akiyama,K., Ono,Y., Muramatsu,M., Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
 Functional annotation of a full-length Arabidopsis cDNA collection
 11910074
 296 (5565), 141-145 (2002)
 On Jun 20, 2004 this sequence version replaced gi:48977139.
 Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: msek@rkc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a

modified plusucscript vector as a SctI/XhoI insert. Please visit our web site (<http://pfigweb.gsc.riken.go.jp/>) for further details.

FEATURES
 source
 1..424
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL06-86-Pl9"
 /dev_stage="plants at various developmental stages from germination to mature seeds"
 /lab_host="DH10B"
 /clone_1lb="RAFL6"
 /note="Site 1: SctI; Site 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

ORIGIN
 Query Match 1.8%; Score 75; DB 3; Length 424;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4154 TTGGAAGATTTATGAAAGAAAGTGAAGTACATTATGAAAGAAAGACGAAA 4213
 |||||
 85 TTGGAAGATTTATGAAAGAAAGTGAAGTACATTATGAAAGAAAGACGAAA 144
 |||||

QY 4214 CCAGAAAAAGAAACC 4228
 |||||

Db 145 CCAGAAAAAGAAACC 159
 |||||

RESULT 18
 BH934314 694 bp DNA linear GSS 01-OCT-2002
 LOCUS BH934314
 DEFINITION od65g10.g1 B. oleracea002 Brassica oleracea genomic, genomic survey sequence.
 ACCESSION BH934314
 VERSION BH934314.1 GI:23414380
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 694)
 Mash,W., Rabinowicz,P.D. and Wilson,R.K.
 Mash,W., Rabinowicz,P.D. and Wilson,R.K.
 Whole genome shotgun reads from Brassica oleracea
 Unpublished (2002)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: rsubmissions@wustl.wustl.edu
 Plate: od65 row: 9 column: 10
 Seq primer: -28RPOT reverse
 Class: shotgun
 High quality sequence stop: 551.
FEATURES
 source
 1..694
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_1lb="B.oleracea002"
 /note="Vector: pOTW13. Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN
 Query Match 1.7%; Score 73; DB 9; Length 694;
 Best Local Similarity 100.0%; Pred. No. 9.9e-20;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3928 AAGTAAGAAAGCTTTTCTCATTAAGACACGATCCACGAGATTCAACGCAAT 3987
 |||||
 Db 75 AAGTAAGAAAGCTTTTCTCATTAAGACACGATCCACGAGATTCAACGCAAT 134
 |||||

QY 3988 TTGNGCTTGCTC 4000
 |||||
 Db 135 TTGTGCTTGCTC 147
 |||||

RESULT 19
 AL756782 268 bp DNA linear GSS 01-APR-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-113A12-012505,
 DEFINITION genomic survey sequence.
 ACCESSION AL756782
 VERSION AL756782.1 GI:21489280
 KEYWORDS GSS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.

REFERENCE 1
 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
 GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL 12874060
 PUBMED
 REFERENCE 2
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Weishaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL 14756321
 PUBMED
 REFERENCE 3
 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
 Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL 14682050
 PUBMED
 REFERENCE 4 (bases 1 to 268)
 Li, Y., Rosso, M.G., Strizhov, N. and Weishaar, B.
 Direct Submission
 Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion within the locus defined by BAC clone
 T8119. Details on the protocols used for generation of the
 sequence are described in References 1-3. The sequences are
 generated at the MPI for Plant Breeding Research in the context of
 the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
 program designated 'GABI'. Information on line availability can be
 found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

COMMENT Location/Qualifiers
 1..268
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-113A12-012505"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match 1.7%; Score 71; DB 10; Length 268;
 Best Local Similarity 100.0%; Fred. No. 7.7e-19;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2026 TAGTAATTACACATTTTAAACCGTCCATCCAGATTGTAATAGTGAATTCGAACA 2085
 |||||
 Db 29 TAGTAATTACACATTTTAAACCGTCCATCCAGATTGTAATAGTGAATTCGAACA 88
 |||||

QY 2086 TTTT TTTT TTTT 2096
 |||||
 Db 89 TTTT TTTT TTTT 99
 |||||

RESULT 20
 CB260786 594 bp mRNA linear EST 06-NOV-2003
 LOCUS CB260786
 DEFINITION 65-B9572-012-004-B17-T7R MP1Z-ADIS-012 Arabidopsis thaliana cDNA
 clone MP1ZP769B174Q 5-PRIME, mRNA sequence.
 ACCESSION CB260786
 VERSION CB260786.1 GI:32885559
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.

REFERENCE 1 (bases 1 to 594)
 Schmidt, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altman, T.,
 Mitchell-Olds, T. and Weishaar, B.
 Large-scale identification and analysis of genome-wide
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 Genome Res. 13 (6), 1250-1257 (2003)

JOURNAL 12799357
 PUBMED
 REFERENCE 2
 Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 594 Std Error: 0.00
 Plate: 4 row: B column: 17
 Seq primer: T7R, CTATATGCACTCACTATAGGA.
 Location/Qualifiers
 1..594
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /ecotype="landsberg erecta"
 /db_xref="GABI:590183"
 /db_xref="taxon:3702"
 /clone="MP1ZP769B174Q"
 /issue_type="whole plant"
 /lib_stage="adult plant, mixed stressses"
 /lib_host="E. coli XL1-Blue MFP"
 /clone="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; cDNA
 library from Arabidopsis thaliana, accession landsberg
 erecta; six weeks old total plants grown under long-day
 conditions in soil, whole adult plants were treated for 24
 hours with different stressses, (1) at 4M-0 C in the dark,
 (2), at 37 Grad C in the dark, (3) lying in the lab after
 removing from soil, (4) in the greenhouse after wounding
 leaves with a forceps, (5) in the lab watering with a 150
 mM NaCl solution, (6) at 26 Grad C in the light/UV; equal
 quantities of stressed plant material were pooled; library
 was made at the Max-Planck-Institute for Plant Breeding
 Research, Cologne, Germany; cloning sites SalI-NotI,
 primer sites and orientation:
 T7-SalI-CCACCGCTCCG-5prime-cDNA-polyA-CC-NotI-SP6; Note:
 Sequencing granted in the context of the GABI Arabidopsis
 Verbund II: Genetic Diversity, 'Reestablishment of
 high-efficiency SNP-based mapping tools and development of

methods for genome-wide mutation detection' Pi: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 1.6%; Score 68; DB 6; Length 594;
Best Local Similarity 99.2%; Pred. No. 1.4e-11; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 1;

Qy 4110 GGTGTCTTCCTGTGTAACCAATGATGGTTTACCTTACTTCTGAGAGATTATTAAG 4169
Db 24 GGTGTCTTCCTGTGTAACCAATGATGGTTTACCTTACTTCTGAGAGATTATTAAG 83

Qy 4170 AAGAAAGAGTGAAGATCACTTATAGAAAGAGAGCAAGAACCAAAAGAAACC 4228
Db 84 AAGAGAGAGTGAAGATCACTTATAGAAAGAGAGCAAGAACCAAAAGAAACC 142

RESULT 21
AL769557 110 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-087D01-012440,
DEFINITION genomic survey sequence.

ACCESSION AL769557
VERSION AL769557.1 GI:21531759
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060

REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321

REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050

REFERENCE 4
AUTHORS Rosso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.
TITLE Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
JOURNAL It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

1..110
location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-087D01-012440"

/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AF537514). The lines contain one or more T-DNA insertions. The DNA fragment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 1.5%; Score 65; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2210 ATATCTTTTGTCTTGTATTTAGAAAACAATTTATTCGAGAAAAAGCTTTCTT 2269
Db 46 ATATCTTTTGTCTTGTATTTAGAAAACAATTTATTCGAGAAAAAGCTTTCTT 105

Qy 2270 CTCTA 2274
Db 106 CTCTA 110

RESULT 22
AL754991 96 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-060D01-013875,
DEFINITION genomic survey sequence.

ACCESSION AL754991
VERSION AL754991.1 GI:21487489
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060

REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321

REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050

REFERENCE 4
AUTHORS Rosso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.
TITLE Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
JOURNAL It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

1..96
location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-087D01-012440"

TITLE Shim, P., Zimmerman, J. and Ecker, J. R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

FEATURES
source Location/Qualifiers
1..56
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_1lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 1.0%; Score 43; DB 9; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2524 TCATAGGCGCTTACGTATTTGAGCTTACTGTAAGTAAAGCT 2566
14 TCATAGGCGCTTACGTATTTGAGCTTACTGTAAGTAAAGCT 56

RESULT 26
BH451280/c 335 bp DNA linear GSS 12-DEC-2001
LOCUS BOGNN777R BOGN Brassica oleracea genomic clone BOGNN77, genomic
DEFINITION Survey sequence.
ACCESSION BH451280
VERSION BH451280.1 GI:17636991
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 335)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Mortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)

JOURNAL PUBMED 15805490
COMMENT Other GSSs: BOGNN777F
Contact: Chris Town
TIGR
9112 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source Location/Qualifiers
1..335
/organism="Brassica oleracea"
/mol_type="genomic DNA"

/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_1lb="BOGNN77"
/clone_1lb="BOGN"
/note="Vector: pHOSt, Site 1. BectXI, 2-3 kb sheared
genomic DNA inserted into pHOSt using BectXI linkers"

ORIGIN

Query Match 0.8%; Score 32; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2855 GTACAAACATGTACATATATAGACAGACAT 2886
96 GTACAAACATGTACATATATAGACAGACAT 65

RESULT 27
BH510257/c 796 bp DNA linear GSS 13-DEC-2001
LOCUS BOHKU787R BOHK Brassica oleracea genomic clone BOHKU78, genomic
DEFINITION Survey sequence.
ACCESSION BH510257
VERSION BH510257.1 GI:17718347
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 796)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Mortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)

JOURNAL PUBMED 15805490
COMMENT Other GSSs: BOHKU787F
Contact: Chris Town
TIGR
9112 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES

source Location/Qualifiers
1..796
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_1lb="BOHKU78"
/note="Vector: pHOSt, Site 1. BectXI, 2-3 kb sheared
genomic DNA inserted into pHOSt using BectXI linkers"

ORIGIN

Query Match 0.8%; Score 32; DB 9; Length 796;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2855 GTACAAACATGTACATATATAGACAGACAT 2886
644 GTACAAACATGTACATATATAGACAGACAT 613

RESULT 28
CW938563/c 897 bp DNA linear GSS 20-DEC-2004
LOCUS TCBI8.3_F08_T7 Tribolium BAC library Tribolium castaneum genomic,
DEFINITION genomic survey sequence.


```

ACCESSION      CM938563
VERSION        CM938563.1
SOURCE         GSS
ORGANISM       Tribolium castaneum (red flour beetle)
REFERENCE      1
AUTHORS        Savaard,J. and Tautz,D.
TITLE          Tribolium castaneum BAC-ends sequencing project
JOURNAL        Unpublished (2003)
COMMENT        Contact: Savaard, J.
                Abteiling fur Evolutionsgenetik, AG Tautz
                Institut fur Genetik, Universitat zu Koin
                Weyerstra 121, 50931 Koin, Germany
                Tel: 49 221 470 6911
                Fax: 49 221 470 5975
                Email: savaard@uni-koeln.de
                Class: BAC ends.

FEATURES
  source
    1..897
    /organism="Tribolium castaneum"
    /mol_type="genomic DNA"
    /db_xref="taxon:7070"
    /clone_id="Tribolium BAC library"
    /note="Vector: pBAC3.6, Site_1: EcoRI, Site_2: EcoRI,
    library constructed by Exelixis Inc."

ORIGIN
Query Match      0.6%; Score 27; DB 10; Length 897;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 24 TAATACGACTCATTATGAGGAGCTCGA 50
Db 67 TAATACGACTCATTATGAGGAGCTCGA 41

RESULT 29
LOCUS          CM938873      901 bp      DNA      linear      GSS 20-DEC-2004
DEFINITION     TB19.1_C07.T7 Tribolium BAC library Tribolium castaneum genomic,
ACCESSION      CM938873
VERSION        CM938873.1
KEYWORDS       GSS.
SOURCE         Tribolium castaneum (red flour beetle)
ORGANISM       Tribolium castaneum
REFERENCE      1
AUTHORS        Savaard,J. and Tautz,D.
TITLE          Tribolium castaneum BAC-ends sequencing project
JOURNAL        Unpublished (2003)
COMMENT        Contact: Savaard, J.
                Abteiling fur Evolutionsgenetik, AG Tautz
                Institut fur Genetik, Universitat zu Koin
                Weyerstra 121, 50931 Koin, Germany
                Tel: 49 221 470 6911
                Fax: 49 221 470 5975
                Email: savaard@uni-koeln.de
                Class: BAC ends.

FEATURES
  source
    1..901
    /organism="Tribolium castaneum"
    /mol_type="genomic DNA"
    /db_xref="taxon:7070"
    /clone_id="Tribolium BAC library"
    /note="Vector: pBAC3.6, Site_1: EcoRI, Site_2: EcoRI,

```

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ORIGIN          Library constructed by Exelixis Inc."

Query Match      0.6%; Score 27; DB 10; Length 901;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 24 TAATACGACTCATTATGAGGAGCTCGA 50
Db 70 TAATACGACTCATTATGAGGAGCTCGA 44

RESULT 30
LOCUS          BF925688      298 bp      mRNA      linear      EST 19-JAN-2001
DEFINITION     CM2-NT0192-291100-578-h07 NT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BF925688
VERSION        BF925688.1
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
                Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
                Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
                O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                Simpson,A.J.
                Shotgun sequencing of the human transcriptome with ORF expressed
                sequence tags
                Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                10737800
                Contact: Simpson A.J.G.
                Laboratory of Cancer Genetics
                Ludwig Institute for Cancer Research
                Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                Brazil
                Tel: +55-11-2704922
                Fax: +55-11-2707001
                Email: asimpson@ludwig.org.br
                This sequence was derived from the FAPESP/LICR Human Cancer Genome
                Project. This entry can be seen in the following URL
                (http://www.ludwig.org.br/scripts/gethtml2.pl?fl=CM2&ct=CM2-NT0192-
                291100-578-h07&ct3=2000-11-29&ct4=1)
                Seq primer: puc 18 forward
                High quality sequence start: 27
                High quality sequence stop: 298.

FEATURES
  source
    1..298
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /dev_stage="Adult"
    /clone_id="NT0192"
    /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
    Site 2: SmaI; A mini-library was made by cloning products
    derived from ORSTES PCR (U.S. Letters Patent application
    No. 196,716 - Ludwig Institute for Cancer Research)
    profiles into the pUC 18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
    low stringency conditions."

ORIGIN
Query Match      0.6%; Score 26; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3910 AAAATTAATAATTAATAATTAAGTAA 3935
Db 249 AAAATTAATAATTAATAATTAAGTAA 274

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RESULT 31
BE145442

LOCUS BE145442 225 bp mRNA linear EST 21-JUN-2000

DEFINITION IL5-HT0198-291099-009-F06 HT0198 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE145442

VERSION BE145442.1 GI:8608166

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Negrão,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT 10737800

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

TEL: +55-11-2704922
FAX: +55-11-2707001
EMAIL: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5-HT0198-291099-009-F06&ct3=1999-10-29&ct4=1)

Seq primer: puc 18 forward

High quality sequence stop: 224.

FEATURES

source Location/Qualifiers

1..225

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_id="HT0198"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 0.6%; Score 25; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAGTTTCAATT 3495
|||||
Db 197 AAAAAAAAAAGTTTCAATT 221

RESULT 32
CE734860/c

LOCUS CE734860 388 bp DNA linear GSS 30-SEP-2003

DEFINITION tigr-gss-dog-17000330204499 Dog Library Canis familiaris genomic,

ACCESSION CE734860

VERSION CE734860.1 GI:37074980

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 388)

AUTHORS Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

COMMENT 14512627

CONTACT: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org

Class: shotgun.

FEATURES

source Location/Qualifiers

1..388

/organism="Canis familiaris"

/mol_type="genomic DNA"

/strain="Standard Poodle"

/db_xref="taxon:9615"

/clone_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 388;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3911 AAAAAAAAAATGAAAGTAA 3935
|||||
Db 128 AAAAAAAAAATGAAAGTAA 104

RESULT 33
AZ088538

LOCUS AZ088538 488 bp DNA linear GSS 08-MAY-2000

DEFINITION RPCI-23-470D9.TJ RPCI-23 Mus musculus genomic clone RPCI-23-470D9,

ACCESSION AZ088538

VERSION AZ088538.1 GI:7730586

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 488)

AUTHORS Zhao,S., Mierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akintet,B., Levina,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.

TITLE Mouse BAC End Sequences from Library RPCI-23

JOURNAL Unpublished (1999)

COMMENT Other_GSSs: RPCI-23-470D9.TV

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pletier de Jong (pieterdejong.med.buhalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buhalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 470 row: D column: 9

Seq primer: SP6
Class: BAC ends.

FEATURES
Source Location/Qualifiers

1..488
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPC1-23-470D9"
/sex="Female"
/lab_host="DH10B"
/clone_1lb="RPC1-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI, Site 2: EcoRI, Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI MethyIase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 0.6%; Score 25; DB 9; Length 488;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 TTCTCTGTAGCTGTGTGTGTCT 97
Db 339 TTCTCTGTAGCTGTGTGTGTGT 363

RESULT 34

AG013324/c 715 bp DNA linear GSS 16-FEB-2005
LOCUS Homo sapiens genomic DNA, 21q region, clone: S82AN, genomic survey
DEFINITION
ACCESSION AG013324 AG005647
VERSION AG013324.2 GI:55788761
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REFERENCE 2 (bases 1 to 715)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1998) Masahira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
226-0045, Japan (E-mail:hattori@gscc.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
COMMENT On Nov 16, 2004 this sequence version replaced gi:3513370.
AG005647: Submitted (07-Mar-1998).

FEATURES
Source Location/Qualifiers

1..715
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="S82AN"

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 715;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 GCCTAATACGACTCCTATAGGAG 45
|||||

Db 510 GCCTAATACGACTCCTATAGGAG 486

RESULT 35

CNS01002/c 755 bp DNA linear GSS 14-JUN-2001
LOCUS Anopheles gambiae GSS SP6 end of clone 26M24 of NotreDamel library
DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.

ACCESSION AL153762
VERSION AL153762.1 GI:7014681
KEYWORDS GSS.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Culicidae; Anophelinae; Anopheles.

REFERENCE 1 (bases 1 to 755)
AUTHORS Genoscope.

TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage ;
BP 191 91006 Evry cedex - FRANCE (E-mail : seqret@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

REFERENCE 2 (bases 1 to 755)
AUTHORS Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) BMRB, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France

COMMENT This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES
Source Location/Qualifiers

1..755
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="26M24"
/clone_1lb="NotreDamel"
/note="end : SP6"

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 755;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3910 AAAATTAATAATTAATAATTAAGTAA 3934
Db 653 AAAATTAATAATTAATAATTAAGTAA 629
|||||

RESULT 36

BH510250 793 bp DNA linear GSS 13-DEC-2001
LOCUS BOHKU8TR BOHK Brassica oleracea genomic clone BOHKU8, genomic
DEFINITION survey sequence.
ACCESSION BH510250
VERSION BH510250.1 GI:17718340
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 793)
AUTHORS Aylee,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utechtack,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490

COMMENT Other_GSSs: BOHKU8TR

Contact: Chris Town
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TP

Class: sheared ends.

FEATURES

Source

Location/Qualifiers

1..793

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOHKU78"

/note="Vector: pHOSt; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt using BstXI linkers"

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 31;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

1788 AATGCTTAATCATTAATAAATAAG 1812

Db

609 AATGCTTAATCATTAATAAATAAG 633

RESULT 37

CM949303/c

LOCUS TCB33.4_F02.T7 Tribolium BAC library Tribolium castaneum genomic, 798 bp DNA linear GSS 20-DEC-2004

DEFINITION genomic survey sequence.

ACCESSION

CM949303

VERSION CM949303.1 GI:56731923

KEYWORDS

GSS.

SOURCE

Tribolium castaneum (red flour beetle)

ORGANISM Tribolium castaneum Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tribolium.

REFERENCE 1 (bases 1 to 798)

Savard, J. and Tautz, D.

Tribolium castaneum BAC-ends sequencing project

Unpublished (2003)

Contact: Savard, J.

Abteilung fur Evolutionsgenetik, AG Tautz

Institut fur Genetik, Universitat zu Koln

Meyeral 121, 50931 Koln, Germany

Tel: 49 221 470 6911

Fax: 49 221 470 5975

Email: savard@uni-koeln.de

Class: BAC ends.

Location/Qualifiers

1..798

/organism="Tribolium castaneum"

/mol_type="genomic DNA"

/strain="GA-2"

/db_xref="taxon:7070"

/clone_lib="Tribolium BAC library"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Library constructed by Exelixis Inc."

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 31;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

24 TAATACGACTCATATAGGAGCTC 48

Db

69 TAATACGACTCATATAGGAGCTC 45

RESULT 38

AG409273

LOCUS AG409273 860 bp DNA linear GSS 21-DEC-2004

DEFINITION Mus musculus molossinus DNA, clone:MSMg01-269A12.T7, genomic survey sequence.

ACCESSION AG409273

VERSION AG409273.1 GI:48051959

KEYWORDS

GSS.

Mus musculus molossinus (Japanese wild mouse)

Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 Abe, K., Noguchi, H., Tagawa, K., Yuzurina, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwa, K. and Shiroishi, T.

Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end

sequence-SNP analysis

Genome Res. 14 (12), 2439-2447 (2004)

2 (bases 1 to 860)

15574823

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suenho-chou, Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan

(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/),

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

clones are derived from the mouse BAC library MSMg01. For BAC library availability, Bio Resource Center,

Tsukuba Institute, The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rc.riken.jp

PRIMERS

Sequencing : T7

LIBRARY : pBAC3.6

Vector : EcoRI

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1..860

/organism="Mus musculus molossinus"

/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMg01-269A12.T7"

/sex="male"

/issue_type="mixture of kidney and spleen"

/clone_lib="MSMg01 Mouse Male BAC library"

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 31;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

21 GCCTAATACGACTCATATAGGAG 45

Db

10 GCCTAATACGACTCATATAGGAG 34

RESULT 39

CM940939/c

LOCUS CM940939 898 bp DNA linear GSS 20-DEC-2004

DEFINITION TCB22.1_A08.T7 Tribolium BAC library Tribolium castaneum genomic, genomic survey sequence.

ACCESSION

CM940939

VERSION CM940939.1 GI:56723552

KEYWORDS
SOURCE GSS.
ORGANISM Tribolium castaneum (red flour beetle)

REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tribolium.
TITLE 1 (bases 1 to 898)
JOURNAL Savard, J. and Tautz, D.
 Tribolium castaneum BAC-ends sequencing project
 Unpublished (2003)
COMMENT Contact: Savard, J.
 Abteilung fur Evolutionsgenetik, AG Tautz
 Institut fur Genetik, Universitat zu Koln
 Weyertal 121, 50931 Koln, Germany
 Tel.: 49 221 470 6911
 Fax: 49 221 470 5975
 Email: savard@uni-koeln.de
 Class: BAC ends.

FEATURES
source
 1..898
 /organism="Tribolium castaneum"
 /mol_type="genomic DNA"
 /strain="GA-2"
 /db_xref="taxon:7070"
 /clone_lib="Tribolium BAC library"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Library constructed by Exelixis Inc."

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 898;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCCTATAGGAGCTC 48
 |||
 64 TAATACGACTCCTATAGGAGCTC 40

Db

RESULT 40
 AG400158 924 bp DNA linear GSS 21-DEC-2004
LOCUS Mus musculus molossinus DNA, clone:MSMg01-234D03.T7, genomic survey
DEFINITION
 AG400158
ACCESSION
 AG400158.1 GI:48041813
VERSION
 GSS.
KEYWORDS
 Mus musculus molossinus (Japanese wild mouse)
SOURCE
 Mus musculus molossinus
ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwa, K. and Shitoh, T.
REFERENCE
AUTHORS Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
TITLE Genome Res. 14 (12), 2439-2447 (2004)
JOURNAL 15574823
 2 (bases 1 to 924)
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
REFERENCE
AUTHORS Direct Submision
TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Yokohama, Kanagawa, 230-0045, Japan
JOURNAL 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
 (E-mail: hattori@sc.riken.jp, URL: http://hsp.gsc.riken.go.jp/, Tel.: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp

PRIMERS
 Sequencing : T7
LIBRARY
 Vector : pBACe3.6
 R Site 1 : EcoRI
 R Site 2 : EcoRI.

FEATURES
source
 1..924
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-234D03.T7"
 /sex="male"
 /tissue type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 924;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 GCCTAATACGACTCCTATAGGAG 45
 |||
 80 GCCTAATACGACTCCTATAGGAG 104

Db

RESULT 41
 CM937215/c 1036 bp DNA linear GSS 20-DEC-2004
LOCUS TcB16.1_F06.T7 Tribolium BAC library Tribolium castaneum genomic,
DEFINITION
 genomic survey sequence.
ACCESSION
 CM937215
VERSION
 CM937215.1 GI:56719828
KEYWORDS
 GSS.
SOURCE
 Tribolium castaneum (red flour beetle)
ORGANISM
 Tribolium castaneum
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tribolium.
 1 (bases 1 to 1036)
 Savard, J. and Tautz, D.
REFERENCE
AUTHORS Tribolium castaneum BAC-ends sequencing project
TITLE Unpublished (2003)
JOURNAL
COMMENT Contact: Savard, J.
 Abteilung fur Evolutionsgenetik, AG Tautz
 Institut fur Genetik, Universitat zu Koln
 Weyertal 121, 50931 Koln, Germany
 Tel.: 49 221 470 6911
 Fax: 49 221 470 5975
 Email: savard@uni-koeln.de
 Class: BAC ends.

FEATURES
source
 1..1036
 /organism="Tribolium castaneum"
 /mol_type="genomic DNA"
 /strain="GA-2"
 /db_xref="taxon:7070"
 /clone_lib="Tribolium BAC library"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Library constructed by Exelixis Inc."

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 1036;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCCTATAGGAGCTC 48
 |||
 66 TAATACGACTCCTATAGGAGCTC 42

Db

RESULT 42
CK121482/c 161 bp mRNA linear EST 01-JUN-2004
DEFINITION 202020.p1 AWM1 Arabidopsis thaliana cDNA clone MPMGP2011020202
5-PRIME, mRNA sequence.
ACCESSION CK121482
VERSION CK121482.1 GI:47831798
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
COMMENT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosid II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 161)
AUTHORS Fellner,T., Immink,R.G.H., Cahill,D.J. and Kersten,B.
TITLE Generation of a cDNA expression library from Arabidopsis inflorescence meristem
JOURNAL Unpublished (2003)
COMMENT Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Insestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
Fax: +49(0)30/84131128
Email: Kersten@molgen.mpg.de
Insert Length: 161 Std Error: 0.00
Plate: 202 row: 0 column: 20
Seq primer: P0E65.
FEATURES
source
Location/Qualifiers
1..161
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="GABI:951967"
/db_xref="taxon:3702"
/clone="MPMGP2011020202"
/cbase_type="inflorescence meristem"
/dev_stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSE111"
/clone_1lb="AtM1"
/note="Vector: POE-30NAST-actb (AY386205); Site 1: SalI; Site 2: NotI; About 1 week after bolting, cDNA synthesis using SuperscriptTM-system (Invitrogen) with an oligo(dT)-primer containing NotI restriction site and a SalI adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at <https://gabi.rzp.de>"

ORIGIN
Query Match 0.6%; Score 24; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAAATGAGCTCATTAGGGAGCT 47
Db 111 TAAATGAGCTCATTAGGGAGCT 88

RESULT 43
AQ955990/c 191 bp DNA linear GSS 28-JAN-2000
LOCUS AQ955990
DEFINITION LERRA118TR LERA Arabidopsis thaliana genomic clone LERRA118, genomic survey sequence.
ACCESSION AQ955990
VERSION AQ955990.1 GI:6783819
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
COMMENT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosid II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 191)
AUTHORS Buell,C.R., Lin,X., Pal,G., Barnstead,M., Bowman,C., Uterbach,T., Feldjlyum,T., Liang,F., Creasy,T. and Fraser,C.M.
TITLE Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
JOURNAL Unpublished (2000)
COMMENT Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For additional information, see <http://www.tigr.org/cdb/ac/at.html>
Seq primer: TR
Class: shotgun.
FEATURES
source
Location/Qualifiers
1..191
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERRA118"
/clone_1lb="LERA"
/note="Organ: Leaf; Vector: PHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."

ORIGIN
Query Match 0.6%; Score 24; DB 9; Length 191;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CCTAATGAGCTCATTAGGGAG 45
Db 79 CCTAATGAGCTCATTAGGGAG 56

RESULT 44
CK573161 278 bp mRNA linear EST 01-MAR-2004
LOCUS CK573161
DEFINITION 1172 Plasmodium yoelii liver stage LCM cDNA library Plasmodium yoelii cDNA, mRNA sequence.
ACCESSION CK573161
VERSION CK573161.1 GI:44827251
KEYWORDS EST.
SOURCE Plasmodium yoelii
ORGANISM Plasmodium yoelii
COMMENT Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 278)
AUTHORS Blair,P.L., Witney,A., Carnucci,D.J., Azad,A.F. and Aguilar,J.C.
TITLE Transcriptional analysis of in vivo Plasmodium yoelii liver stage gene expression
JOURNAL Mol. Biochem. Parasitol. 142 (2), 177-183 (2005)
PUBMED 15876462
COMMENT Contact: Sacchi JB
Department of Microbiology and Immunology
University of Maryland School of Medicine
BRB 13-009, 655 W. Baltimore Street, Baltimore, MD 21201, USA
Tel: 410 706 4071
Email: jsacc001@umaryland.edu
POLYA=Yes.
FEATURES
source
Location/Qualifiers
1..278
/organism="Plasmodium yoelii"
/mol_type="mRNA"
/strain="17X NL"
/db_xref="taxon:5861"
/dev_stage="40 hour liver schizont"

/clone_lib="Plasmodium yoelii liver stage LCM cDNA library"
 /note="Vector: pTriplEx2; Plasmodium yoelii liver stage parasites were harvested by laser capture microdissection, from infected Balb/c mouse liver cryosections, 40 hours after inoculation with sporozoites. Total RNA was then isolated using the Strataprep Total RNA microprep kit from Stratagene."

ORIGIN

Query Match 0.6%; Score 24; DB 7; Length 278;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAAGTTTCAAT 3494
 Db 183 AAAAAAAAAAAGTTTCAAT 206

RESULT 45 DR973784 278 bp mRNA linear EST 03-AUG-2005
 LOCUS CHUT008f12.b1 Primary Chick Utricle Subtraction Gallus gallus cDNA
 DEFINITION 3, mRNA sequence.

ACCESSION DR973784.1 GI:71775897
 VERSION DR973784.1
 KEYWORDS Gallus gallus (chicken)
 SOURCE Gallus gallus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 278)
 Lovett, M., Clifton, S., Page, D., Hillier, L., Martin, J., Wylie, T., Dane, M., Theising, B., Bowers, Y., Gibbons, M., Rittler, E., Bennett, J., Ronko, I., Teagareishvili, R., Kennedy, S., Waterston, R. and Wilson, R.
 AUTHORS WashU Chicken EST Project
 JOURNAL Unpublished (2003)
 COMMENT Contact: Mike Lovett
 Washington University School of Medicine
 Email: lovett@genetics.wustl.edu
 DNA sequencing by: Washington University Genome Sequencing Center
 For information on obtaining a clone please contact: Mike Lovett (lovett@genetics.wustl.edu) This library was directionally cloned.
 FEATURES Location/Qualifiers

1..278
 source
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /lab_host="DH5alpha"
 /clone_lib="Primary Chick Utricle Subtraction"
 /note="Vector: pAMP1; 1st strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in pAMP1 vector in annealing reaction with Uracil DNA Glycosylase (UDG)."

ORIGIN

Query Match 0.6%; Score 24; DB 8; Length 278;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATATGAGCTCACTATGAGGAGC 46
 Db 217 CTATATGAGCTCACTATGAGGAGC 194

RESULT 46 A0955989 310 bp DNA linear GSS 28-JAN-2000
 LOCUS LERAI18TF LERA Arabidopsis thaliana genomic clone LERAI18, genomic
 DEFINITION

survey sequence.

ACCESSION A0955989
 VERSION A0955989.1 GI:6783818
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 310)
 Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Uterbach, T., Feldlynn, T., Liang, F., Creasy, T. and Fraser, C.M.
 AUTHORS Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
 JOURNAL Unpublished (2000)
 COMMENT Contact: Xiaoying Lin
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: at@tigr.org
 For additional information, see <http://www.tigr.org/tdb/at.html>
 Seq primer: TF
 Class: shotgun.

JOURNAL

FEATURES Location/Qualifiers
 1..310
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecoli_type="Landsberg erecta"
 /db_xref="taxon:3702"
 /clone_lib="LERAI18"
 /note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."

FEATURES

1..310
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecoli_type="Landsberg erecta"
 /db_xref="taxon:3702"
 /clone_lib="LERAI18"
 /note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."

ORIGIN

Query Match 0.6%; Score 24; DB 9; Length 310;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATGAGCTCACTATGAGGAGC 45
 Db 9 CCTAATGAGCTCACTATGAGGAGC 32

RESULT 47 BH451271 318 bp DNA linear GSS 12-DEC-2001
 LOCUS BOGN77TF BOGN Brassica oleracea genomic clone BOGN77, genomic survey sequence.
 DEFINITION BH451271
 ACCESSION BH451271.1 GI:17636982
 VERSION BH451271
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea

JOURNAL

REFERENCE 1 (bases 1 to 318)
 Ayala, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Uterbach, T.R., Wortman, J.R., White, O.R. and Town, C.D.
 AUTHORS Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
 JOURNAL Genome Res. 15 (4), 487-495 (2005)
 PUBMED 15805490
 COMMENT Other_GSSs: BOGN77TR
 Contact: Chris Town

COMMENT

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
 Seg primer: TF
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..318

/organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone_1fb="BOGN77"
 /clone_1lb="BOGN"
 /note="Vector: PHOS1, Site 1: BstXI, 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 0.6%; Score 24; DB 9; Length 318;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1310 ATCATACCAAAATCAAGGAGG 1333
 Db 25 ATCATACCAAAATCAAGGAGG 48

RESULT 48
 CV263561 320 bp mRNA linear EST 22-SEP-2004
 LOCUS WS02022.B21_C24 PTXN-IB-N-A-11 Populus trichocarpa x Populus nigra
 DEFINITION cDNA clone WS02022_C24 3', mRNA sequence.
 ACCESSION CV263561
 VERSION CV263561.1 GI:52516536
 KEYWORDS EST.

SOURCE
 ORGANISM
 Populus trichocarpa x Populus nigra
 Populus trichocarpa x Populus nigra
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
 1 (bases 1 to 320)

REFERENCE
 AUTHORS
 Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
 Kirpatrick,R., Liu,Y., Palmquist,D., Stott,J., Barber,S., Yang,G.,
 Babakaliff,R., Brown-John,M., Chand,S., Featherstone,R., Mason,A.,
 Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
 Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
 Bohlmann,J.
 The poplar transcriptome: Analysis of expressed sequence tags from
 multiple cDNA libraries
 Unpublished (2004)

JOURNAL
 COMMENT
 Genome BC forest genomics program
 University of British Columbia
 Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
 Vancouver, British Columbia, Canada, V6T 1Z3
 Tel: 1-604-822-0282
 Fax: 1-604-822-2114
 Email: bohlmann@mel.ubc.ca
 Plate: WS02022 row: C column: 24
 High quality sequence scop: 320
 POLY=A=yes.

FEATURES
 source
 Location/Qualifiers
 1..320

/organism="Populus trichocarpa x Populus nigra"
 /mol_type="mRNA"
 /cultivar="NXM6"
 /db_xref="taxon:293756"
 /clone="WS02022_C24"
 /sex="Male"
 /lab_host="R. coli DH10B T1 phage resistant cells"
 /clone_1lb="PTXN-IB-N-A-11"
 /note="Vector: pBluescript II SK (+) XR, Site 1: EcoRI (5'
 end of cDNA); Site 2: XhoI (3' end of cDNA); Sapling trees
 two metres in height and grown under greenhouse conditions
 were exposed to continuous feeding by Cryptorhynchus
 lapathi (poplar and willow borer) adults caged on the

sapling using mesh bags. Bark (with phloem and cambium
 attached) from within the caged region was harvested 2
 hours, 6 hours and 48 hours after the onset of treatment.
 mRNA was isolated from each tissue source independently
 and equal quantities of mRNA from each tissue were then
 pooled. cDNA was prepared from 5 micrograms of mRNA and
 directionally ligated into the pBluescript II SK (+) XR
 vector using the pBluescript II XR cDNA library
 construction kit according to manufacturer's instructions
 with modifications (Stratagene). Plasmid DNA was then
 transformed by electroporation into DH10B cells
 (Invitrogen) for propagation. Normalization was applied
 according to published methods [Bonaldo M.F. et al. (1996)
 Genome Research 6(9):791] in order to reduce the abundance
 of highly expressed transcripts."

ORIGIN

Query Match 0.6%; Score 24; DB 7; Length 320;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3909 GAAAAATAAATTAATTAAGT 3932
 Db 303 GAAAAATAAATTAATTAAGT 280

RESULT 49
 CE127892 339 bp DNA linear GSS 25-SEP-2003
 LOCUS tigr-gss-dog-17000326042655 Dog library Canis familiaris genomic,
 DEFINITION genomic survey sequence.
 ACCESSION CE127892
 VERSION CE127892.1 GI:35224637
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

REFERENCE
 AUTHORS
 1 (bases 1 to 339)
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 14512627

JOURNAL
 COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES
 source
 Location/Qualifiers
 1..339

/organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_1lb="Dog library"
 /note="Site 1: BstXI, Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 0.6%; Score 24; DB 9; Length 339;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3910 AAAAAATAAATTAATTAAGTA 3933
 Db 170 AAAAAATAAATTAATTAAGTA 193

RESULT 50
BM163414
LOCUS
DEFINITION
EST565948 PyBS Plasmodium yoelii yoelii cDNA clone PYCLB94.5' end,
mRNA sequence.
BM163414
ACCESSION
BM163414.1 GI:17309106
SOURCE
EST.
Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 349)
Carlton J.M., Daly T.M., Long C.A., Bergman, L.W., Valdivia A.B.,
Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@igr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mrg.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
source
1..349
location/Qualifiers
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17XL"
/db_species="yoelii"
/db_xref="taxon:73239"
/clone="PYCLB94"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBYJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcytalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HydrizAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HydrizAP vector and plasmid DNA isolated."

ORIGIN
Query Match 0.6%; Score 24; DB 3; Length 349;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAGTTTCAAT 3494
|||||
Db 81 AAAAAAAAAAGTTTCAAT 104
|||||

RESULT 51
AG229188
LOCUS
DEFINITION
Lotus corniculatus var. japonicus DNA, clone:ljB17K01_f, genomic
survey sequence.
AG229188

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AG229188.1 GI:26539812
GSS.
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.

REFERENCE
1
Sato, S., Nakamura, Y. and Tabata, S.
Lotus japonicus BAC End sequences
Published Only in Database (2002)
2 (bases 1 to 350)
Sato, S.
Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)
Location/Qualifiers
1..350
/organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/variety="japonicus"
/db_xref="taxon:34305"
/clone="LjB17K01_f"
/clone_1lb="genomic BAC library"
/note="VECTOR: pBeloBAC11
synonym: Lotus japonicus"

ORIGIN
Query Match 0.6%; Score 24; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3554 TGATTGCAAGTTGCAACAGATG 3577
|||||
Db 160 TGATTGCAAGTTGCAACAGATG 137
|||||

RESULT 52
BZ239509/c
LOCUS
DEFINITION
CH230-456M24.TVB CHORI-230 Segment 2 Rattus norvegicus genomic
clone CH230-456M24, genomic survey sequence.
BZ239509
ACCESSION
BZ239509.1 GI:23899773
GSS.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 390)
Zhao, S., Shetty, J., Shatman, S., Teegate, G., Geer, K.,
Shvartsbeyn, A., Gebreyorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, P., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-456M24.TVB
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@igr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources

QY 22 CCTATACGACTCCTATAGGAG 45
 |||||
 DB 4 CCTATACGACTCCTATAGGAG 27

RESULT 55
 BM163834
 LOCUS
 DEFINITION BM163834 398 bp mRNA linear EST 04-DEC-2001
 EST56357 PyBS Plasmodium yoelii yoelii cDNA clone PYCLK30 5' end.
 mRNA sequence.
 ACCESSION BM163834 GI:17309515
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Plasmodium yoelii yoelii
 Plasmodium yoelii yoelii
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 398)
 Carlson, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Valdivia, A.B.,
 Frazer, C.M. and Carucci, D.J.
 Plasmodium yoelii EST project at TIGR
 Unpublished (2001)
 Contact: Jane Carlson
 Parasite Genomics Group
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-530-9319
 Fax: 301-838-0208
 Email: carlont@tigr.org
 For clone info, please contact the Malaria Research and Reference
 Reagent Resource Center, ATCC
 http://www.malaria.mri.org/mr4pages/index.html
 Seq primer: ADP.

FEATURES

source

Location/Qualifiers
 1..398
 /organism="Plasmodium yoelii yoelii"
 /mol_type="mRNA"
 /strain="7XL"
 /sub_species="yoelii"
 /db_xref="taxon:73239"
 /clone="PYCLK30"
 /dev_stage="asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /clone_1lb="PyBS"
 /note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was
 collected from BALB/cByJ mice infected with Py17XL
 parasites, and leukocytes removed by passage over
 microcrystalline cellulose columns. Total RNA was
 isolated using the guanidinium isothiocyanate method, and
 mRNA isolated using oligo(dT)-cellulose chromatography.
 First strand cDNA synthesis was completed using a 50-base
 primer and reverse transcriptase in the presence of
 5-methyl dCTP. After second strand synthesis, uneven
 termini were treated with Pfu DNA polymerase and EcoRI
 adapters ligated to the blunt ends. The sample was cleaved
 with XhoI and separated on a Sephacryl S-500 column.
 Size-fractionated cDNA was precipitated and ligated to
 HybriZAP arms directionally using EcoRI-XhoI cleaved arms.
 After packaging, the phagemid vector (PAD-GAL4) was
 excised from the HybriZAP vector and plasmid DNA
 isolated."

ORIGIN

Query Match 0.6%; Score 24; DB 3; Length 398;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAAGTTTCAAT 3494
 |||||
 DB 312 AAAAAAAAAAAGTTTCAAT 335

RESULT 56
 BM966009

LOCUS
 DEFINITION BM966009 399 bp mRNA linear EST 20-MAR-2002
 h20f03.y1 Toxocara canis adult PAMPI v1 Toxocara canis cDNA 5'
 PARTIAL LACZ GENE ; mRNA sequence.

ACCESSION BM966009 GI:19558726
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Toxocara canis
 Toxocara canis
 Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
 Ascaridoidea; Toxocaridae; Toxocara.
 1 (bases 1 to 399)
 McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J.,
 Wylie, T., Dante, M., Maria, M., Hillier, L., Kucaba, T., Theising, B.,
 Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
 Tsagarashevili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
 Underwood, K., Steptoe, M., Allen, M., Person, B., Shaller, T.,
 Harvey, N., Schurk, R., Kohn, S., Shih, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. DNA Sequencing by: Washington
 University Genome Sequencing Center
 High quality sequence stop: 118.

FEATURES

source

Location/Qualifiers
 1..399
 /organism="Toxocara canis"
 /mol_type="mRNA"
 /db_xref="taxon:6265"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="Toxocara canis adult PAMPI v1"
 /note="Vector: PAMPI (Gibco); Site 1: NotI; Site 2: SalI;
 The library was constructed by Claire Murphy and Dr. James
 McCarter at Washington University, St. Louis. The cDNA was
 made by using Dynabead oligo-dT priming (Dynal). PCR based
 library using a modified protocol from the SMART PCR cDNA
 Synthesis Kit from Clontech. Directionally cloned into the
 UNO sites of PAMPI. Adult nematodes were collected from
 infected dogs and provided by Dr. Prema Arasu of North
 Carolina State University, Raleigh, NC
 (Prema_Arasu@ncsu.edu)."

ORIGIN

Query Match 0.6%; Score 24; DB 3; Length 399;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CCTATACGACTCCTATAGGAGC 46
 |||||
 DB 11 CCTATACGACTCCTATAGGAGC 34

RESULT 57
 CR057094/c
 LOCUS
 DEFINITION CR057094 418 bp DNA linear GSS 05-JUL-2004
 Forward strand read from insert in 5'HPT insertion targeting and
 chromosome engineering clone MHPN70n09, genomic survey sequence.
 ACCESSION CR057094 GI:49790240
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

GSS; genome survey sequence; MTCR.
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE 1 (bases 1 to 418)
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,T., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>

FEATURES
 source
 1..418
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone_1fb="MHPN0n09"
 /clone_1fb="MHPN"

ORIGIN
 Query Match 0.6%; Score 24; DB 11; Length 418;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAAAATTAATTAAGTAAAGAAA 3939
 Db 309 AAAAAATTAATTAAGTAAAGAAA 286

RESULT 58
 LOCUS AZ301311 423 bp DNA linear GSS 29-DEC-2000
 DEFINITION UP 315-19A T7 RPlC11 Human Male BAC Library Homo sapiens genomic
 clone RP11-315A19, genomic survey sequence.
 ACCESSION AZ301311
 VERSION AZ301311.2 GI:11996067
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 423)
 1 (bases 1 to 423)
 Cheung,Y.G., Dailymple,H.L., Narasimhan,S., Watts,J., Schler,G.,
 Raap,A.K., Morley,M. and Bruzel,A.
 A resource of mapped human bacterial artificial chromosome clones
 Genome Res. 9 (10), 989-993 (1999)
 10523527
 On Dec 29, 2000 this sequence version replaced gi:9795907.
 Contact: Arcaro MA, Morley M, Burdick J, Cheung VG
 Department of Pediatrics
 University of Pennsylvania
 3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, USA
 Tel: 215 590 2664
 Fax: 215 590 3709
 Email: mlennox@mail.med.upenn.edu
 Plate: 315 row: A column: 19
 Seg primer: T7
 Class: BAC ends.

FEATURES
 source
 1..423
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="RP11-315A19"
 /sex="Male"
 /cell_type="lymphocytes"
 /clone_1fb="RPlC11 Human Male BAC Library"
 /note="Vector: pBAC3.6; RPlC11 Human Male BAC Library"

ORIGIN
 Query Match 0.6%; Score 24; DB 9; Length 423;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATGAGGAG 45

Db 5 CCTAATACGACTCATTATGAGGAG 28
 |||||

RESULT 59
 LOCUS AQ959559 429 bp DNA linear GSS 28-JAN-2000
 DEFINITION LEREL47TF LERE Arabidopsis thaliana genomic clone LEREL47, genomic
 survey sequence.
 ACCESSION AQ959559
 VERSION AQ959559.1 GI:6787260
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 429)
 Buell,C.R., Lin,X., Pal,G., Barnstead,M., Bowman,C., Utterbach,T.,
 Feldblyum,T., Liang,F., Cressy,T. and Fraser,C.M.
 Genomic survey sequencing of landberg erecta ecotype of
 Arabidopsis thaliana and identification of sequence-based
 polymorphisms
 Unpublished (2000)
 CONTACT: Xiaoying Lin
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: atc@igr.org
 For additional information, see <http://www.tigr.org/cdb/at/c.html>
 Seg primer: TF
 Class: shotgun.

FEATURES
 source
 1..429
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="landberg erecta"
 /db_xref="taxon:3702"
 /clone="LEREL47"
 /clone_1fb="LERE"
 /note="Organ: leaf; Vector: pUC19UK; Total genomic DNA was
 sheared to 0.6-0.8 Kbp before ligation."

ORIGIN
 Query Match 0.6%; Score 24; DB 9; Length 429;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATGAGGAG 45
 Db 13 CCTAATACGACTCATTATGAGGAG 36

RESULT 60
 LOCUS BM171421 440 bp mRNA linear EST 04-DEC-2001
 DEFINITION EST573944 PyBS Plasmodium yoelii yoelii CDNA clone PYCQ44 5' end,
 mRNA sequence.
 ACCESSION BM171421
 VERSION BM171421.1 GI:17304653
 KEYWORDS EST.
 SOURCE Plasmodium yoelii yoelii
 ORGANISM Plasmodium yoelii yoelii
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 440)
 Carlson,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
 Fraser,C.M. and Carnucci,D.J.
 Plasmodium yoelii EST project at TIGR
 Unpublished (2001)
 CONTACT: Jane Carlson
 Parasite Genomics Group
 The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org

For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mri4.org/mr4pages/index.html

Seq primer: ADP.

FEATURES

source

Location/Qualifiers
1. .440
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17XL"
/sub_species="yoelii"
/db_xref="taxon:73239"
/clone="PYC004"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_1lb="PyBS"
/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybridAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybridAP vector and plasmid DNA isolated."

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 24; DB 3; Length 440;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAAGTTTCAT 3494

Db 139 AAAAAAAAAAAGTTTCAT 162

RESULT 61

AQ959560/c

LOCUS 444 bp DNA linear GSS 28-JAN-2000

DEFINITION LEREL477R LERE Arabidopsis thaliana genomic clone LEREL47, genomic

survey sequence.

ACCESSION AQ959560

VERSION AQ959560.1 GI:6787261

KEYWORDS GSS.

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 444)

Buell, C.R., Lin, X., Pal, G., Barnstead, M., Bowman, C., Uterbach, T.,

Feldblum, T., Liang, F., Creasy, T. and Fraser, C.M.

Genomic survey sequencing of Landsberg erecta ecotype of

Arabidopsis thaliana and identification of sequence-based

polymorphisms

Unpublished (2000)

CONTACT: Xiaoying Lin

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: ac@tigr.org

For additional information, see <http://www.tigr.org/cdb/ac/ac.html>
Seq primer: TR
Class: Shotgun.

FEATURES

source

Location/Qualifiers
1. .444
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LEREL47"
/clone_1lb="LERE"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.6-0.8 kbp before ligation."

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 24; DB 9; Length 444;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATGGAG 45

Db 425 CCTAATACGACTCATTATGGAG 402

RESULT 62

AQ028235/c

LOCUS 454 bp DNA linear GSS 30-JUN-1998

DEFINITION CIT-HSP-2325L11.TR CIT-HSP Homo sapiens genomic clone 2325L11,

genomic survey sequence.

ACCESSION AQ028235

VERSION AQ028235.1 GI:3268457

KEYWORDS GSS.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 454)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Basu, S., Linher, K.,

Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,

Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building (1998)

Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdamad@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.

FEATURES

source

Location/Qualifiers
1. .454
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2325L11"
/sex="Male"
/cell_type="Sperm"
/clone_1lb="CIT-HSP"
/note="Vector: pBelOBAC11, Site_1: HindIII, Site_2:
HindIII"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 24; DB 9; Length 454;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3470 CAAAAAAAAAAGTTTCA 3493
 |||||
 Db 254 CAAAAAAAAAAGTTTCA 231

RESULT 63
 BM16570 469 bp mRNA linear EST 04-DEC-2001
 LOCUS EST569093 PyBS Plasmodium yoelii yoelii cDNA clone PYCNT81 5' end,
 DEFINITION mRNA sequence.
 ACCESSION BM16570 GI:17299802
 VERSION BM16570
 KEYWORDS EST.
 SOURCE Plasmodium yoelii yoelii
 ORGANISM Plasmodium yoelii yoelii
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 REFERENCE 1 (bases 1 to 469)
 Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Valdiva,A.B.,
 Fraser,C.M. and Carucci,D.J.
 Plasmodium yoelii EST project at TIGR
 COMMENT Unpublished (2001)
 TITLE Contact: Jane Carlton
 JOURNAL Parasite Genomics Group
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-530-9319
 Fax: 301-838-0208
 Email: carlton@tigr.org
 For clone info, please contact the Malaria Research and Reference
 Reagent Resource Center, ATCC
 http://www.malaria.mri4.org/mr4pages/index.html
 Seq primer: ADP.

FEATURES
 source Location/Qualifiers

1..469
 /organism="Plasmodium yoelii yoelii"
 /mol_type="mRNA"
 /strain="17XL"
 /sub_species="yoelii"
 /db_xref="taxon:73239"
 /clone="PYCNT81"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was
 collected from BALB/cByJ mice infected with PY17XL
 parasites, and leukocytes removed by passage over
 microcrystalline cellulose columns. Total RNA was
 isolated using the guanidinium isothiocyanate method, and
 mRNA isolated using oligo(dT)-cellulose chromatography.
 First strand cDNA synthesis was completed using a 50-base
 primer and reverse transcriptase in the presence of
 5-methyl dCTP. After second strand synthesis, uneven
 termini were treated with Pfu DNA polymerase and EcoRI
 adaptors ligated to the blunt ends. The sample was cleaved
 with XhoI and separated on a Sephacryl S-500 column.
 Size-fractionated cDNA was precipitated and ligated to
 HybriZAP arms directionally using EcoRI-XhoI cleaved arms.
 After packaging, the phagemid vector (PAD-GAL4) was
 excised from the HybriZAP vector and plasmid DNA
 isolated."

ORIGIN

Query Match 0.6%; Score 24; DB 3; Length 469;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3471 AAAAAAAAAAAGTTTCAAT 3494
 |||||
 Db 139 AAAAAAAAAAAGTTTCAAT 162

RESULT 64
 BU303919/c

LOCUS BU303919 478 bp mRNA linear EST 27-NOV-2002
 DEFINITION 603737371F1 CSEQCHN56 Gallus gallus cDNA clone CHEST629m18 5', mRNA
 sequence.
 ACCESSION BU303919 GI:25753631
 VERSION BU303919.1
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 478)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 12445392
 CONTACT: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source Location/Qualifiers

1..478
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton line 151"
 /db_xref="taxon:9031"
 /clone="CHEST629m18"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN56"
 /note="Organ: small intestine; Vector: pBluescript II
 KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
 library was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer,
 using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adaptors, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 0.6%; Score 24; DB 5; Length 478;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2073 AAATCGAAAACATTTT TTTT 2096
 |||||
 Db 442 AAATCGAAAACATTTT TTTT 419

RESULT 65

BU396654/c 478 bp mRNA linear EST 27-NOV-2002
 LOCUS BU396654 603533803F1 CSEQCHN58 Gallus gallus cDNA clone CHEST492e2 5', mRNA
 DEFINITION sequence.
 ACCESSION BU396654
 VERSION BU396654
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE
1 (bases 1 to 478)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, M.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
JOURNAL
Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

SOURCE

1. 478
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHST19262"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CEBCHN58"
/note="Organ: small intestine; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer.
Following methylation C in the first strand synthesis reaction,
this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 0.6%; Score 24; DB 5; Length 478;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2073 AAATCGAAACATTTTCTTTT 2096
Db 442 AAATCGAAACATTTTCTTTT 419

RESULT 66
BF558277/c 487 bp mRNA linear EST 12-DEC-2000
LOCUS
DEFINITION
UI-R-AI-eo-c-08-0-UI-r1 UI-R-AI Rattus norvegicus cDNA clone
BF558277
ACCESSION
BF558277.1 GI:11668007
VERSION
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 487)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
clones will be available through Research Genetics (www.regen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LNL (info@image.llnl.gov). IMAGE ID= 1778863
Seq primer: M13 forward.
Location/Qualifiers

FEATURES

SOURCE

1. 487
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AI-eo-c-08-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-AI"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AI
library is a subtracted library derived from the UI-R-A0
library. The UI-R-A0 library consisted of a mixture of
individually tagged normalized libraries constructed from
rat placenta, adult lung, brain, liver, kidney, heart,
spleen, ovary, and muscle. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-AI) was constructed as follows: PCR
amplified cDNA inserts from a pool of approximately 3,840
UI-R-A0 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-A0
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-AI library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"

ORIGIN

Query Match 0.6%; Score 24; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3461 TTCTTAGCACAACAAAAA 3484
Db 33 TTCTTAGCACAACAAAAA 10

RESULT 67
AL720059/c 511 bp mRNA linear EST 18-APR-2002
LOCUS
DEFINITION
AL720059 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BNOA044ZD11 5', mRNA sequence.
AL720059
ACCESSION
AL720059.1 GI:20184663
VERSION
KEYWORDS
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 511)
Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M.,
Hardelin, J.P., Weissenbach, J. and Petit, C.
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
JOURNAL
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. 511

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="BN0AA044ZD11"

/tissue_type="inner ear"

/dev_stage="embryonic"

/clone_lib="Danio rerio embryonic inner ear subtracted cDNA"

/note="subtracted cDNA library"

ORIGIN

Query Match 0.6%; Score 24; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAATTAATTAAGTAAGAAA 3939
Db 342 AAAATTAATTAAGTAAGAAA 319

RESULT 68
AL720155 523 bp mRNA linear EST 18-APR-2002
LOCUS AL720155 Danio rerio embryonic inner ear subtracted cDNA Danio
DEFINITION xerio cDNA clone BN0AA044ZD11 3', mRNA sequence.
ACCESSION AL720155
VERSION AL720155.1 GI:20184759
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 523)
Hardelin,J.P., Weissenbach,U. and Petit,C.
A subtracted cDNA library from the zebrafish (Danio rerio) embryonic inner ear
Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers

1. 523

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="BN0AA044ZD11"

/tissue_type="inner ear"

/dev_stage="embryonic"

/clone_lib="Danio rerio embryonic inner ear subtracted cDNA"

/note="subtracted cDNA library"

ORIGIN

Query Match 0.6%; Score 24; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAATTAATTAAGTAAGAAA 3939
Db 182 AAAATTAATTAAGTAAGAAA 205

RESULT 69
AL715025 525 bp mRNA linear EST 18-APR-2002
LOCUS AL715025 Danio rerio embryonic inner ear subtracted cDNA Danio
DEFINITION

erio cDNA clone BN0AA009ZE06 5', mRNA sequence.
AL715025
AL715025.1 GI:20179628
EST.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 525)
Hardelin,J.P., Weissenbach,U. and Petit,C.
A subtracted cDNA library from the zebrafish (Danio rerio) embryonic inner ear
Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers

1. 525

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="BN0AA009ZE06"

/tissue_type="inner ear"

/dev_stage="embryonic"

/clone_lib="Danio rerio embryonic inner ear subtracted cDNA"

/note="subtracted cDNA library"

ORIGIN

Query Match 0.6%; Score 24; DB 1; Length 525;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAATTAATTAAGTAAGAAA 3939
Db 332 AAAATTAATTAAGTAAGAAA 309

RESULT 70
DR576414/c 529 bp mRNA linear EST 08-JUL-2005
LOCUS DR576414/c MS00743_C21_F18 MS-PS-N-A-8 Picea glauca cDNA clone MS00743_F18 3,
DEFINITION mRNA sequence.
ACCESSION DR576414
VERSION DR576414.1 GI:70641131
KEYWORDS EST.
SOURCE Picea glauca (white spruce)
ORGANISM Picea glauca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 529)
Ralph,S., Kolosova,N., Oddy,C., Cooper,D., Butterfield,Y., Kirkpatrick,R., Liu,J., Palmquist,D., Stolt,J., Barber,S., Yang,G., Babakoff,R., Brown-John,M., Chand,S., Featherstone,R., Mason,A., Mayo,M., Moran,J., Olson,T., Wong,D., Friedmann,M.F., Ritland,C.E., Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and Bohlmann,J.
The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2005)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@mel.ubc.ca
Plate: MS00743 row: F column: 18
High quality sequence stop: 529

FEATURES POLYA=Yes.
source Location/Qualifiers
1. 529
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/mol_type="mRNA"
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/db_xref="taxon:3330"
/clone="WS00743 P18"
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/tissue_type="Pushing buds harvested May 16th, young shoots harvested June 15th, and mature shoots harvested June 15th"
/lab_host="E. coli DH10B cells"
/clone_lib="WS-PS-N-A-8"
/note="Organ: Foliage from 25 year old trees harvested at Kalamalka Research Station in Vernon, British Columbia in 2001; Vector: Bluescript II SK (+) XR; Site 1: EcoRI (5' end of CDNA); Site 2: XhoI (3' end of CDNA); mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

ORIGIN
Query Match 0.6%; Score 24; DB 8; Length 529;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3470 CAAAAAAAAAGGTTTCAA 3493
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182 CAAAAAAAAAGGTTTCAA 159

RESULT 71
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LOCUS AL723652
DEFINITION Danio rerio embryonic inner ear subtracted cDNA Danio
ACCSSION AL723652
VERSION AL723652.1 GI:20188256
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 540)
Colomba.R., Well.D., Broctier.P., Blanchard.S., Levi.M., Hardekin.J.P., Weisenbach.J. and Petit.C.
A subtracted cDNA library from the zebrafish (Danio rerio) embryonic inner ear
Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 540
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0A0672A07"
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/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted

FEATURES CDNA"
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/clone="WS00743 P18"
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/tissue_type="Pushing buds harvested May 16th, young shoots harvested June 15th, and mature shoots harvested June 15th"
/lab_host="E. coli DH10B cells"
/clone_lib="WS-PS-N-A-8"
/note="Organ: Foliage from 25 year old trees harvested at Kalamalka Research Station in Vernon, British Columbia in 2001; Vector: Bluescript II SK (+) XR; Site 1: EcoRI (5' end of CDNA); Site 2: XhoI (3' end of CDNA); mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

ORIGIN
Query Match 0.6%; Score 24; DB 1; Length 540;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3916 AAAAAAAAAAGTAAAGAA 3939
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171 AAAAAAAAAAGTAAAGAA 194

RESULT 72
BM168186 564 bp mRNA linear EST 04-DEC-2001
LOCUS BM168186
DEFINITION EST570709 PyBS Plasmodium yoelii yoelii cDNA clone PYCOW73 5' end, mRNA sequence.
ACCSSION BM168186
VERSION BM168186.1 GI:17301418
KEYWORDS EST.
SOURCE Plasmodium yoelii yoelii
ORGANISM Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 564)
Carlton,T.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@igr.org
For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
http://www.malaria.mrg.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
source Location/Qualifiers
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/clone="PYCOW73"
/dev_stage="asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBYJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybridZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybridZAP vector and plasmid DNA isolated."

ORIGIN
Query Match 0.6%; Score 24; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAGTTTCAT 3494
 DB 89 AAAAAAAAAAGTTTCAT 112

RESULT 73
 LOCUS BZ293554 581 bp DNA linear GSS 31-OCT-2002
 DEFINITION CG0392.r1 Candida glabrata Random Genomic Library Candida glabrata
 accession BZ293554 genomic clone CG0392, genomic survey sequence.
 VERSION BZ293554
 KEYWORDS BZ293554.1 GI:24433641
 SOURCE GSS.
 ORGANISM Candida glabrata
 Candida glabrata
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 581)
 Wong,S., Fares,M.A., Zimmermann,W., Butler,G. and Wolfe,K.H.
 Evidence from comparative genomics for a complete sexual cycle in
 the 'asexual' pathogenic yeast Candida glabrata
 Genome Biol. 4 (2), R10 (2003)
 12620120
 CONTACT: Wong S
 Department of Genetics, Smurfit Institute
 Trinity College Dublin
 Dublin 2, Ireland
 Tel: 353 1 6082319
 Fax: 353 1 6798558
 Email: swong@tcd.ie
 Class: plasmid ends.
 Location/Qualifiers
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 /db_xref="taxon:5478"
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 mRNA sequence.
 VERSION BM170115
 ACCESSION BM170115.1 GI:17303347
 KEYWORDS EST.
 SOURCE Plasmodium yoelii yoelii
 ORGANISM Plasmodium yoelii yoelii
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 631)
 Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
 Frazer,C.M. and Carucci,D.J.
 Plasmodium yoelii EST project at TIGR
 Unpublished (2001)
 CONTACT: Jane Carlton
 Parasite Genomics Group
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-530-9319
 Fax: 301-838-0208

FEATURES
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 /organism="Plasmodium yoelii yoelii"
 /mol_type="mRNA"
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 /clone="PYCGB42"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /clone_1lb="PyBS"
 /note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was
 collected from BALB/cBYJ mice infected with Py17XL
 parasites, and leukocytes removed by passage over
 microcrystalline cellulose columns. Total RNA was
 isolated using the guanidium isothiocyanate method, and
 mRNA isolated using oligo(dT)-cellulose chromatography.
 First strand cDNA synthesis was completed using a 50-base
 primer and reverse transcriptase in the presence of
 5-methyl dCTP. After second strand synthesis, uneven
 termini were treated with Pfu DNA polymerase and EcoRI
 adaptors ligated to the blunt ends. The sample was cleaved
 with XhoI and separated on a Sephacryl S-500 column.
 Size-fractionated cDNA was precipitated and ligated to
 HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
 After packaging, the phagemid vector (PAD-GAL4) was
 excised from the HybridZAP vector and plasmid DNA
 isolated."

ORIGIN
 source
 1..631
 /organism="Plasmodium yoelii yoelii"
 /mol_type="mRNA"
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 /sub_species="yoelii"
 /db_xref="taxon:73239"
 /clone="PYCGB42"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /clone_1lb="PyBS"
 /note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was
 collected from BALB/cBYJ mice infected with Py17XL
 parasites, and leukocytes removed by passage over
 microcrystalline cellulose columns. Total RNA was
 isolated using the guanidium isothiocyanate method, and
 mRNA isolated using oligo(dT)-cellulose chromatography.
 First strand cDNA synthesis was completed using a 50-base
 primer and reverse transcriptase in the presence of
 5-methyl dCTP. After second strand synthesis, uneven
 termini were treated with Pfu DNA polymerase and EcoRI
 adaptors ligated to the blunt ends. The sample was cleaved
 with XhoI and separated on a Sephacryl S-500 column.
 Size-fractionated cDNA was precipitated and ligated to
 HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
 After packaging, the phagemid vector (PAD-GAL4) was
 excised from the HybridZAP vector and plasmid DNA
 isolated."

QY 3471 AAAAAAAAAAGTTTCAT 3494
 DB 139 AAAAAAAAAAGTTTCAT 162

RESULT 75
 LOCUS CE784932 637 bp DNA linear GSS 30-SEP-2003
 DEFINITION tigr-gss-dog-1700030840001 Dog library Canis familiaris genomic,
 genomic survey sequence.
 VERSION CE784932
 ACCESSION CE784932.1 GI:37125695
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.
 1 (bases 1 to 637)
 Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 14512627
 CONTACT: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
 Location/Qualifiers

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source          1. .637
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Query Match          0.6%; Score 24; DB 10; Length 637;
Best local Similarity 100.0%; Pred. No. 86;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      84 GTGTGTGTGTGTGTTTAACTCA 107
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Db      167 GTGTGTGTGTGTGTTTAACTCA 190

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Job time : 10442 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 20:21:42 ; Search time 13879 Seconds

(without alignments)
17316.385 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtcgactctcgcctcactg.....agaacccaagaacc 4228

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

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1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcs:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4228	100.0	4228	6	BD274517
2	4228	100.0	4228	6	AR316368
3	4228	100.0	4228	6	AR427902
4	2619	61.9	110766	15	ATC28119
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20	55	1.3	3049	6	AX449167	AX449167 Sequence
21	55	1.3	3869	15	AB026549	AB026549 Arabidops
22	55	1.3	5651	4	RABAMYA	M98536 Rabbit seru
23	55	1.3	8072	8	AB031009	AB031009 Homo sapi
24	55	1.3	11716	6	CS070402	CS070402 Sequence
25	55	1.3	13701	15	AB124593	AB124593 Oryza sat
26	55	1.3	27078	6	CS070389	CS070389 Sequence
27	53	1.3	1955	15	ATU44028	U44028 Arabidopsis
28	46	1.1	4026	6	CS070390	CS070390 Sequence
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33	32	0.8	4162	6	AR029517	AR029517 Sequence
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35	32	0.8	4162	6	AR494979	AR494979 Sequence
36	32	0.8	4162	6	AX441395	AX441395 Sequence
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38	31	0.7	4165	6	I41430	I41430 Sequence 26
39	31	0.7	147619	8	AL512368	AL512368 Human DNA
40	29	0.7	177938	14	AL512455	AL512455 Homo sapi
41	29	0.7	204712	14	AC134627	AC134627 Rattus no
42	29	0.7	215429	14	AC123561	AC123561 Rattus no
43	29	0.7	276881	14	AC095481	AC095481 Rattus no
44	28	0.7	105	11	SYNLAMSH1	M37056 Cloning vec
45	28	0.7	3484	6	A91914	A91914 Sequence 1
46	28	0.7	3484	6	AR309120	AR309120 Sequence
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48	28	0.7	3484	6	BD007602	BD007602 Nematoda-
49	28	0.7	140069	9	AL355005	AL355005 Mouse DNA
50	28	0.7	183958	14	BX530096	BX530096 Mus muscu
51	28	0.7	220894	9	AL732410	AL732410 Mouse DNA
52	27	0.6	374	6	CS088900	CS088900 Sequence
53	27	0.6	374	6	CS088904	CS088904 Sequence
54	27	0.6	374	6	CS088909	CS088909 Sequence
55	27	0.6	2912	11	CVGEM92FM	X65312 Cloning vec
56	27	0.6	5824	11	CVB311872	AJ311872 Cloning v
57	27	0.6	6063	11	CVB311873	AJ311873 Cloning v
58	27	0.6	7038	6	BD263403	BD263403 Compositi
59	27	0.6	8815	6	BD263400	BD263400 Compositi
60	27	0.6	14271	11	AY189825	AY189825 Hls-3 int
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63	27	0.6	230502	9	AC151836	AC151836 Mus muscu
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74	26	0.6	4157	11	AY720440	AY720440 Plant exp
75	26	0.6	6337	6	BD235520	BD235520 Desaturas
76	26	0.6	65222	14	AC136361	AC136361 Homo sapi
77	26	0.6	119903	8	AC004662	AC004662 Homo sapi
78	26	0.6	152100	8	AL133332	AL133332 Human DNA
79	26	0.6	168496	9	AC157098	AC157098 Mus muscu
80	26	0.6	182662	8	AC023830	AC023830 Homo sapi
81	26	0.6	183838	8	AC104332	AC104332 Homo sapi
82	26	0.6	193965	9	AC158650	AC158650 Mus muscu
83	26	0.6	195156	14	AC019034	AC019034 Homo sapi
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85	26	0.6	206021	8	AC012065	AC012065 Homo sapi
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OY	1021	TCTGTCTTAAGATATCTACAGCTGCTTCCGCTGTGAATAGAGAAATTTGAATGATGA	1080
Db	1021	TCTGTCTTAAGATATCTACAGCTGCTTCCGCTGTGAATAGAGAAATTTGAATGATGA	1080
OY	1081	GAGATCCCATTAAGAGTATCTACAGCTGCTTCCGCTGTGAATAGAGAAATTTGAATGATGA	1140
Db	1081	GAGATCCCATTAAGAGTATCTACAGCTGCTTCCGCTGTGAATAGAGAAATTTGAATGATGA	1140
OY	1141	TTTTTCTTAAGAGTATCTACAGCTGCTTCCGCTGTGAATAGAGAAATTTGAATGATGA	1200
Db	1141	TTTTTCTTAAGAGTATCTACAGCTGCTTCCGCTGTGAATAGAGAAATTTGAATGATGA	1200
OY	1201	AATATTCGAAAGGAAAGAAAAAGGCAAGAAACTATTTGTCGAAAGACATTAATGAC	1260
Db	1201	AATATTCGAAAGGAAAGAAAAAGGCAAGAAACTATTTGTCGAAAGACATTAATGAC	1260
OY	1261	ACTATAAATTTGGATTATTAATAATGATATATGTTGGTGAAATTTATTAACATTAACAA	1320
Db	1261	ACTATAAATTTGGATTATTAATAATGATATATGTTGGTGAAATTTATTAACATTAACAA	1320
OY	1321	AATATAAGGAAGGAGAGGAGCCTCTTCGCTTATGATTTCCCTCCTAATAACAATGCT	1380
Db	1321	AATATAAGGAAGGAGAGGAGCCTCTTCGCTTATGATTTCCCTCCTAATAACAATGCT	1380

Qy	1381	CCGACATCCTTTTTCCTTCCACAAATGATTCACGAGAAATCTGTGTGATC	1440
Db	1381	CCGACATCCTTTTTCCTTTCACAAATATTCACGAGAAATCTGTGTGATC	1440
Qy	1441	ACTTTCAGCAAAATTAACAAATTTTGTGATTTTGTCAAGTCTTGCTGTTTAAAG	1500
Db	1441	ACTTTCAGCAAAATTAACAAATTTTGTGATTTTGTCAAGTCTTGCTGTTTAAAG	1500
Qy	1501	TCGATTAATTGGTAATACATATGTGTGATATACATCCAGCTAATCAATATGAT	1560
Db	1501	TCGATTAATTGGTAATACATATGTGTGATATACATCCAGCTAATCAATATGAT	1560
Qy	1561	CTCCTTCGCTATCAATTAATTAACACATGAGCTAATGAGCTAATTAATACCA	1620
Db	1561	CTCCTTCGCTATCAATTAATTAACACATGAGCTAATGAGCTAATTAATACCA	1620
Qy	1621	CATTCTCTATCAATTTTATATGATTAATAAACAACGAGCTAATAGCTACAGATT	1680
Db	1621	CATTCTCTATCAATTTTATATGATTAATAAACAACGAGCTAATAGCTACAGATT	1680
Qy	1681	GGTATTAAGGATTAATGCTTCTAGTCGAAGAAATTTTGTATGATTAACCTGCTG	1740
Db	1681	GGTATTAAGGATTAATGCTTCTAGTCGAAGAAATTTTGTATGATTAACCTGCTG	1740
Qy	1741	GGAAAAAATCCAGCTTAATATGCTAATTAAGGATTAATGATTAATATGCTTAATCA	1800
Db	1741	GGAAAAAATCCAGCTTAATATGCTAATTAAGGATTAATGATTAATATGCTTAATCA	1800
Qy	1801	TTAAATTAAGGATTTTGTGCTTTAAAGTTACACGCTTAATTCATTAAGAGAT	1860
Db	1801	TTAAATTAAGGATTTTGTGCTTTAAAGTTACACGCTTAATTCATTAAGAGAT	1860
Qy	1861	ATTATCTTGATGCAAAATTCGAAATACTTTTAAACATATAGAAATTTTCAGATT	1920
Db	1861	ATTATCTTGATGCAAAATTCGAAATACTTTTAAACATATAGAAATTTTCAGATT	1920
Qy	1921	TTAAATTAAGGATTAATATGCTTCAATATATGCTTCCAGTAAATTTTGAGGT	1980
Db	1921	TTAAATTAAGGATTAATATGCTTCAATATATGCTTCCAGTAAATTTTGAGGT	1980
Qy	1981	TTAAACACATGATGTTTTTGTATTAATAAACAATTAATTTCTAGTATTAACATT	2040
Db	1981	TTAAACACATGATGTTTTTGTATTAATAAACAATTAATTTCTAGTATTAACATT	2040
Qy	2041	TTTAACCGTCCATCCAGATGTAATAGTGACAAATCTGAATAATTTTTTTTTCTTG	2100
Db	2041	TTTAACCGTCCATCCAGATGTAATAGTGACAAATCTGAATAATTTTTTTTTCTTG	2100
Qy	2101	AATCTTGTTTAAATTTCTCTGCTGCAATCTTGCAAGGATTTGACCAACGATATACATA	2160
Db	2101	AATCTTGTTTAAATTTCTCTGCTGCAATCTTGCAAGGATTTGACCAACGATATACATA	2160
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Db	2161	TTGAAACCAAAATATCCACGAGGATGATAGGTTAGATCCCAATTCATATCTTTTGT	2220
Qy	2221	CTTGTGTTATTTATGAAAAAACAATATTTATCAGGAAAAAAAGCTTTCTCTAGTGATA	2280
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Db	2581	TAGTTCATCTGTACAAACAAACAAATTCGTAACATATATTAACAAATCTACTA	2640
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Db	2701	CAAACTTGAATGTTTGTGTTGTAATTAATCTTAACCAAAAGTTTGAATGTGCAATGGG	2760
Qy	2761	AGCTACACTGTAGTCCCTTTTTCGCCAAATTAATCTCCTTAATGACGCGTTAAAGT	2820
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Qy	2821	ATTAAACCAACAAATTTTAAATTTGTGCTGAAGGTAACAAATGTCAATATTAAGAGA	2880
Db	2821	ATTAAACCAACAAATTTTAAATTTGTGCTGAAGGTAACAAATGTCAATATTAAGAGA	2880
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Db	2881	CAGCATGTTTATTAACAATAATGTTGATGTAATGGAATCAATAATTAATTAAGAAATTA	2940
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Qy	3001	CAGAGCTATATATGCGGTCATTTAGAGCGGTAACCAAAAGTTTGGTGGTATTTCTAC	3060
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Qy	3121	TGTCGATTAATATTTGTAATGTAATTTTGTGTTCTATATATGATACGTAATTTCA	3180
Db	3121	TGTCGATTAATATTTGTAATGTAATTTTGTGTTCTATATATGATACGTAATTTCA	3180
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Db	3361	TTTCCAAATGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3420
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Qy	3481	AAAAAGTTTTCATTAATTAATTAATTAATTTTGTGATTTTGAAGTTTAAATGATGCT	3540
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Qy	3541	GAAGTTTGAATGAATTTGCAAGTTTGCACAGAAATGCTGATTAATCAATCAAAA	3600
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RESULT 2
AR316368
LOCUS AR316368 4228 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6559357.
ACCESSION AR316368
VERSION AR316368.1 GI:31711159
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4228)
AUTHORS Fischer, R.L. and Mizukami, Y.
TITLE Methods for altering mass and fertility in plants
JOURNAL Patent: US 6559357-A 3 06-MAY-2003;
The Regents of the University of California; Oakland, CA
FEATURES
source
1. 4228
/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 0;
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Db 1 GTGACTCTAGGCTCACTGCGCTTAATACATCACTATAGGAGCTCGAGATCTTTA 60
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DEFINITION	Sequence 3 from patent US 6639128.				
ACCESSION	AR427902				
VERSION	AR427902.1	GI:40186931			
KEYWORDS					
SOURCE	Unknown.				

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 4228)
TITLE	Fischer, R.L., and Mizukami, Y.
JOURNAL	Methods for altering organ mass, controlling fertility and enhancing asexual reproduction in plants
FEATURES	Patent: US 6639128-A 3 28-OCT-2003;
source	National Science Foundation; Arlington, VA
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Matches 4228; Conservative	0; Mismatches 0; Indels 0; Gaps 0
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AUTHORS	Bevan,M., Robben,J., Grymoprez,B., Volckaert,G., Bancroft,I., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.					
REFERENCE	Unpublished					
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AUTHORS	Direct Submission					
TITLE	Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk					
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ .					
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REFERENCE 1 (bases 1 to 23823)
AUTHORS Rose, M., Hempel, S., Entlian, K.-D., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
JOURNAL Unpublished
REFERENCE 2 (bases 3704 to 114469)
AUTHORS Robben, J., Grynopmez, B., Volckaert, G., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
JOURNAL Unpublished
REFERENCE 3 (bases 114416 to 198493)
AUTHORS Wedler, H., Kutzner, M., Wambutt, R., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
JOURNAL Unpublished
REFERENCE 4 (bases 1 to 198493)
AUTHORS EU Arabidopsis sequencing project.
JOURNAL Direct Submission
TITLE Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de/proj/thal/
JOURNAL Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
COMMENT Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/> this fragment has an overlap with ATCHRIV87 at the 5' end and an overlap with ATCHRIV89 at the 3' end.
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 4159; Conservative 0; Mismatches 8; Indels 12; Gaps 7;
QY 52 GATCCTTTAGTAAAGAACTTTCTTTGTAAGTGTGTGTGTGTTTAAGTCAATTA 111
DB 38046 GATCCTTTAGTAAAGAACTTTCTTTGTAAGTGTGTGTGTTTAAGTCAATTA 38105
QY 112 TAACCTAGTCAGTGTATCACTATATATTTGAATTTGAATTTATCATTTAATG 171
DB 38106 TAACCTAGTCAGTGTATCACTATATATTTGAATTTGAATTTATCATTTAATG 38165
QY 172 AGTAGCATTAATATATATAGCTGATTAACCAACCAAAATGTTTCGTTTATGGATA 231
DB 38166 AGTAGCATTAATATATATAGCTGATTAACCAACCAAAATGTTTCGTTTATGGATA 38225
QY 232 GTTCTATATGTGACTTGAATTATAGTACTATATAAACGTGGTTTATTTAAATCGT 291
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DB 38286 ACCCATTAACAAAGTGAACCAACGAGATCCATGTTTGTGTGTTTCTTTGTGTTAA 38345
QY 352 CGAGATTAATGATTATGAAAGATTAATCTTACTAAATTTATTAATTAATTTGGAATA 411
DB 38346 CGAGATTAATGATTATGAAAGATTAATCTTACTAAATTTATTAATTAATTTGGAATA 38405

QY 412 CAACCTAAATATGTTAGTGTCTTGAGTCTGACGTTCAGATTAATATATCGGTATATC 471
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QY 1192 AAGAAACCTAATTTGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1251
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QY 4130 AATGATTTGGGTTTAAAGTTACTTCTGAGAGATTATTAAGAAAGAGATTAACA 4189
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DB 42176 TTATAGAAAGAGAGACAAACCAAAAAAGAAAC 42214

RESULT 6
ATHS30550
LOCUS 371 bp DNA linear PLN 29-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 212A06.
ACCESSION AJ530550
VERSION AJ530550.1 GI:26798810
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
1
REFERENCE
AUTHORS Brunaud, V., Balzerge, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE
AUTHORS 2 (bases 1 to 371)
Balzerge, S.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzerge S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgip.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics

program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante.info.inbio.gen.fr>).
Location/Qualifiers
1.371

FEATURES
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left border"

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Best Local Similarity 100.0%; Pred. No. 1,1e-148;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2459 ATTCTCAGCAAAACGCGCGCTAGAGGTGTTATCTTACATTACAGCTGGTGGGC 2518
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QY 2579 GTTAGTCTCAGCTGTACAAACAAATCCAAATCGTATATATCAATATCTAC 2638
DB 126 GTTAGTCTCAGCTGTACAAACAAATCCAAATCGTATATATCAATATCTAC 185
QY 2639 TAGTACTAGATTAAGCTAGCATATGCTTTTGGCAATTTCTAACTATCTATAC 2698
DB 186 TAGTACTAGATTAAGCTAGCATATGCTTTTGGCAATTTCTAACTATCTATAC 245
QY 2699 AACCAACTTGAATCTTTGTTGTAATTTATCTTAAACCAAGTTGAATGCGATTG 2758
DB 246 AACCAACTTGAATCTTTGTTGTAATTTATCTTAAACCAAGTTGAATGCGATTG 305
QY 2759 GAGACTACACTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAA 2818
DB 306 GAGACTACACTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAA 365
QY 2819 GATATT 2824
DB 366 GATATT 371

RESULT 7
ATHS31085
LOCUS 371 bp DNA linear PLN 29-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 225B08.
ACCESSION AJ531085
VERSION AJ531085.1 GI:26799345
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
1
REFERENCE
AUTHORS Brunaud, V., Balzerge, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE
AUTHORS 2 (bases 1 to 371)
Balzerge, S.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzerge S., UMRGV, INRA/CNRS, 2 rue

COMMENT
 Gaston Cremlieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.inbio.gen.fr>).
 Location/Qualifiers
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 left border"

ORIGIN
 Query Match 8.7%; Score 366; DB 15; Length 371;
 Best Local Similarity 100.0%; Pred. No. 1.1e-148;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2459 ATTCTTCAGCAAAACGGCGCGTGAAGTGTCTTATCTTACATTACAGCTGGTTGGC 2518
 DB 6 ATCTTCAGCAAAACGGCGCGTGAAGTGTCTTATCTTACATTACAGCTGGTTGGC 65
 QY 2519 AGACATCAATGCGCTTACGTAATTTGAGCTTTACCTGACGTAAGCTTTACATATCTA 2578
 DB 66 AGACATCAATGCGCTTACGTAATTTGAGCTTTACCTGACGTAAGCTTTACATATCTA 125
 QY 2579 GTTAGTTCACGTGCAAAACAAATCCAAATCGTAACATATCAATATCTAC 2638
 DB 126 GTTAGTTCACGTGCAAAACAAATCCAAATCGTAACATATCAATATCTAC 185
 QY 2639 TAGTACTAGATTAGCTACGTATACATCGCTTTTCGCAATTTCTAACTAATCTATAC 2698
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 QY 2759 GAGAGTACACTGATGCTCCCTTTTTCGCAAAATATCTCTACATGACCGGTTAAA 2818
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 QY 2819 GTATTT 2824
 DB 366 GTATTT 371

RESULT 8
 BD274516 2148 bp DNA linear PAT 17-JUL-2003
 LOCUS
 DEFINITION Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant.
 ACCESSION BD274516
 VERSION BD274516.1 GI:33084284
 KEYWORDS JP 2002534078-A/1.
 SOURCE
 ORGANISM
 Arabidopsis thaliana (thale cress)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 2148)
 AUTHORS Fischer,R.L. and Mizukami,Y.

TITLE
 JOURNAL
 COMMENT
 Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant
 Patent: JP 2002534078-A 1 15-OCT-2002;
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 OS Arabidopsis thaliana (thale cress)
 PN JP 2002534078-A/1
 PD 15-OCT-2002
 PF 07-JAN-2000 JP 2000592392
 PR 08-JAN-1999 US 09/227421
 PI ROBERT L FISCHER, YUKIKO MIZUKAMI
 PC A01H1/00,C12N5/10,C12N15/09,C12N5/00,C12N15/00 CC
 AINTEGUMENTA (ANT)
 CC encodes first Ap2 domain
 CC encodes linker region
 CC encodes second Ap2 domain
 FH Key Location/Qualifiers
 FT CDS (269)..(1936)
 FT misc_feature (1109)..(1339)
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ORIGIN
 Query Match 6.3%; Score 268; DB 6; Length 2148;
 Best Local Similarity 100.0%; Pred. No. 5.1e-106;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3961 AGATCCCAACGGATTCACAGCAAAATTTGCTTTGCTTCCTTCCTTATTAATATC 4020
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 QY 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGCTTCTTGTTACCAATGTTGGGT 4140
 DB 121 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGCTTCTTGTTACCAATGTTGGGT 180
 QY 4141 TTAGCTTACTACTTGAGAGATTATAGAAAGAAAGATGATCATTAAGAAAGA 4200
 DB 181 TTAGCTTACTACTTGAGAGATTATAGAAAGAAAGATGATCATTAAGAAAGA 240
 QY 4201 AGAAGCAGAAACCAAAAGAAAGAAC 4228
 DB 241 AGAAGCAGAAACCAAAAGAAAGAAC 268

RESULT 9
 AR316367 2148 bp DNA linear PAT 12-JUN-2003
 LOCUS
 DEFINITION Sequence 1 from patent US 6559357.
 ACCESSION AR316367
 VERSION AR316367.1 GI:31711158
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 2148)
 AUTHORS Fischer,R.L. and Mizukami,Y.
 TITLE Methods for altering mass and fertility in plants
 JOURNAL Patent: US 6559357-A 1 06-MAY-2003;
 The Regents of the University of California; Oakland, CA
 LOCATION/Qualifiers
 1..2148
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Db 241 AGAAGACAGAAACCAAAAAAGAAACC 268

RESULT 12
AY080706 2056 bp mRNA linear PLN 18-SEP-2002
LOCUS Arabidopsis thaliana putative ovule development protein
DEFINITION atinegumenta (At4g37750) mRNA, complete cds.

ACCESSION
AY080706
VERSION
AY080706.1 GI:19310586
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Bukayocja, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1 (bases 1 to 2056)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shim,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Arabidopsis Full Length cDNA Clones
Unpublished

TITLE
JOURNAL
AUTHORS
REFERENCE
2 (bases 1 to 2056)
Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
Sakurai,T., Satou,M., Seki,M., Shim,P., Southwick,A.,
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Direct Submission

TITLE
JOURNAL
COMMENT
Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: RIKEN
Arabidopsis Full-length cDNA.): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J.,
Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,
Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,
Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shim,P.,
Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGSC) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGSC)
contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.
Location/Qualifiers
1..2056
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="4"
/clone="RAFL06-86-F19 (RI1873)"
/ecotype="Columbia"
/note="This clone is in a modified pBluescript vector
(lambda ZAP) as a XhoI/SacI insert."
1..2056
/gene="At4g37750"
1..157
/gene="At4g37750"

gene
5'UTR

misc_difference 2
/gene="At4g37750"
/note="not present in genomic sequence"
158..1825
/gene="At4g37750"
/codon_start=1
/evidence=experimental
/product="putative ovule development protein atinegumenta"
/protein_id="AA185024.1"
/db_xref="GI:19310587"
/translation="MKSFCDDNDNHSNTTNLLIGSLSSNMKMGCRGREALYSSST
SSAATSSSVPPQLVVDNTSNFVCYGVNPGGIVSHMSVMPLRSDGSLCLMEALNR
SSSHNHQDSFKVEDPFGTHHNTSHKEMDLSDLSFNTTHERPTTNPQEFPS
POTRNHEERTRYNDPSSLTHGSEFVGYGEQQLSLSPSGSQSSCTGSHHQ
NONNHQSTHOOIISALVETSGVPTTMAAKKRGQGVVGVGQVIGYDMERKARAYDL
FGKRSQRYGVTTRHRTGVEYHLMDSFKGSHKRGQVYIGYDMERKARAYDL
AALKRWQPSHTNPSAENYQKELEDMKNTRQSYVAHLKRSQSFSGASITYGVTTRH
HGHGWQARIGVAGKNDLYLFTFGQEAALAEYDVAALKRGTNAVTNFDITRYDV
RIMSSNTLLSGELARRNNNSIVRVTEDDTALAVALVGGSSNKEVSTPERLSPALFA
LPOVQKMGESNMGNMSPWTSNPNAELKTVALLTPQMVFVFAAMADS"
1826..2056
/gene="At4g37750"

ORIGIN
3'UTR

Query Match 3.7%; Score 155; DB 15; Length 2056;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4074 ACCGCAACAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTTCTGTGTAACCAATG 4133
DB 3 ACCGCAACAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTAACCAATG 62

QY 4134 ATTGGGTTTTAGCTTCTCTCTCGAGAGATTATAGAAAGAAAGAGATACATTAT 4193
DB 63 ATTGGGTTTTAGCTTCTCTCTCGAGAGATTATAGAAAGAAAGAGATACATTAT 122

QY 4194 AGAAGACAGAAAGCAAGAAACCAAAAAAGAAACC 4228
DB 123 AGAAGACAGAAAGCAAGAAACCAAAAAAGAAACC 157

RESULT 13
XXU02426
LOCUS XXU02426 20125 bp DNA linear SYN 29-JAN-1997
DEFINITION Cloning vector lambda EMBL3 SP6/T7, left arm.
ACCESSION U02426
VERSION U02426.1 GI:413792
KEYWORDS
SOURCE Cloning vector lambda EMBL3 SP6/T7
ORGANISM Cloning vector lambda EMBL3 SP6/T7
REFERENCE
1 (bases 1 to 20125)
other sequences; artificial sequences; vectors.
AUTHORS Kites,P.A.
TITLE ClonteCH Vectors On Disc version 1.3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 20125)
Kites,P.A.
AUTHORS Kites,P.A.
DIRECT SUBMISSION
Submitted (07-OCT-1993) Paul A. Kites, ClonteCH Laboratories, Inc.,
1020 East Meadow Circle, Palo Alto, CA 94303, USA
This sequence has been compiled from information in the sequence
databases, published literature and other sources. If you suspect
there is an error in this sequence, please contact ClonteCH's
Technical Service Department at (415) 424-8222 or (800) 662-2566,
extension 3 or E-mail TECH@CLONTECH.COM.
Location/Qualifiers
1..20125
/organism="Cloning vector lambda EMBL3 SP6/T7"
/mol_type="genomic DNA"
/db_xref="taxon:31784"

ORIGIN
Query Match 1.3%; Score 57; DB 11; Length 20125;

Best Local Similarity 100.0%; Pred. No. 6.6e-14;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATCCT 57
Db 20044 GTGACTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATCCT 20100

RESULT 14
AF121976 1421 bp DNA linear ROD 07-DEC-1999
LOCUS Mus musculus odorant receptor Sl9 gene, complete cds.
DEFINITION AF121976
ACCESSION AF121976
VERSION AF121976.2 GI:6532000
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1421)
AUTHORS Malnic,B., Hirono,U., Sato,T. and Buck,L.B.
TITLE Combinatorial receptor codes for odors
JOURNAL Cell 96 (5), 713-723 (1999)
PUBMED 10089886
REFERENCE 2 (bases 442 to 1421)
AUTHORS Malnic,B., Hirono,U., Sato,T. and Buck,L.B.
TITLE Direct Submision
JOURNAL Submitted (20-JUN-1999) Neurobiology, Harvard Medical School, 220
Longwood Avenue, Boston, MA 02115, USA
REFERENCE 3 (bases 1 to 1421)
AUTHORS Malnic,B., Hirono,U., Sato,T. and Buck,L.B.
TITLE Direct Submision
JOURNAL Submitted (07-DEC-1999) Neurobiology, Harvard Medical School, 220
Longwood Avenue, Boston, MA 02115, USA
REMARK Sequence update by submitter
COMMENT On Dec 7, 1999 this sequence version replaced gi:4680261.
FEATURES
source
location/Qualifiers
1. .1421
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="BALB/C"
/db_xref="taxon:10090"
/catalytic_activity=">1310
/product="odorant receptor Sl9"
/note="G-protein-coupled receptor"
/codon_start=1
/product="odorant receptor Sl9"
/protein_id="P427596.2"
/db_xref="GI:6532001"
/translation="MPEKMLSKLAVLLIESCRQALVKGRIIVDSRPHMNTTH
YRELEDOHWIAIPFGSMYIALVNGCTIIYITIDRALHBPWYLFCLISITDLYC
STTLPKMLAFMLRSHVSYHGLCTOMFPAVATRSALILMAPRYVALICRPLHY
TSILNAVVIKIGLACTRGLIPFVPIVILIRLPFGCHITIPHTICENHGIACACA
SLKPNITVGLVALSTGMVNLATSYIILQAVLPLSKDAQFRAFSTCGAHCIVL
LVPIPAFSPFTHRGHNVPPQVHIIILAVLPLVPLVYGVINTKQIRLIIDF
FVGR"

ORIGIN
Query Match 1.3%; Score 55; DB 9; Length 1421;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 387 GTGACTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 441

RESULT 15
AR059581 2408 bp DNA linear PAT 29-SEP-1999
LOCUS AR059581
DEFINITION Sequence 69 from patent US 5840498.

ACCESSION AR059581
VERSION AR059581.1 GI:5986031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5840498-A 69 24-NOV-1998;
FEATURES
source
location/Qualifiers
1. .2408
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 666 GTGACTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 720

RESULT 16
AR063063 2408 bp DNA linear PAT 29-SEP-1999
LOCUS AR063063
DEFINITION Sequence 69 from patent US 5844072.
ACCESSION AR063063
VERSION AR063063.1 GI:5990754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5844072-A 69 01-DEC-1998;
FEATURES
source
location/Qualifiers
1. .2408
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 666 GTGACTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 720

RESULT 17
193548 2408 bp DNA linear PAT 01-DEC-1998
LOCUS 193548
DEFINITION Sequence 69 from patent US 5731149.
ACCESSION 193548
VERSION 193548.1 GI:3938018
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.E. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5731149-A 69 24-MAR-1998;
FEATURES
source
location/Qualifiers
1. .2408
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 1.3%; Score 55; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 55
Db 666 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 720

RESULT 18
AR370418 2408 bp DNA linear PAT 12-SEP-2003
LOCUS Sequence 69 from patent US 6300470.
DEFINITION AR370418
ACCESSION AR370418
VERSION AR370418.1 GI:34606949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsled,M.E. and Onelleite,A.J.
TITLES Antidiotic cryptdin peptides and methods of their use
JOURNAL Patent: US 6300470-A 69 09-OCT-2001;
The Regents of the University of California; Oakland, CA
FEATURES
source 1..2408
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 55
Db 666 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 720

RESULT 19
AX430197 3049 bp DNA linear PAT 28-JUN-2002
LOCUS Sequence 4 from Patent EP1207204.
DEFINITION AX430197
ACCESSION AX430197
VERSION AX430197.1 GI:21655562
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLES Tissue-specific promoters from sugar beet
JOURNAL Patent: EP 1207204-A 4 22-MAY-2002;
KWS Saat AG (DE)
FEATURES
source 1..3049
/organism="Beta vulgaris"
/mol_type="unassigned DNA"
/db_xref="taxon:161934"

FEATURES
promoter 1..2998
TATA_signal 2877..2883
mRNA 2928..3049

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 3049;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 55
Db 666 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 720

Db 2656 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 2710

RESULT 20
AX449167 3049 bp DNA linear PAT 03-JUL-2002
LOCUS Sequence 4 from Patent WO0240687.
DEFINITION AX449167
ACCESSION AX449167
VERSION AX449167.1 GI:21697968
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLES Tissue specific promoters
JOURNAL Patent: WO 0240687-A 4 23-MAY-2002;
KWS Saat AG (DE)
FEATURES
source 1..3049
/organism="Beta vulgaris"
/mol_type="unassigned DNA"
/db_xref="taxon:161934"

FEATURES
promoter 1..2998
TATA_signal 2877..2883
mRNA 2928..3049

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 3049;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 55
Db 2656 GTGACTCTAGGCTCACTGGCTTAATACGACTCATATAGGAGGCTCGAGATC 2710

RESULT 21
AB026549 3869 bp DNA linear PLN 24-OCT-2001
LOCUS Arabidopsis thaliana gene for neoxanthin cleavage enzyme, complete cds.
DEFINITION AB026549
ACCESSION AB026549
VERSION AB026549.1 GI:16416373
KEYWORDS neoxanthin cleavage enzyme.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Iuchi,S., Kobayashi,M. and Shinozaki,K.
TITLES Characterization of neoxanthin cleavage enzyme from Arabidopsis thaliana
JOURNAL Unpublished
AUTHORS Iuchi,S. and Shinozaki,K.
TITLES Direct Submision
JOURNAL Submitted (22-APR-1999) Satoshi Iuchi, RIKEN, Plant Mol. Bio.; 3-1-1 Kouyadai, Tsukuba 305-0074, Japan
(E-mail:iuchi@rtc.riken.go.jp, Tel:81-298-36-4359)
FEATURES
source 1..3869
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/ecotype="Columbia"
1831..3530
/codon_start=1
/product="neoxanthin cleavage enzyme"
/protein_id="BAB70609.1"

/db_xref="GI:16416374"
 /translation="MASTPATAAAGSGWLGNGHTQPPSSQSSDLSYCSLPMASTV
 TRKLVASALHTPPALHPFKQSSNSPALVVPKAKESNTKQMNIFQRAAAALDAAG
 FLVSHKRLHPKTAADPSVOAGNAPAPNAPVARNLPVVGKLPDSIKGVVNGANP
 LHEVNTGHHPFDGQVYAVKVEHGSASVACRFQTRFVYEROLGHPVPEKALGELH
 GHTGIALMLFVAAAAGIVDPAGTGVANGLVYFNGRLAMSEDDLPVOVOTTPNG
 DLKTVGHPFDGQVSTMIAPKVPDPSGELFALSYVNSKPYKVRFPDQKSPD
 VEIOLDQPTMMHDEFAITENPVYVDDQVPEFLPMIRIGSPVYVDKKNVAREGILDKY
 AEDSSNTKMIADAPDCFCFHLNNABEPETIDVYVIGSCMTPEDSIFNESDENKSVLS
 EIRLNLKVGESTRRPIISNEDQVNLGAGNRNMLGRKTKFAYLALAEWPVKVSGFA
 KVDLTTEGVKHLVGNRYGGEPLFLPGEQGEDEGYILCFVHDEKTKWSKLQIVNAV
 SLVEATVTKLPSRVYGFHGFICADDLAKQV"

ORIGIN

Query Match 1.3%; Score 55; DB 15; Length 3869;
 Best Local Similarity 100.0%; Pred. No. 8.3e-13;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGCACTCTAGGCGCTCACTGGCCTAATACGACTACTATAGGAGCTCGAGATC 55
 Db 1 GTGCACTCTAGGCGCTCACTGGCCTAATACGACTACTATAGGAGCTCGAGATC 55

RESULT 22
 RABAMYA 5651 bp DNA linear MAM 27-APR-1993
 LOCUS DEFINITION Rabbid serum amyloid A gene, exons 1, 2, 3, and 4.
 ACCESSION M98536
 VERSION M98536.1 GI:164769
 KEYWORDS acute phase reactant; serum amyloid A.
 SOURCE Oryctolagus cuniculus (rabbit)
 ORGANISM Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
 Leporidae; Oryctolagus.
 1 (sites)
 Ray, B.K. and Ray, A.
 Complementary DNA cloning and nucleotide sequence of rabbit serum
 amyloid A protein
 Biochem. Biophys. Res. Commun. 178 (1), 68-72 (1991)

REFERENCE
 AUTHORS Ray, B.K. and Ray, A.
 JOURNAL Biochem. Biophys. Res. Commun. 180 (3), 1258-1264 (1991)
 PUBMED 1953777
 COMMENT Original source text: Oryctolagus cuniculus (strain New Zealand)
 TITLE Rabbid serum amyloid A gene: cloning, characterization and sequence analysis

FEATURES

source
 1. 5651
 /organism="Oryctolagus cuniculus"
 /mol_type="genomic DNA"
 /strain="New Zealand"
 /db_xref="taxon:9986"
 /feature_type="liver"
 TATA_signal
 mRNA
 exon join(626..659,1089..1181,4322..4462,4904..5148)
 exon 626..659
 /number=1
 intron 660..1088
 exon /number=1
 1089..1181
 /number=2
 intron 1182..4321
 exon /number=2
 4322..4462
 /number=3
 intron 4463..4903
 exon /number=3
 4904..5148
 /number=4

polya_signal 5129..5134
 ORIGIN

Query Match 1.3%; Score 55; DB 4; Length 5651;
 Best Local Similarity 100.0%; Pred. No. 7.3e-13;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGCACTCTAGGCGCTCACTGGCCTAATACGACTACTATAGGAGCTCGAGATC 55
 Db 5651 GTGCACTCTAGGCGCTCACTGGCCTAATACGACTACTATAGGAGCTCGAGATC 5597

RESULT 23

AB031009 8072 bp DNA linear PRI 19-FEB-2000
 LOCUS Homo sapiens DNA, MHC class I CL region, 7.1 ancestral haplotype.
 DEFINITION AB031009
 ACCESSION AB031009.1 GI:7008034
 VERSION
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (sites)
 Leelayuwat, C., Abraham, L.J., Tabarias, H., Christiansen, F.T. and
 Dawkins, R.L.
 Genomic organization of a polymorphic duplicated region centromeric
 of HLA-B
 Immunogenetics 36 (4), 208-212 (1992)
 2 (bases 1 to 8072)
 Dawkins, R.L., Gaudieri, S. and Leelayuwat, C.
 Direct Submission
 Submitted (12-AUG-1999) Silvana Gaudieri, University of Western
 Australia, Centre for Molecular Immunology and Instrumentation;
 Stirling Hwy, Nedlands, WA 6009, Australia
 (E-mail:sgaudier@lab.nig.ac.jp, Tel:61-8-93464414,
 Fax:61-8-93464578)

FEATURES

source
 1. 8072
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21.3"
 /haplotype="MHC 7.1 Ancestral Haplotype HLA-A3 HLA-B7
 HLA-DR15"
 /cell_type="B lymphoblastoid"
 /dev_stage="Adult"
 490..517
 /note="AT rich"
 533..832
 /rpt_family="AluSq"
 complement(1825..1983)
 /rpt_family="L2"
 1984..2552
 /rpt_family="MER61B"
 2598..3373
 /note="Haplospecific geometric element Homologous region"
 2868..2962
 /note="(GA)n"
 complement(3005..3110)
 /rpt_family="MERSA"
 3871..3901
 /note="AT rich"
 complement(4318..4388)
 /rpt_family="7SIRNA"
 complement(4551..4682)
 /rpt_family="LIM3"
 complement(4716..4939)
 /rpt_family="L2"
 5083..5286
 repeat_unit

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misc_feature      /rpt_family="L1ME1"
5569..6766
/note="PERB3 homologous region"
repeat_unit      5678..6090
/rpt_family="HERV16"
repeat_unit      6118..6573
/rpt_family="HERV1"
misc_feature      complement(6600..8072)
/note="PERB7 homologous region"
repeat_unit      6679..6893
/rpt_family="HERV16"
repeat_unit      6959..7040
/rpt_family="HERV1"
repeat_unit      7136..7464
/rpt_family="HERV1"
repeat_unit      7705..8072
/rpt_family="HERV1"

ORIGIN
Query Match      1.3%; Score 55; DB 8; Length 8072;
Best Local Similarity 100.0%; Pred. No. 6.6e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 55
1 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 55
Db 1 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 55

RESULT 24
LOCUS      CS070402      11716 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION      Sequence 31 from Patent WO2001023541.
ACCESSION      CS070402
VERSION      CS070402.1      GI:63087970
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
              synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Fodor, W.L. and Ramsondar, J.J.
TITLE      Compositions and methods for altering gene expression
              Patent: WO 2001023541-A 31 05-APR-2001;
              Alexion Pharmaceuticals, Inc. (US)
FEATURES
source      1..11716
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="gene targeting vector"
              4852..4937
              /note="Nucleotides at positions 4852 to 4937 are n wherein
              n = nucleotides between the end of Intron 3 and beginning
              of Intron 4"

ORIGIN
Query Match      1.3%; Score 55; DB 6; Length 11716;
Best Local Similarity 100.0%; Pred. No. 5.9e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 55
1 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 55
Db 1 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 55

RESULT 25
LOCUS      AB124593      13701 bp      DNA      linear      PLN 12-NOV-2004
DEFINITION      Oryza sativa (indica cultivar-group) DNA, endogenous rice tungro
              bacilliform virus-like sequence, clone:IR36-BRTBV3.
ACCESSION      AB124593
VERSION      AB124593.1      GI:46409013
KEYWORDS
SOURCE      Oryza sativa (indica cultivar-group)
```

```
ORGANISM      Oryza sativa (indica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1
AUTHORS      Kunii, M., Kanda, M., Nagano, H., Uyeda, I., Kishima, Y. and Sano, Y.
TITLE      Reconstruction of putative DNA virus from endogenous rice tungro
              bacilliform virus-like sequences in the rice genome: implications
              for integration and evolution
JOURNAL      (er) BMC Genomics 5 (1), 80 (2004)
PUBMED      15488154
REFERENCE      2 (bases 1 to 13701)
AUTHORS      Kishima, Y. and Sano, Y.
TITLE      Direct Submission
JOURNAL      Submitted (17-OCT-2003) Yuji Kishima, Hokkaido University,
              Laboratory of Plant Breeding, Graduate School of Agriculture;
              Kita-ku Kita 9, Nishi 9, Sapporo, Hokkaido, 060-8589, Japan
              (E-mail:kishima@aps.agr.hokudai.ac.jp, Tel:81-11-706-2439,
              Fax:81-11-706-4934)
FEATURES
source      1..13701
              Location/Qualifiers
              /organism="Oryza sativa (indica cultivar-group)"
              /mol_type="genomic DNA"
              /cultivar="IR36"
              /db_xref="taxon:39946"
              /clone_jib="IR36-BRTBV3"
              /clone_jib="EMBL3 etiolated shoots genomic DNA (CLONTECH,
              F110413)"
              158..5914
              /note="endogenous rice tungro bacilliform virus-like
              sequence"

ORIGIN
Query Match      1.3%; Score 55; DB 15; Length 13701;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 55
1 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 55
Db 13669 GTCGACTCTAGGCTCAGCTGAGCTTAATACGACTCATTATAGGAGCTCGAGATC 13615

RESULT 26
LOCUS      CS070389      27078 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION      Sequence 18 from Patent WO2001023541.
ACCESSION      CS070389
VERSION      CS070389.1      GI:63087957
KEYWORDS
SOURCE      .
ORGANISM      Sus scrofa (pig)
              Sus scrofa (pig)
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
              Sus.
REFERENCE      1
AUTHORS      Fodor, W.L. and Ramsondar, J.J.
TITLE      Compositions and methods for altering gene expression
              Patent: WO 2001023541-A 18 05-APR-2001;
              Alexion Pharmaceuticals, Inc. (US)
FEATURES
source      1..27078
              Location/Qualifiers
              /organism="Sus scrofa"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9823"
              /note="porcine Gal alpha (1,3) galactosyl transferase
              gene"
              4852..4937
              /note="Nucleotides 4852 to 4937 are n wherein n =
              nucleotides within the Exon 4 region"
              11717..11752
              /note="Nucleotides 11717 to 11752 are n wherein n =
              nucleotides within the Exon 5 region"
              13748..13811

misc_feature      13748..13811
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misc_feature
misc_feature
misc_feature

/note="Nucleotides 13748 to 13811 are n wherein n =
nucleotides within the Exon 6 region"
14359..14463
/note="Nucleotides 14359 to 14463 are n wherein n =
nucleotides within the Exon 7 region"
21628..21765
/note="Nucleotides 21628 to 21765 are n wherein n =
nucleotides within the Exon 8 region"
27049..27078
/note="Nucleotides 21628 to 21765 are n wherein n =
nucleotides within the Exon 9 region"

ORIGIN

Query Match 1.3%; Score 55; DB 6; Length 27078;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGACTCTAGGCTCACTGCGCTAATACGACTCACTATAGGGAGCTCGAGGATC 55
Db 1 GTCGACTCTAGGCTCACTGCGCTAATACGACTCACTATAGGGAGCTCGAGGATC 55

RESULT 27
ATU44028 1955 bp mRNA linear PLN 30-JAN-1996
LOCUS Arabidopsis thaliana transcription factor CKC mRNA, complete cds.
DEFINITION U44028
ACCESSION U44028
VERSION U44028.1 GI:1171428
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bakteriota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsida.
1 (bases 1 to 1955)
Verzani P., Morandini P. and Soave C.
Submitted (29-DEC-1995) Paola Verzani, Dept. of Biology 'L.
Gorini', University of Milan, Via Celoria 26, Milan, 20133, Italy
Location/Qualifiers
1..1955
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
76..1743
/function="transcription factor; complements a yeast
protein kinase C 1 mutant; Method: conceptual translation
supplied by author."
/codon_start=1
/product="CKC"
/protein_id="AA06281.1"
/db_xref="GI:1171429"
/translation="MKSFCNDNDNNHNTNLGFSLSNMWKGKRGREATYSST
CSAATSSSVPOI.VYGDNTNSNGVCYSGNSGITYHMSMPLRSGSICIMALNR
SSSHNHODSSPKVEDPFGTHNNTSHKENDLSLDLFTNTHETVTTNFOEFESF
PQRNHEETRNNGDNDLSLTHGSEFNGVGEFQSLSTLSPSSQSCITGSHHQ
NQNMNSQNHQOISEALVETSVGFETTTMAAKKGOEDVVVVGQKQVHRKSIDT
FGORTSGYRGVTRHRTGRYEAHLMDNSPKKEGSRKGRGVYLGQYMERKAAAYDL
AALKYMGSTHTNSAENYOKETEDMNMTRQEVVAHLRRKSSGFSRGSADTGYVTL
HOGKRMQARIGRAVAKNDLYLGTGQGBEAAEAVDAVATKRCGNATNTNDDIRYVD
RIMSSNTLISGELARRNNNSIVANNTEDQTALNAVVGSGSKKEVSTPERLSPFALTA
LPVNMQMFSGNMGNMSPMTPSNALKTVALTLPPMPVFAAWADS"

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

CDS
1..1955
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
76..1743
/function="transcription factor; complements a yeast
protein kinase C 1 mutant; Method: conceptual translation
supplied by author."
/codon_start=1
/product="CKC"
/protein_id="AA06281.1"
/db_xref="GI:1171429"
/translation="MKSFCNDNDNNHNTNLGFSLSNMWKGKRGREATYSST
CSAATSSSVPOI.VYGDNTNSNGVCYSGNSGITYHMSMPLRSGSICIMALNR
SSSHNHODSSPKVEDPFGTHNNTSHKENDLSLDLFTNTHETVTTNFOEFESF
PQRNHEETRNNGDNDLSLTHGSEFNGVGEFQSLSTLSPSSQSCITGSHHQ
NQNMNSQNHQOISEALVETSVGFETTTMAAKKGOEDVVVVGQKQVHRKSIDT
FGORTSGYRGVTRHRTGRYEAHLMDNSPKKEGSRKGRGVYLGQYMERKAAAYDL
AALKYMGSTHTNSAENYOKETEDMNMTRQEVVAHLRRKSSGFSRGSADTGYVTL
HOGKRMQARIGRAVAKNDLYLGTGQGBEAAEAVDAVATKRCGNATNTNDDIRYVD
RIMSSNTLISGELARRNNNSIVANNTEDQTALNAVVGSGSKKEVSTPERLSPFALTA
LPVNMQMFSGNMGNMSPMTPSNALKTVALTLPPMPVFAAWADS"

ORIGIN

Query Match 1.3%; Score 53; DB 15; Length 1955;
Best Local Similarity 100.0%; Pred. No. 7.7e-12;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4176 AGACTGAAGATACCTTATAGAAAGAGAGAAACCAAAAAAGAAACC 4228
Db 23 AGAGTGAAGATACCTTATAGAAAGAGAGAAACCAAAAAAGAAACC 75

RESULT 28
CS070390 4026 bp DNA linear PAT 05-MAY-2005
LOCUS CS070390
DEFINITION Sequence 19 from Patent WO2001023541.
ACCESSION CS070390
VERSION CS070390.1 GI:63087958
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Podor W.L. and Ramsondar J.J.
Compositions and methods for altering gene expression
Patent: WO 2001023541-A 19 05-APR-2001;
Alexion Pharmaceuticals, Inc. (US)
Location/Qualifiers
1..4026
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Gal alpha (1,3) galactosyl transferase gene"

ORIGIN

Query Match 1.1%; Score 46; DB 6; Length 4026;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 AGGCTCAGTGGCTTAATACGACTCACTATAGGAGCTCGAGGATC 55
Db 10 AGGCTCAGTGGCTTAATACGACTCACTATAGGAGCTCGAGGATC 55

RESULT 29
AB080913 13143 bp DNA linear PRI 05-FEB-2004
LOCUS Homo sapiens gene for Fc-epsilon receptor I beta-chain, complete
DEFINITION AB080913
ACCESSION AB080913
VERSION AB080913.1 GI:29420482
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bakteriota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Akiwaza Y., Nishiyama C., Hasegawa M., Maeda K., Nakahata T.,
Okumura K., Ra C. and Ogawa H.
Regulation of human FcepsilonRI beta chain gene expression by Oct-1
Int. Immunol. 15 (5), 549-556 (2003)
2 (bases 1 to 13143)
Nishiyama C. and Hasegawa M.
Submitted (06-MAR-2002) Chiharu Nishiyama, Juntendo University
School of Medicine, Allergy Research Center; 2-1-1 Hongo,
Bunkyo-ku, Tokyo 113-8421, Japan
(E-mail: chiharu@med.juntendo.ac.jp, Tel: 81-3-5802-1591,
Fax: 81-3-3813-5512)
Location/Qualifiers
1..13143
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1383..1540
join(1485..1540,2411..2540,3055..3189,5509..5565,
6117..6275,6677..6775,8269..8367)
/codon_start=1
/product="Fc-epsilon receptor I beta-chain"
/protein_id="BAC6486.1"
/db_xref="GI:29420483"
/translation="MOTESRRANLALPOEPPSVPAFVLEISPOEVSGLTKSAS
PLHTWLTVAKEQEPFLGVQIITLMTICLCFRTVCSVDLSIHEDIPSSFAGYGF

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

13143
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1383..1540
join(1485..1540,2411..2540,3055..3189,5509..5565,
6117..6275,6677..6775,8269..8367)
/codon_start=1
/product="Fc-epsilon receptor I beta-chain"
/protein_id="BAC6486.1"
/db_xref="GI:29420483"
/translation="MOTESRRANLALPOEPPSVPAFVLEISPOEVSGLTKSAS
PLHTWLTVAKEQEPFLGVQIITLMTICLCFRTVCSVDLSIHEDIPSSFAGYGF

exon 2411..2540
 exon 3055..3189
 exon 5509..5565
 exon 6117..6275
 exon 6677..6775
 exon 8269..11251
 ORIGIN

Query Match	1.1%;	Score 45;	DB 8;	Length 13143;
Best Local Similarity	100.0%;	Pred. No. 1,4e+08;		
Matches 45;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	11	GGCTCACTGGCCCTAATTCAGACTCACTCTATTAGGAGACTTGAGAGATC	55	
Db	13143	GGCTCACTGGCCCTAATTCAGACTCACTCTATTAGGAGACTTGAGAGATC	13099	

RESULT 30					
S49654S2					
LOCUS	S49654S2	1228 bp	DNA	linear	ROD 25-JAN-2005
DEFINITION	Mus sp. sperm mitochondria-associated cysteine-rich protein gene,				
	5' UTR and complete cds.				
ACCESSION	S49657				
VERSION	S49657.1	GI:259841			
KEYWORDS	.				
SEGMENT	2 of 2				
SOURCE	Mus sp.				
ORGANISM	Mus sp.				

REFERENCE AUTHORS TITLE
1 (pages 1 to 1228) Karimpour I., Cutler, M., Shih, D., Smith, J. and Kleene, K. C. Sequence of the gene encoding the mitochondrial capsule

JOURNAL DNA Cell Biol. 11 (9), 693-699 (1992)
 PUBMED 1418626
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbon 118581] from the original journal article.

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source
1..1228
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
join(SA4654.1<787..928,391..842)
/product="sperm mitochondria-associated cysteine-rich
protein
join(SA4654.1<787..928,391..410)
5' UTR
411..842
CDS

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/translation="MSDPSKINQCEPPCCCPKPCCPAPKACCRQKRPCPCPKSPCCCPKPKS  
PCCPPKPCPCPPCCPCPCAPCPCPLKPKCCPKQKSCCPKCKCTCCPPDPCCADPTCC  
SSNKTESDSDTSGCTLEKGSQSPOSPGAQGNMVKKSNP"
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Query Match	1.0%;	Score 44;	DB 9;	Length 1228;
Best Local Similarity	100.0%;	Pred. No. 7.8e-08;		
Matches	44;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	12	GCCTCACTGGCCTTATACGACTCACTATTAGGAGCTCGAGATC	55	
db	98	GCCTCACTGGCCTTATACGACTCACTATTAGGAGCTCGAGATC	141	

FEATURE	source
RESULT 31	
LOCUS	ATU41339
DEFINITION	Arabidopsis thaliana ANT (AINTEGUMENTA)
VERSION	U41339
KEYWORDS	U41339.1 GI:1244707
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales, Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 1905) Elliot, R.C., Betzner, A.S., Hutner, E., Oakes, M.P., Tucker, W.Q., Geregenes, D., Perez, P. and Smyth, D.R.
TITLE	AINTEGUMENTA, an APT2LA2-like gene of Arabidopsis with pleiotropic roles in ovule development and floral organ growth
JOURNAL	Plant Cell 8 (2), 155-168 (1996)
PIUMED	8742707
REFERENCE	2 (bases 1 to 1905) Smyth, D.R.
AUTHORS	Direct Submission
TITLE	Submitted (27-NOV-1995) David Smyth, Genetics and Dev. Biology,
JOURNAL	Monash University, Wellington Road, Clayton, VIC 3168, Australia
FEATURES	Location/Qualifiers
source	1..1905

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  1. .1905
  38. .1705
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  Accession Number U12546"
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  /product="ANT"
  /protein_id="AAB17364.1"
  /db_xref="GI:1244708"
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  SNAATSSSVPPOLVVGDNNTSNFGCYGSPNGGIIYSHMVPMLRISGLCLMBALNR
  SSSHHNDESSPVEYDFGTHNNHNSHKEAMDLSDLPNTHTPEVTTTFQPSFS
  PQRNHEBETFRNYGNDPESLTHGSGFNVGYYGEEQSLSLSPSGSSCITGSHHHQQ
  NQNMQNSQNHQOISEALVETSVGFETTTAAAKKRGQDVLVVGQKQIVHRSKIDT
  FGQRTSQRGVTRHRTWGRYEALHMDNPSFKEGHSRKGROVUYLGQYMEKRAAYDL
  AALKYMGPSRHTNPSAENVYKKEIDEMKNMRQSVYALHRSKGSFGSAIYIGVTH
  HCGKRWARICRVAGNKDLYLGTPTGQFEAAEAYDAVALKEFGNTAVTNDITRYVD
  RINSSNTLISGELARRNNNSIYVRNTEDQYALAAVYVGGSKNSKESVPERLLSPALFA
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  878. .1108
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  /note="encodes first Ap2 domain"
  1184. .1391
  /gene="AINTEGUMENTA"
  /note="encodes second Ap2 domain"

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[illegible]

DEFINITION C. albicans (Ca74) SAP7 gene for aspartyl protease.
ACCESSION 230193
VERSION 230193.1 GI:456253
KEYWORDS aspartyl protease; SAP7 gene.
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetaceae; mitosporic Saccharomycetaceae; Candida.
REFERENCE 1 (bases 1 to 2317)
AUTHORS Monod,M., Togni,G., Hube,B. and Sanglard,D.
TITLE Multiplicity of genes encoding aspartic proteinases in
Candida species
JOURNAL Mol. Microbiol. 13 (2), 357-368 (1994)
PUBMED 7984113
REFERENCE 2 (bases 1 to 2317)
AUTHORS Monod,M., Togni,G., Hube,B. and Sanglard,D.
TITLE Multiplicity of genes encoding secreted aspartic proteases in
Candida species
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2317)
AUTHORS Sanglard,D.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-1994) Dominique SANGLARD, Inst. de Microbiologie
F509/Biochimie, Centre, Hôpitalier Universitaire Vaudois (CHUV),
155, Ch. de Boveresses, Epalinges, 1066, Switzerland
FEATURES
source
1. .2317
/organism="Candida albicans"
/mol_type="genomic DNA"
/strain="Ca74"
/db_xref="taxon:5476"
283. .2049
/gene="SAP7"
283. .2049
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/codon_start=1
/transl_table=12
/product="aspartyl protease"
/protein_id="CA82925.1"
/db_xref="GI:578123"
/db_xref="GOA:P43096"
/db_xref="InterPro:IPR001461"
/db_xref="InterPro:IPR001969"
/db_xref="UniProt/Swiss-Prot:P43096"
/translacion="MQRVLELLSLSTALVIGPFTALPVHKLQAGEGSAHPNRLP
IPFVNGVAKSVEDVNOIIOPIFGNGIFSGSIOGTHSGNGSVKYEVLPSASAK
GASGSPSTDKDTPSKTSPSLDLMNSITDPMNLGLKPPSTNGSKDAPPS
AVSQVQPTSKSVSTAPGSASSSSSSSEBLASSQPSDSDQSSANKTKGAPLS
LDNTOYLTYATLVKSPAQEVQVMDTGSSDLNPFSSGNSQCKVNGSISDCRXGVD
KSSSSSWNDKTDYSSISYDGDKASGTMGQDNITPAGPSIENANPAVIDNTTSIGV
FGVGYPELEAVKRYTLPAMKEQNLIAKVAISLYSDSDAVQGYLLPGIDHAFT
GDKAPDIVOCNDKXYYSOIPLTSVASLNNYNAVGLPAGSNHPKGAIVYNGTDSF
NGGVLDKDTLLDGTGTVSLSKDOVESIVGLYGVNTYADGAKAYPVCWNGNPGVY
LEENPKREQYIKYPTSEFVYISGVYASGAEICVFGIILPETHSILGDNFMSVYAVFDL
EDHVISIAQAAYNDHNAVPIE"
916. .2046
/gene="SAP7"
/product="aspartyl protease (putative)"
ORIGIN
Query Match 0.8%; Score 33; DB 15; Length 2317;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTAATAGACTCACTATAGAGCTCGAGATC 55
DB 2296 CTAATAGACTCACTATAGAGCTCGAGATC 2264
RESULT 33
AR029517/c 4162 bp DNA linear PAT 29-SEP-1993
LOCUS

DEFINITION Sequence 26 from patent US 5859336.
ACCESSION AR029517
VERSION AR029517.1 GI:5941490
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 4162)
AUTHORS Koziet,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Eyoia,S.V.,
Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L., Bowman,C.G.,
Dawson,J.L., Dunder,B.M., Pace,G.M. and Suttie,J.L.
TITLE Synthetic DNA sequence having enhanced activity in maize
JOURNAL Patent: US 5859336-A 26 12-JUN-1999;
FEATURES
source
1. .4162
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 TGGCTATAGACTCACTATAGAGCTCGA 50
DB 4162 TGGCTATAGACTCACTATAGAGCTCGA 4131
RESULT 34
AR098470/c 4162 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 26 from patent US 6075185.
ACCESSION AR098470
VERSION AR098470.1 GI:12807727
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 4162)
AUTHORS Koziet,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Eyoia,S.V.,
Wright,M.S., Launis,K.L., Rochsteijn,S.J., Bowman,C.G., Dawson,J.L.,
Dunder,B.M., Pace,G.M. and Suttie,J.L.
TITLE Synthetic DNA sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: US 6075185-A 26 13-JUN-2000;
FEATURES
source
1. .4162
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 TGGCTATAGACTCACTATAGAGCTCGA 50
DB 4162 TGGCTATAGACTCACTATAGAGAGCTCGA 4131
RESULT 35
AR494979/c 4162 bp DNA linear PAT 15-MAY-2004
LOCUS
DEFINITION Sequence 26 from patent US 6720488.
ACCESSION AR494979
VERSION AR494979.1 GI:47270333
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 4162)
AUTHORS Koziet,M., Desai,N., Pace,G.M., Suttie,J., Carozzi,N., Boyce,C.,
Dawson,J.L., Dunder,B., Wright,M., Launis,K., Rochsteijn,S.J.,

TITLE Lewis, K., Warren, G., and Ewola, S.
JOURNAL Transgenic maize seed and method for controlling insect pests
Patent: US 6720486-A 26 13-APR-2004;
Syngenta Investment Corporation; Wilmington, DE

FEATURES
source
1. .4162
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TGCCCTAATCGACTCACTATAGGAGCTCGA 50
Db 4162 TGCCCTAATCGACTCACTATAGGAGCTCGA 4131

RESULT 36
AX441395/c 4162 bp DNA linear PAT 03-JUL-2002

LOCUS Sequence 26 from Patent EP1209237.
DEFINITION AX441395
ACCESSION AX441395
VERSION AX441395.1 GI:21690378
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
AUTHORS 1
Kozielec, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,
Ewola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launus, K.L.
and Rothstein, S.J.
TITLE Synthetic dna sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: EP 1209237-A 26 29-MAY-2002;
Syngenta Participations AG (CH)

FEATURES
source
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/organism="Zea mays"
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/db_xref="taxon:4577"
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1418..1427
/note="start of mRNA"

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intron 2367..2451
exon 2452..2602
intron 2603..2690
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intron 2805..2906
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intron 3076..3177
exon 3178..3304
intron 3305..3398
exon 3399..3498
intron 3499..3713
exon 3714..3811

ORIGIN

DEFINITION Sequence 26 from Patent EP1213356.
ACCESSION AX453891
VERSION AX453891.1 GI:21713549
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
AUTHORS 1
Kozielec, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,
Ewola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launus, K.L.
and Rothstein, S.J.
TITLE Synthetic dna sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: EP 1213356-A 26 12-JUN-2002;
Syngenta Participations AG (CH)

FEATURES
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exon 1481..2366
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exon 2452..2602
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intron 3499..3713
exon 3714..3811

ORIGIN

Query Match 0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TGCCCTAATCGACTCACTATAGGAGCTCGA 50
Db 4162 TGCCCTAATCGACTCACTATAGGAGCTCGA 4131

RESULT 38
LOCUS 4165 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 26 from patent US 5625136.
ACCESSION 141430
VERSION 141430.1 GI:2082020
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 4165)
Kozielec, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,
Ewola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launus, K.L.,
Rothstein, S.J., Bowman, C.G., Dawson, J.L., Dunder, E.M., Pace, G.M.
and Sutcliffe, J.L.
TITLE Synthetic DNA sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: US 5625136-A 26 29-APR-1997;
Syngenta Participations AG (CH)

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ORIGIN		
Query Match	0.7%; Score 29; DB 14; Length 177938;	
Best Local Similarity	100.0%; Pred. No. 0.061;	
Matches 29; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Dy	3471 AAAAAAAAAAAGCTTTTCATTAATA 3499	
Db	20564 AAAAAAAAAAAGCTTTTCATTAATA 20592	
RESULT 41		
LOCUS	AC134627	204712 bp DNA linear HTG 20-NOV-2002
DEFINITION	Rattus norvegicus clone CH230-36BN4, WORKING DRAFT SEQUENCE, 5	
ACCESSION	AC134627	
VERSION	AC134627.2 GI:25138679	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRIFT; HTGS_FULLTOP.	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Rattus. 1 (bases 1 to 204712) Muzny,D.,Marie, Metzker,M.,Lee, Abrazon,S., Adams,C., Alder,J., Allen,C., Allen,H., Albrooks,S., Amin,A., Angiano,D., Anyalebechi,V., Ayogaji,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Blawie,K., Blair,J., Blankenburg,K., Blythe,P., Brown,M., Bryant,N., Bunay,C., Burch,P., Burrell,K., Calderon,E., Cadenas,V., Carter,K., Cavazos,I., Cesaar,H., Chen,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Cher,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., David,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Diaper,H., Dugan-Rocha,S., Dunn,A., Durdin,K., Duval,B., Bayes,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foister,P., Fraser,C.M., Gabisi,A., Gatta,R., Garcia,A., Garner,T., Garra,M., Georgescu,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guerrero,K., Gunaratne,P., Healand,W., Hamill,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Henningsen,B., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulik,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpachy,S., Kelly,S., Khan,Z., King,L., Kovac,C., Kovats,C., Krefc,C.L., Lebow,H., Levau,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshaw,L., Louisedge,H., Lozada,R.J., Lu,X., Ma,J., Maheshwari,C., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A., Margum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mehriney,S., McLeod,M.P., McNeill,T.Z., Meenen,B., Milosavljevic,A., Miner,G., Munja,E., Montemayor,J., Moore,S., Moragan,M., Morris,K., Morris,S., Mundasa,M., Murphy,M., Nair,L., Narkewicz,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwokolemoh,O., Okunolu,G., Olarnpinagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfankoch,C., Plopper,F., Polnatekter,A., Popovic,D., Primus,B., Pu,L., Reigh.R., Plazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Relgh.R.,	

REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rivers,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,U., Shvartsbeyn,A., Sison,,., Sitter,C.D., Smay,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,U., Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wodden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,U., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausen,A., Weis,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.	Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Submitted (28-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequencing version replaced gi:23343609. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.	On Nov 20, 2002 this sequencing version replaced gi:23343609. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.	On Nov 20, 2002 this sequencing version replaced gi:23343609. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.	On Nov 20, 2002 this sequencing version replaced gi:23343609. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Project Information Center project name: KC20 Center clone name: CH230-36BN4	Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Project Information Center project name: KC20 Center clone name: CH230-36BN4	Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Project Information Center project name: KC20 Center clone name: CH230-36BN4	Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Project Information Center project name: KC20 Center clone name: CH230-36BN4
Assembly program: Phrap; version 0.990329 Consensus quality: 186320 bases at least Q40 Consensus quality: 18835 bases at least Q30 Consensus quality: 189791 bases at least Q20 Estimated insert size: 187550; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation	Assembly program: Phrap; version 0.990329 Consensus quality: 186320 bases at least Q40 Consensus quality: 18835 bases at least Q30 Consensus quality: 189791 bases at least Q20 Estimated insert size: 187550; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation	Assembly program: Phrap; version 0.990329 Consensus quality: 186320 bases at least Q40 Consensus quality: 18835 bases at least Q30 Consensus quality: 189791 bases at least Q20 Estimated insert size: 187550; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation	Assembly program: Phrap; version 0.990329 Consensus quality: 186320 bases at least Q40 Consensus quality: 18835 bases at least Q30 Consensus quality: 189791 bases at least Q20 Estimated insert size: 187550; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html). * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.	* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html). * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.	* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html). * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.	* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html). * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
1 6702: contig of 6702 bp in length 6703 6802: gap of unknown length 6803 contig of 69966 bp in length 76789 76888: gap of unknown length 127889: contig of 51011 bp in length 127900 127999: gap of unknown length	1 6702: contig of 6702 bp in length 6703 6802: gap of unknown length 6803 contig of 69966 bp in length 76789 76888: gap of unknown length 127889: contig of 51011 bp in length 127900 127999: gap of unknown length	1 6702: contig of 6702 bp in length 6703 6802: gap of unknown length 6803 contig of 69966 bp in length 76789 76888: gap of unknown length 127889: contig of 51011 bp in length 127900 127999: gap of unknown length	1 6702: contig of 6702 bp in length 6703 6802: gap of unknown length 6803 contig of 69966 bp in length 76789 76888: gap of unknown length 127889: contig of 51011 bp in length 127900 127999: gap of unknown length

FEATURES	source	1.	204712	Location/Qualifiers
*	128000	153581	contig of 25582 bp in length	
*	153582	153681	gap of unknown length	
*	153682	204712	contig of 51031 bp in length.	
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gap				
misc_feature				
gap				
gap				
misc_feature				
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Matches	29;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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Db	164536	ACATACACATATATTTTGTGTTTGTGTTT	164564	
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DEFINITION				
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VERSION				
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SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
AC123561				
AC123561.2				
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Rattus norvegicus (Norway rat)				
Rattus norvegicus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
Schirognathi; Murioidea; Muridae; Rattus;				
1 (bases 1 to 215429)				
Munry, D. Marie, Metzker, M. Lee, Abrazon, S., Amin, A., Angiano, C., Alder, J.,				
Allen, C., Allen, H., Albrooks, S., Amlin, A., Argüello, D.,				
Ayala, A., Ayala, V., Ayala, A., Ayodeji, M., Bacc, R., Baden, H.,				
Baldwin, D., Banderman, D., Barber, M., Barnstead, M., Benham, F.,				
Blawie, K., Blair, J., Blankenship, K., Blyth, P., Brown, M.,				
Byrnes, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,				
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, J.,				
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,				
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,				
Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,				
Diaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K.,				
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,				
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,				
Freder, C. M., Gabisi, A., Garcia, R., Garcia, A., Garner, T., Garza, M.,				
Georgiev, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,				
Gunnarsson, P., Haaland, W., Hamli, C., Hamilton, C., Hamilton, K.,				
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,				
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Hollins, B., Howell, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A.,				
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,				
Kapachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,				

Kwois, C., Kraft, C.L., Lebou, H., Levay, J., Lewis, L., Li, Z., Liu, J.,
 Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J.,
 Lorenzenhewa, L., Louisedge, H., Lozada, R.J., Lu, X., Ma, J.,
 Maneshwari, M., Mahindaratne, M., Mahmoud, M., Mallory, K., Mangum, A.,
 Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Manthey, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
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 Nankerville, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
 Nwokedemeh, O., Okwom, G., Olarinmason, A., Pal, S., Parks, K.,
 Paternacki, S., Paul, H., Perez, A., Perez, L., Plamnick, C.,
 Plomp, F., Polidexter, A., Popovic, D., Primus, E., Pu, L.,
 Puzo, M., Quirco, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
 Rely, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
 Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
 Sanders, W., Savary, G., Scheier, S., Scott, G., Shatsman, S., Shen, H.,
 Shetty, J., Shvartsbeyn, A., Sisson, I., Silter, C.D., Sma, S.D.,
 Sneed, A., Sodergren, E., Song, X.-Z., Sorcelle, R., Sosa, J.,
 Steimle, M., Strong, R., Sutton, A., Swack, A., Taber, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejs, Z., Usmani, K.,
 Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, D.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Weidenhausen, G., Weiser, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Widenstock, E., and Gibbs, R.A.
 Unpublished
 2 (bases 1 to 215429)
 Direct Submission
 Submitted (31-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 215429)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (11-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Oct 10, 2002 this sequence version replaced gi:21281285.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GXSW
 Center clone name: CH230-165B21
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 178656 bases at least Q40
 Consensus quality: 181922 bases at least Q30
 Consensus quality: 184135 bases at least Q20
 Estimated insert size: 186300; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the pieces
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 1 215429: contig of 215429 bp in length.

FEATURES

source

1. 215429
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-165B21"

misc_feature

720..1470
 /note="clone boundary
 clone_end:17
 site:ECORI
 end_sequence:BH272105"

ORIGIN

Query Match 0.7%; Score 29; DB 14; Length 215429;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

704 ACATACACATATTTTGTGTTGTTT 732

Db 212351 ACATACACATATTTTGTGTTGTTT 212379

RESULT 43

AC095481/C

LOCUS AC095481 276881 bp DNA linear HTG 09-MAY-2003
 DEFINITION Rattus norvegicus clone CH230-7K20. *** SEQUENCING IN PROGRESS ***
 5 unordered pieces.

ACCESSION

AC095481

AC095481.6 GI:30467658

VERSION

HTG: HTGS_PHASE1, HTGS_DRAFT, HTGS_ENRICHED.

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE

AUTHORS

Muzny,D,Marrie, Metzker,M, Lee, Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alibonco, S., Amin, A., Anguiano, D.,
 Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Bismalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
 Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
 Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, W.,
 Gebregergs, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
 Gunatirre, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
 Harvey, J., Hawlak, P., Hawes, A., Henderson, N., Hernandez, J.,
 Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,
 Hollins, B., Howells, S., Hu, Y. S., Hume, J., Idlebird, D., Jackson, A.,
 Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
 Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kowls, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
 Lorenzini, L., Louie, H., Lozano, R. J., Lu, X., Ma, J.,
 Maheshwari, M., Mahindaratne, M., Mahmoud, K., Malloy, K., Mangum, A.,
 Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department

JOURNAL

of Molecular and Human Genetics, Baylor College of Medicine, One

REFERENCE

Baylor Plaza, Houston, TX 77030, USA

AUTHORS

3 (bases 1 to 276881)

TITLE

Rat Genome Sequencing Consortium.

JOURNAL

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department

REFERENCE

of Molecular and Human Genetics, Baylor College of Medicine, One

AUTHORS

Baylor Plaza, Houston, TX 77030, USA

TITLE

The sequence in this assembly is a combination of BAC based reads

COMMENT

and whole genome shotgun sequencing reads assembled using Atlas

JOURNAL

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

REFERENCE

in the feature table below represents a scaffold in the Atlas

AUTHORS

assembly (a 'contig-scaffold'). Within each contig-scaffold,

TITLE

individual sequence contigs are ordered and oriented, and separated

COMMENT

by sized gaps filled with Ns to the estimated size. The sequence

JOURNAL

may extend beyond the ends of the clone and there may be sequence

REFERENCE

contigs within a contig-scaffold that consist entirely of whole

AUTHORS

genome shotgun sequence reads. Both end sequences and whole genome

TITLE

shotgun sequence only contigs will be indicated in the feature

COMMENT

table.

JOURNAL

----- Genome Center

REFERENCE

Center: Baylor College of Medicine

AUTHORS

Center code: BCM

TITLE

Web site: http://www.hgsc.bcm.tmc.edu/

COMMENT

Contact: hgsc-help@bcm.tmc.edu

JOURNAL

----- Project Information

REFERENCE

Center project name: GCKM

AUTHORS

Center clone name: CH230-7K20

TITLE

----- Summary Statistics

COMMENT

Assembly program: Atlas

JOURNAL

Consensus quality: 222954 bases at least Q40

REFERENCE

Consensus quality: 228004 bases at least Q30

AUTHORS

Consensus quality: 230763 bases at least Q20

TITLE

Estimated insert size: 23155; sum-of-contigs estimation

COMMENT

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

JOURNAL

REFERENCE

* NOTE: Estimated insert size may differ from sequence length

AUTHORS

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

TITLE

* NOTE: This is a 'working draft' sequence. It currently

COMMENT

* consists of 5 contigs. The true order of the pieces

JOURNAL

* is not known and their order in this sequence record is

REFERENCE

* arbitrary. Gaps between the contigs are represented as

AUTHORS

* runs of N, but the exact sizes of the gaps are unknown.

TITLE

* This record will be updated with the finished sequence

COMMENT

* as soon as it is available and the accession number will

```
* be preserved.
* 1 241308: contig of 241308 bp in length
* 241309 241408: gap of unknown length
* 241409 270462: contig of 29054 bp in length
* 270463 270562: gap of unknown length
* 270563 271681: contig of 1119 bp in length
* 271682 271781: gap of unknown length
* 271782 272810: contig of 1029 bp in length
* 272811 272910: gap of unknown length
* 272911 276881: contig of 3971 bp in length.
FEATURES
    source
        1..276881
            /organism="Rattus norvegicus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10116"
            /clone="CH230-7K20"
            1..1235
                /note="wgs contig"
                /note="wgs_contig"
                /note="wgs_contig"
                /note="wgs_contig"
                /note="wgs_contig"
            241309..241408
                /estimated_length=unknown
            270463..270562
                /estimated_length=unknown
            271682..271781
                /estimated_length=unknown
            272811..272910
                /estimated_length=unknown
ORIGIN
Query Match 0.7%; Score 29; DB 14; Length 276881;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 704 ACATACGACATATTTTGTGTTTGTGTTT 732
Db 156792 ACATACGACATATTTTGTGTTTGTGTTT 156764

RESULT 44
SYNLMASH1
LOCUS Cloning vector lambda-SHLX1 DNA, partial sequence.
ACCESSION M37056
VERSION M37056.1 GI:208752
KEYWORDS lambda-SHLX.
SOURCE unidentified cloning vector
ORGANISM unidentified cloning vector
REFERENCE 1 (bases 1 to 105)
AUTHORS Palazzolo,M.J., Hamblen,B.A., Ding,D.L., Martin,C.H., Mead,D.A.,
Mierendorf,R.C., Raghavan,K.V., Meyerowitz,E.M. and Lipshitz,H.D.
TITLE Phage lambda cDNA cloning vectors for subtractive hybridization,
fusion-protein synthesis and Cre-loxP automatic plasmid subcloning
JOURNAL Gene 88 (1), 25-36 (1990)
PUBMED 2140336
COMMENT Original source text: Cloning vector DNA.
FEATURES
    source
        1..105
            /organism="unidentified cloning vector"
            /mol_type="genomic DNA"
            /db_xref="taxon:45196"
            /clone="pSHLX1"
ORIGIN
Query Match 0.7%; Score 28; DB 11; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCGA 50
|||||
```

```
Db 15 CTATACGACTCACTATAGGAGCTCGA 42

RESULT 45
A91914
LOCUS Sequence 1 from Patent WO9822599.
DEFINITION A91914
ACCESSION A91914
VERSION A91914.1 GI:6740781
KEYWORDS
    Arabidopsis thaliana (thale cress)
    Arabidopsis thaliana
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 3484)
AUTHORS OHL,S.A. and Klapp,J.
TITLE NEMATODE-INDUCIBLE REGULATORY DNA SEQUENCES
JOURNAL Patent: WO 9822599-A 1 28-MAY-1998;
LBB FREDERIQUE MARIANNE V D (NL); OHL STEPHAN ANDREAS (NL)
FEATURES
    source
        1..3484
            /organism="Arabidopsis thaliana"
            /mol_type="unassigned DNA"
            /db_xref="taxon:3702"
            /ecotype="C24"
            <3481..3484
                /note="unnamed protein product"
                /codon_start=2
                /protein_id="CAB69451.1"
                /db_xref="GI:6740782"
                /translation="M"
CDS
ORIGIN
Query Match 0.7%; Score 28; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCGA 50
|||||
```

```
Db 698 CTATACGACTCACTATAGGAGCTCGA 725

RESULT 46
AR309120
LOCUS AR309120
DEFINITION Sequence 1 from patent US 6555529.
ACCESSION AR309120
VERSION AR309120.1 GI:31700962
KEYWORDS
    Unknown.
    Unclassified.
REFERENCE 1 (bases 1 to 3484)
AUTHORS Funaba,Y., Koike,J., Tanahashi,M., Okazaki,S. and Ito,M.
TITLE Remedies for intermedullary diseases
JOURNAL Patent: US 6555529-A 1 29-APR-2003;
Toray Industries, Inc.; Tokyo;
JPK;
FEATURES
    source
        1..3484
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match 0.7%; Score 28; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCGA 50
|||||
```

[illegible]

Matches	28; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	------------------	----	------------	----	--------	----	------	----

OY 23 CTATACGACTCACTATAGGAGCTCGA 50
|||||
Db 698 CTAATACGACTCACTATAGGAGCTCGA 725

```

RESULT 49
LOCUS   ALJ355005
DEFINITION Mouse DNA sequence from clone RP21-429M4 on chromosome X, complete
sequence.
ACCESSION ALJ355005
VERSION   ALJ355005.3    GI:9797242
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Bukharov; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 140069)
REFERENCE
AUTHORS Mathewa, J.
TITLE   Direct Submission
JOURNAL Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humbug@wanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:7940000.
During sequence assembly date is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL, Sw:
SWISSPROT, Tr: TREMBL, Wp: WormPep; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP21-429M4 is
from the RPCI-21 Mouse PAC library
constructed by the group of Plier de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pPAC4

----- Genome Center
Center: UK Medical Research Council
Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk

----- Location/Qualifiers
     1..140069
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /db_xref="taxon:10090"
        /chromosome="X"
        /clone="RP21-429M4"
        /clone_1fb="RPCI-21"

```


OY 84 GTGGTGATGTGTTTAAGTCATA 111
|||||
Db 74821 GTGGTGATGTGTTTAAGTCATA 74848

```

FEATURES
     source
         location/qualifiers
             1..140069
                 /organism="Mus musculus"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:10090"
                 /chromosome="X"
                 /clone="RP21-429M4"
                 /clone_1fb="RPCI-21"

```


Query Match 0.7% ; Score 28; DB 9; Length 140069;
Best Local Similarity 100.0% ; Pied. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

COMMENT
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL, Sw:
SWISSPROT, Tr: TREMBL, Wp: WormPep; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP21-429M4 is
from the RPCI-21 Mouse PAC library
constructed by the group of Plier de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pPAC4

----- Genome Center
Center: UK Medical Research Council
Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk

----- Location/Qualifiers
     1..140069
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /db_xref="taxon:10090"
        /chromosome="X"
        /clone="RP21-429M4"
        /clone_1fb="RPCI-21"

```

```

RESULT 50
BX530096
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

BX530096 183958 bp DNA linear HTG_03-JUL-2003
Mus musculus chromosome X clone RP23-476H16, WORKING DRAFT
SEQUENCE.
BX530096.2 GI:32451242
HTG, HTGS PHASE2; HTGS ACTIVERPIN; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
Musaropota, Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 183958)
Chapman, J.
Direct Submision
Submitted (02-JUL-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk
On Jul 3, 2003 this sequence version replaced gi:31335658.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a paired quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: Bw476H16
----- Summary Statistics
Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 183848 bases at least Q40
Consensus quality: 183909 bases at least Q30
Consensus quality: 183938 bases at least Q20
Insert size: 183958; sum-of-contigs
Insert size: 185334; 2.3% error; agarose-fp
Quality coverage: 9.32x in Q20 bases; sum-of-contigs Quality
coverage: 9.48x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 183958: contig of 183958 bp in length.
Location/Qualifiers
1. 183958
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-476H16"
/clone_1fb="RPCI-23"
1. 183958
/notes="assembly_fragment:01273"

```

```

ORIGIN
Query Match 0.7%; Score 28; DB 14; Length 183958;
Best Local Similarity 100.0%; Pred. NO. 0.17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

84 GGTGTGTGTGTGTTTAAGTCAATTA 111
DB 80990 GGTGTGTGTGTGTTTAAGTCAATTA 81017

```

```

RESULT 51
AL732410/c 220894 bp DNA linear ROD 17-JAN-2003
LOCUS AL732410
DEFINITION Mouse DNA sequence from clone RP23-91L2 on chromosome X, complete
sequence.
ACCESSION AL732410
VERSION AL732410
KEYWORDS GI:27802745
SOURCE HTS.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 220894)
AUTHORS Kay, M.
TITLE Direct Submission
JOURNAL Submitted (17-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunger@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Jan 18, 2003 this sequence version replaced gi:21436719.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep -----
Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: hunger@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
RP23-91L2 is from the RPCI-23 Mouse BAC Library
constructed by the group of Plecter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
Location/Qualifiers
1..220894
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-91L2"
/clone_1lb="RPCI-23"

```

RESULT 52
CS088900/c
LOCUS CS088900 374 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 34 from Patent EP1449849.
ACCESSION CS088900
VERSION CS088900.1 GI:66714222
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Light,D.R., Andrews,W.H., Clarke,J.H., Wydro,R.M. and Young,P.A.
TITLE Protease-resistant thrombomodulin analog
JOURNAL Patent: EP 1449849-A 34 25-AUG-2004;
Paton GmbH (DE)
FEATURES
source
Location/Qualifiers
1..374
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="CLAI-SMAI fragment from pTHR515 containing the 3aa deletion of the Nterminus of DNFL into the CLAI-SMAI partial of pTHR512."

ORIGIN
Query Match 0.6%; Score 27; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAGCTCG 49
Db 147 CTAATACGACTCACTATAGGAGCTCG 121

RESULT 53
CS088904/c
LOCUS CS088904 374 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 38 from Patent EP1449849.
ACCESSION CS088904
VERSION CS088904.1 GI:66714226
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Light,D.R., Andrews,W.H., Clarke,J.H., Wydro,R.M. and Young,P.A.
TITLE Protease-resistant thrombomodulin analog
JOURNAL Patent: EP 1449849-A 38 25-AUG-2004;
Paton GmbH (DE)
FEATURES
source
Location/Qualifiers
1..374
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="NOT1-XBAI fragment from pTHR498 containing the DNFL gene into the NOT1-XBAI sites of pGEM9ZF-. This plasmid is designated 'A' in the strategy for construction of a Patent TM production plasmid."

ORIGIN
Query Match 0.6%; Score 27; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAGCTCG 49
Db 147 CTAATACGACTCACTATAGGAGCTCG 121

RESULT 54
CS088909/c
LOCUS CS088909 374 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 43 from Patent EP1449849.

ACCESSION CS088909
VERSION CS088909.1 GI:66714231
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Light,D.R., Andrews,W.H., Clarke,J.H., Wydro,R.M. and Young,P.A.
TITLE Protease-resistant thrombomodulin analog
JOURNAL Patent: EP 1449849-A 43 25-AUG-2004;
Paton GmbH (DE)
FEATURES
source
Location/Qualifiers
1..374
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="MUU-NOT1 fragment from pTHR514 containing a 7aa deletion at the end of the link region of DNFL, the S474A, the R456G and the H457Q mutations into the MUU-NOT1 sites of pTHR518."

ORIGIN
Query Match 0.6%; Score 27; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAGCTCG 49
Db 147 CTAATACGACTCACTATAGGAGCTCG 121

RESULT 55
CVGEM9ZFM/c
LOCUS CVGEM9ZFM 2912 bp DNA circular SYN 06-FEB-2001
DEFINITION Cloning vector pGEM-9ZF(-).
ACCESSION X65312
VERSION X65312.2 GI:12711304
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Technical Services.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1993) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, WI 53711-5399, USA
REMARK revised by [2]
2
AUTHORS Technical Services.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2001) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, WI 53711-5399, USA
REMARK revised by [3]
3 (bases 1 to 2912)
AUTHORS Technical Services.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2001) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, WI 53711-5399, USA
REMARK On Feb 7, 2001 this sequence version replaced gi:58182.
See X65300-X65335 for related vector sequences
This vector can be obtained from Promega Corporation, Madison, WI.
Call one of the following numbers for order or technical information:
Order or Technical 800-356-9526
In Wisconsin 800-356-9526
Outside U.S. 608-274-4330.
FEATURES
source
Location/Qualifiers
1..2912
/organism="Cloning vector pGEM-9ZF(-)"
/mol_type="other DNA"
/db_xref="taxon:90118"

	misc_feature	1	/note="SP6 transcription initiation site"
	promoter	53..72	/note="T7 promoter"
	misc_feature	55	
	misc_feature	93..321	/note="T7 transcription initiation site"
	misc_feature	102..118	/note="lac operon sequence"
	gene	/note="PUC/M13 reverse primer binding site"	
	misc_feature	complement(104..106)	
	misc_feature	/gene="lacZ"	
	misc_feature	complement(104..106)	
	misc_feature	/gene="lacZ"	
	misc_feature	126..142	/note="lacZ start codon"
	gene	/note="lac operator"	
	CDS	complement(1263..2123)	
		/gene="bla"	
		complement(1263..2123)	
		/gene="bla"	
		/codon_start=1	
		/transl_table=11	
		/product="beta-lactamase"	
		/protein_id="CA46404.1"	
		/db_xref="GI:58183"	
		/translation="MSIQHFRVALIPPEAFCLPVFAPETLVKVKDAEDQLGARVGY IELNDISKILDESFPVERPPMSTFKYLCSGLISRIDAOEOLGRIRIHYSQNDLVEY YSPVTEKHLLTDGMTPRELCSAIIIMSDNTANILLTTIGPKELTAFLAHMGDVTPL DRMPRELNAIAPPNDRDTPTVMATTRIKLLTSBLITLSRQDLIMDEADKTAGPL LRSLAPGWFIAIDRSAGERSRGITALLGPDKPSRIIVITTGSAITDERNRQTAL EIGASLIKHM"	
	misc_feature	2255..2710	/note="phase fl region"
	misc_feature	2712..2868	
	misc_feature	/note="lac operon sequence"	
	misc_feature	2831..2847	
	misc_feature	/note="PUC/M13 reverse primer binding site"	
	misc_feature	2876..2887	
	promoter	/note="multiple cloning sites"	
		2896..2912	
		/note="SP6 promoter"	
ORIGIN			
Query Match		0.6%; Score 27; DB 11; Length 2912;	
Best Local Similarity		100.0%; Pred. No. 1,7';	
Matches	27; Conservative	0; Mismatches	0; Indels
Gaps			0;
Dn	23 CTAAATACGACTCATTATAGGGAGCTCG 49		
	73 CTAATACGACTCATTATAGGGAGCTCG 47		
RESULT 56			
CVE311872			
LOCUS	CVE311872	5824 bp	DNA
DEFINITION	Cloning vector PHANNIBAL.		circular SYN 09-JUL-2002
ACCSSION	AJ311872		
VERSION	AJ311872.1 GI:15982214		
KEYWORDS	AMP gene; ampicillin resistance protein; pdk gene; promoter.		
SOURCE	Cloning vector PHANNIBAL		
ORGANISM	Cloning vector PHANNIBAL		
REFERENCE	Other sequences; artificial sequences; vectors.		
AUTHORS	1 Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q., Gooding,P., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P., Glave,A.P., Green,A.G. and Waterhouse,P.M. Construct design for efficient, effective and high-throughput gene silencing in plants Plant J. 27 (6), 581-590 (2001)		
JOURNAL	PUBMED	11576441	
REFERENCE	2 (bases 1 to 5824)		
AUTHORS	Waterhouse,P.M.		

TITLE	Direct Submission
JOURNAL	Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
FEATURES	Location/Qualifiers
source	1..5824
	/organism="Cloning vector PHANNIBAL"
	/mol_type="other DNA"
	/db_xref="taxon:167047"
	/lab_host="Escherichia coli"
	/focus
	/note="PHANNIBAL is a derivative of cloning vector PART7 which was a derivative of pGEM-9Zf(-)"
	1..2864
source	/organism="Escherichia coli K12"
	/mol_type="other DNA"
	/strain="K12"
	/db_xref="taxon:83333"
source	2865..4210
	/organism="Cauliflower mosaic virus"
	/mol_type="other DNA"
	/db_xref="taxon:10641"
source	4254..4995
	/organism="Flaveria trinervia"
	/mol_type="other DNA"
	/db_xref="taxon:4227"
source	5049..5814
	/organism="Agrobacterium tumefaciens"
	/mol_type="other DNA"
	/db_xref="taxon:358"
gene	775..1635
	/gene="amp"
CDS	775..1635
	/gene="amp"
	/codon_start=1
	/transl_table=11
	/product="ampicillin resistance protein"
	/protein_id="CAC86250.1"
	/db_xref="GI:15982215"
	/translation="MSIQHPRVALIPPEAFCLVPFAPPETLVKVDADPOLGARVGY IELDLSGKILSPREPERPPMWTSPVLICGAVLSRIDAGEOLGRIRHYSONDLVBE YSPTEKGLIDGMTRVRLCSAATMSNTKLANLLTTIGPKKETATLHMGDHYTAL DRWPELNEATPNDERDTPVAVATLTLLTELTILASROQLIDWEDADKVGEPD LRSLPAGWFIADKSGAGSGRSRGIIALPGDKPSRIIVITYTGSQATDERNRQIAL EIGASLIKHM"
promoter	2865..4210
	/function="35S promoter"
gene	4254..4995
	/gene="pdk"
intron	4254..4995
	/gene="pdk"
	/note="from pyruvate orthophosphate dikinase (pdk)"
	/number=2
terminator	5049..5814
	/note="octopine esynthase (ocs) terminator"
ORIGIN	
Query Match	0.64; Score 27; DB 11; Length 5824;
Best Local Similarity	100.04; Pred. No. 1.3;
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0y	23 CTAATACGACTCACTATAGGAGCTCG 49
Db	2826 CTAATACGACTCACTATAGGAGCTCG 2852
RESULT 57	
LOCUS	CVE311873 6063 bp DNA circular SYN 09-JUL-2002
DEFINITION	Cloning vector pKANIBAL.
ACCESSION	AJ311873
VERSION	AJ311873.1 GI:15982216
KEYWORDS	kan gene; kanamycin resistance protein; pdk gene; promoter.
SOURCE	Cloning vector pKANIBAL

ORGANISM Cloning vector pKANNIBAL.
other sequences; artificial sequences; vectors.

REFERENCE 1 Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene silencing in plants

JOURNAL Plant J. 27 (6), 581-590 (2001)

PUBMED 11576441

REFERENCE 2 (bases 1 to 6063)
Waterhouse, P.M.
Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

JOURNAL Location/Qualifiers

FEATURES 1. .6063
/organism="Cloning vector pKANNIBAL"
/mol_type="other DNA"
/db_xref="taxon:167048"
/lab_host="Escherichia coli"
/locus
/note="pKANNIBAL is a derivative of cloning vector pART7 which was a derivative of pGEM-9ZF(-)"
1. .3103
/organism="Escherichia coli K12"
/mol_type="other DNA"
/strain="K12"
/db_xref="taxon:83333"
3104. .4449
/organism="Cauliflower mosaic virus"
/mol_type="other DNA"
/db_xref="taxon:10641"
4493. .5234
/organism="Flaveria trinervia"
/mol_type="other DNA"
/db_xref="taxon:4227"
5288. .6053
/organism="Agrobacterium tumefaciens"
/mol_type="other DNA"
/db_xref="taxon:358"
1075. .1869
/gene="kan"
1075. .1869
/gene="kan"
/gene="kan"
/codon_start=1
/transl_table=11
/product="kanamycin resistance protein"
/protein_id="CAC86251.1"
/db_xref="GI:15982217"
/translation="MAKMRISPLKLIIEKRCVKDTGEGSPAKYVKLVGNNVYLKMTDSRKGITVDREKMMLEGLKVPKVLHFEHDSNMLNSEADGVLCSEBYEDQSPKRIELVAECTRLPHSIDSCPTNSLDSRLADYLLNNDLADVCEWNEEDPPDPRELVDPLKTEKPEBELVPSHGIDGDSNIFVKDGYSGPDLGRSGRADKMVDIAPCVRSIRREIGESQYVELFPDLGLIKPDWEKIKYVILDELFP"
3104. .4449
/function="35S promoter"
4493. .5234
/gene="pdk"
4493. .5234
/gene="pdk"
/note="from pyruvate orthophosphate dikinase (pdk)"
/number=2
5288. .6053
/note="octopine easythase (oce) terminator"

ORIGIN

Query Match 0.6%; Score 27; DB 11; Length 6063;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 CTATACGACTCACTATAGGAGCTCG 49
|||||

Db 3065 CTATACGACTCACTATAGGAGCTCG 3091

RESULT 58
BD263403/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 7038)
AUTHORS
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
TITLE
Compositions and methods for use in recombinational cloning of nucleic acids
JOURNAL Patent: JP 2002537790-A 181 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/181
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
CI 2N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/00, C12N5/00
CC pMAB85
FH Key
FT source

1. .7038 Location/Qualifiers
/organism="Artificial Sequence".
/mol_type="synthetic construct"
/db_xref="taxon:32630"

ORIGIN

Query Match 0.6%; Score 27; DB 6; Length 7038;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 TAATACGACTCACTATAGGAGCTCGA 50
|||||

Db 6005 TAATACGACTCACTATAGGAGCTCGA 5979

RESULT 59
BD263400/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 815)
AUTHORS
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
TITLE
Compositions and methods for use in recombinational cloning of nucleic acids
JOURNAL Patent: JP 2002537790-A 178 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/178
PD 12-NOV-2002 JP 2000602252
PF 02-MAR-2000 US 60/122389, 23-MAR-1999 US 60/126049 PR
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC

C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
00, C12N5/00
CC pDEST33
FH Key Location/Qualifiers
FT source 1. 8815
FT Location/Qualifiers
1. 8815
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 0.6%; Score 27; DB 6; Length 8815;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TAAATACGACTCCTATAGGAGCTCGA 50
|||||
Db 7782 TAAATACGACTCCTATAGGAGCTCGA 7756

RESULT 60
LOCUS AY189825 14271 bp DNA circular SYN 09-APR-2003
DEFINITION H18-3 Integration vector pKYM026, complete sequence.
ACCESSION AY189825
VERSION AY189825.1 GI:28435535
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1. h18-3 integration vector pKYM026
h18-3 integration vector pKYM026
other sequences; artificial sequences; vectors.
AUTHORS
1. Lee, D.W., Haag, J.R. and Aramayo, R.
TITLE
Construction of strains for rapid homokaryon purification after
integration of constructs at the h18-3 (h18-3) locus of
Neurospora crassa
Curt. Genet. 43 (1), 17-23 (2003)

JOURNAL
CURT. GENET. 43 (1), 17-23 (2003)
12684841
2 (bases 1 to 14271)
Lee, D.W., Haag, J.R. and Aramayo, R.
AUTHORS
Direct Submission
JOURNAL
Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
College Station, TX 77843-3258, USA
Location/Qualifiers
1. 14271
/organism="h18-3 integration vector pKYM026"
/mol_type="genomic DNA"
/db_xref="taxon:220723"
/focus
2584. 5465
/organism="Cloning vector pGEM-9ZE (-)"
/mol_type="genomic DNA"
/db_xref="taxon:90118"
complement(1..2583)
/note="benzomyl resistant marker"
5466. 14271
/note="h18-3 HindIII fragment"
10661. 10713
/note="multi-cloning sites"

ORIGIN
Query Match 0.6%; Score 27; DB 11; Length 14271;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATACGACTCCTATAGGAGCTCG 49
|||||
Db 2609 CTAATACGACTCCTATAGGAGCTCG 2583

RESULT 61
AC157620/c

LOCUS AC157620 155363 bp DNA linear HTG 15-MAR-2005
DEFINITION Papio anubis clone Rp41-436B14, WORKING DRAFT SEQUENCE, 9 ordered
pieces.
ACCESSION AC157620.2 GI:61179916
VERSION HTG: HTGS PHASE2; HTGS DRAFT.
KEYWORDS
SOURCE
ORGANISM
Papio anubis (olive baboon)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Papio.
1 (bases 1 to 155363)
REFERENCE
AUTHORS
Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Boake, A.,
Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, H.,
Engle, J., Geisiole, M., Guan, X., Gupta, J., Haghighi, P., Han, J.,
Hansen, N., Ho, S.-L., Hu, P., Hunter, G., Hurle, B., Idol, J.R.,
Kwong, P., Latic, P., Larson, S., Lee-John, S.-O., Legaspi, R.,
Madden, M., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Mastello, C.,
Merkert, B., McDowell, J., Mojidi, H.A., Mullikin, J.C.,
Oestreicher, J.S., Park, M., Portnoy, M.E., Prasad, A., Puri, O.,
Reddix-Dugue, N., Rosas, B., Schandler, K., Schuler, M.G., Sison, C.,
Stantropop, S., Stephen, E., Teye, A., Thomas, J.W., Thomas, P.J.,
Tsipouri, V., Ung, L., Vogt, J.L., Wetherby, K.D., Young, A. and
Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 155363)
REFERENCE
AUTHORS
Green, E.D.
TITLE
Direct Submission
JOURNAL
Submitted (24-FEB-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
3 (bases 1 to 155363)
REFERENCE
AUTHORS
Green, E.D.
TITLE
Direct Submission
JOURNAL
Submitted (15-MAR-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Mar 15, 2005 this sequence version replaced gi:60223183.
COMMENT
Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@bgrl.nih.gov
Project Information
Center project name: Kic
Center clone name: 436B14

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 153372 bases at least Q40
Consensus quality: 154068 bases at least Q30
Consensus quality: 154387 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 154563; sum-of-contigs
Quality coverage: 7.59x in Q20 bases; agarose-fp
Quality coverage: 8.00x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces

```

* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 33922: contig of 33922 bp in length
33923 34022: contig of 8701 bp in length
34023 42723: gap of unknown length
42724 42823: gap of unknown length
42824 67972: contig of 25149 bp in length
67973 68072: gap of unknown length
68073 115800: contig of 47728 bp in length
115801 115900: gap of unknown length
115901 121755: contig of 5855 bp in length
121756 121855: gap of unknown length
121856 123794: contig of 1939 bp in length
123795 123894: gap of unknown length
123895 143354: contig of 19460 bp in length
143355 143454: gap of unknown length
143455 152511: contig of 9057 bp in length
152512 152611: gap of unknown length
152612 155363: contig of 2752 bp in length.
Location/Qualifiers
1. .155363
/organism="Papio anubie"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
/clone_id="RP41-436B14"
/clone_1b="RP41"
/note="BAC resource: http://bacpac.chori.org/"
1. .48923
/note="clone overlaps with GenBank Accession Number
AC150628 clone RP41-38K18 (center project name hbu)"
1. .33922
/note="assembly_fragment
clone_end:77
vector_side:left"
33923. .34022
/estimated_length=unknown
34023. .42723
/note="assembly_fragment"
42724. .42823
/estimated_length=unknown
42824. .67972
/note="assembly_fragment"
67973. .68072
/estimated_length=unknown
68073. .115800
/note="assembly_fragment"
103272. .155363
/note="clone overlaps with GenBank Accession Number
AC149446 clone RP41-168H19 (center project name hbc)"
115801. .115900
/estimated_length=unknown
115901. .121755
/note="assembly_fragment"
121756. .121855
/estimated_length=unknown
121856. .123794
/note="assembly_fragment"
123795. .123894
/estimated_length=unknown
123895. .143354
/note="assembly_fragment"
143355. .143454
/estimated_length=unknown
143455. .152511
/note="assembly_fragment"
152512. .152611
/estimated_length=unknown
152612. .155363
/note="assembly_fragment

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ORIGIN
Query Match 0.6%; Score 27; DB 14; Length 155363;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3910 AAAATTTAAATTTAAATTTAAAGTAAAG 3936
Db 74820 AAAATTTAAATTTAAATTTAAAGTAAAG 74794

RESULT 62
LOCUS AC139294 183363 bp DNA linear ROD 28-JAN-2005
DEFINITION Mus musculus BAC clone RP24-239E14 from 14, complete sequence.
AC139294
VERSION AC139294.4 GI:55058677
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 183363)
Krnchowski,S., Haglund,K., Meyer,R. and Haakenson,W.
The sequence of Mus musculus BAC clone RP24-239E14
Unpublished (2001)
2 (bases 1 to 183363)
McPherson,J.D. and Waterston,R.H.
Direct Submision
Submitted (29-JAN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 183363)
Wilson,R.K.
Direct Submision
Submitted (25-MAY-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 183363)
Wilson,R.K.
Direct Submision
Submitted (01-NOV-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 183363)
Wilson,R.K.
Direct Submision
Submitted (28-JAN-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Nov 1, 2004 this sequence version replaced gi:47605114.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Summary Statistics
Center project name: W_BB0239E14
-----
NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For

```

additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:
The RPCI-24 BAC library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.

FEATURES

source

1. 183363

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="14"

/map="14"

/clone="RP24-239E14"

/clone_lib="RPCI-24"

90991..91258

/note="Sequence derived from one plasmid subclone."

96920..96921

/transposon="Bacterial transposon insertion in clone

excised here."

ORIGIN

Query Match 0.6%; Score 27; DB 9; Length 183363;

Best Local Similarity 100.0%; Pred. No. 0.46;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3913 AATTAATAATTAATAATTAAGTAAAGAAA 3939

Db 53286 AATTAATAATTAATAATTAAGTAAAGAAA 53312

RESULT 63

AC151836

LOCUS

DEFINITION

Mus musculus BAC clone RP23-359F5 from chromosome 14, complete

sequence.

AC151836

VERSION

KEYWORDS

SOURCE

ORGANISM

HTG.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 230502)

Valzer, J., Lewis, S., Kozlowski, A., Bielicki, L. and Haglund, K.

The sequence of Mus musculus BAC clone RP23-359F5

Unpublished (2001)

2 (bases 1 to 230502)

Wilson, R.K.

Direct Submission

Submitted (06-OCT-2004) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 230502)

Wilson, R.K.

Direct Submission

Submitted (13-MAR-2005) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

4 (bases 1 to 230502)

Wilson, R.K.

Direct Submission

Submitted (30-JUL-2005) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

COMMENT

On Jul 20, 2005 this sequence version replaced gi:61098484.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC

Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Summary Statistics
Center Project name: M_BA0359F05

NOTICE:

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e. phred quality
>30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone, fosmid clone or direct clone walk sequence.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to obtain the consensus sequence. The
assembly was confirmed by restriction digest.
This finishing standard has slightly changed from the previous
human standard. Specifically, standards for regions of low sequence
complexity (such as dinucleotide repeats and small unit tandem
repeats) have been relaxed. These regions are very prevalent in the
mouse genome, and the return on extended finishing efforts is
minimal.

If a sequence meets the criteria of the above statement, it needs
no comments or tags. If the criteria are not met, such as ambiguous
bases, then the region is duly annotated.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:

The BAC library has been constructed by Kazutoyo Oeegawa and
Minako Tatenio in the laboratory of Pieter de Jong
(http://www.chori.org) from female C57BL/6J mouse kidney and/or
brain genomic DNA. The clone and detailed information can be
obtained from Research Genetics, Inc. (http://www.resgen.com) or
Pieter de Jong and coworkers at http://www.chori.org

This sequence is the entire insert of the clone.

FEATURES

source

1. 230502

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="14"

/clone="RP23-359F5"

/clone_lib="RPCI-23"

48876..49550

/note="Unresolved tandem repeat."

102204..102242

/note="Sequence derived from PCR product of project DNA"

102747..102809

/note="Unresolved tandem repeat."

ORIGIN

Query Match 0.6%; Score 27; DB 9; Length 230502;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3913 AATTAATAATTAATAATTAAGTAAAGAAA 3939

Db 170689 AATTAATAATTAATAATTAAGTAAAGAAA 170715

RESULT 64

BD272600

LOCUS

DEFINITION

ACCESSION

VERSION

BD272600 38 bp DNA linear PAT 17-JUL-2003

Amplification of CYP24 and uses thereof.

BD272600

BD272600.1 GI:33082368

```
KEYWORDS      JP 2002540798-A/6.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 38)
AUTHORS        Albertson,D.G., Pinkel,D., Collins,C., Gray,J.W. and Yestra,B.
TITLE          Amplification of CYP24 and uses thereof
JOURNAL        Patent: JP 2002540798-A 6 03-DEC-2002;
               THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT        OS Artificial Sequence
               PN JP 2002540798-A/6
               PD 03-DEC-2002
               PR 06-MAR-2000 JP 200609598
               PR 02-APR-1999 US 09/285292
               PI DONNA G ALBERTSON,DANIEL PINKEL, COLIN COLLINS,JOE W GRAY,BAUKE

FEATURES
  source       Location/Qualifiers
               1..38
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

ORIGIN
Query Match   0.6%; Score 26; DB 6; Length 38;
Best Local Similarity 100.0%; Pred.No.18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY            24 TAATACGACTCACTATAGGAGCTCG 49
Db            1 TAATACGACTCACTATAGGAGCTCG 26

RESULT 65
LOCUS         AX020362             40 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION    Sequence 2 from Patent WO9936517.
ACCESSION     AX020362
VERSION       AX020362.1 GI:10044095
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS        Jemne,A.
TITLE          Method for selecting ribozymes which are capable of covalently
               modifying the ribonucleic acids on 2'-oh-groups in trans
JOURNAL        Patent: WO 9936517-A 2 22-JUL-1999;
               JENNE ANDREAS (DE)
FEATURES
  source       Location/Qualifiers
               1..40
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonucleotide"

ORIGIN
Query Match   0.6%; Score 26; DB 6; Length 40;
Best Local Similarity 100.0%; Pred.No.17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY            23 CTAATACGACTCACTATAGGAGCTC 48
Db            1 CTAATACGACTCACTATAGGAGCTC 48

KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS        Glover,D.
TITLE          Materials and methods relating to cell cycle control
JOURNAL        Patent: WO 2005056802-A 216 23-JUN-2005;
               Cancer Research Technology Limited (GB)
FEATURES
  source       Location/Qualifiers
               1..43
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Primer"

ORIGIN
Query Match   0.6%; Score 26; DB 6; Length 43;
Best Local Similarity 100.0%; Pred.No.17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY            23 CTAATACGACTCACTATAGGAGCTC 48
Db            5 CTAATACGACTCACTATAGGAGCTC 30

RESULT 67
LOCUS         AY720436             4151 bp     DNA      circular SYN 18-SEP-2004
DEFINITION    AY720436 Plant expression vector pPESiTa, complete sequence.
ACCESSION     AY720436
VERSION       AY720436.1 GI:51989440
KEYWORDS      .
SOURCE        Plant expression vector pPESiTa
ORGANISM      Plant expression vector pPESiTa
REFERENCE      1 (bases 1 to 4151)
AUTHORS        Berendzen,K.W., Breuer,F., Oberschall,A., Schell,J. and Koncz,C.
TITLE          Direct Submision
JOURNAL        Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
               Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
FEATURES
  source       Location/Qualifiers
               1..4151
               /organism="Plant expression vector pPESiTa"
               /mol_type="Other DNA"
               /db_xref="taxon:292601"
               1..18
               /note="Tchlll1, NcoI, XhoI, KpnI, MCS promoter"
               19..758
               /note="duplicated 35S CaMV (cabb B-VI isolate) ; 35S5;
               overexpression in plants"
               759..793
               /note="HindIII, NcoI, SmaI, XbaI, BglII, MCS upstream"
               794..805
               /note="N-term strep-tag II"
               806..994
               /note="PIV2 optimized; prevents detection of epitope tag
               in bacteria"
               995..1009
               /note="C-term strep-tag II"
               1010..1035
               /note="SalI, BamHI, PstI, EcoRI; MCS downstream"
               1036..1288
               /note="polyadenylation signal from nopaline synthase gene
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of the Agrobacterium Ti plasmid; NOS terminator"
1289. .1358
/note="KpnI, SacI, NotI, SacI, T7, SfiI; MCS terminator"
misc_feature
complement(1359. .1587)
/note="LacI"
gene
complement(12529. .3389)
/gene="bla"
CDS
complement(12529. .3389)
/gene="bla"
/note="resistance to ampicillin"
/codon_start=1
/product="beta-lactamase"
/protein_id="AAU21235.1"
/db_xref="GI:51969441"
/translation="MSIQHFRVALIPFFAAECLEVPFAPETLVVKQAEQDQARVGY
IEIDNSGKILSFRRPFRPMSTFVILCGAVLSRIDGQEQDQGRIRIHSQNDLVE
YSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGPKELTAFLHNGDVTPL
DRWPELNEAI PNDERDTPVAVATTLRLKLTLSRQQLIDMWEADKVAQPL
LRSA L P G W F I A D S G A G E R S R G I I A A L G P D G K P R I V I Y T T G S Q A T M D E R R R Q I A
EIGASLTIKHW"

Query Match 0.6%; Score 26; DB 11; Length 4151;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTAGGAGCTCG 49
Db 1338 TAATACGACTCATTAGGAGCTCG 1313

RESULT 68
LOCUS AY720435 4152 bp DNA circular SYN 18-SEP-2004
DEFINITION Plant expression vector pPES1tb, complete sequence.
ACCESSION AY720435
VERSION AY720435.1 GI:51969438
KEYWORDS
SOURCE Plant expression vector pPES1tb
ORGANISM Plant expression vector pPES1tb
REFERENCE
AUTHORS other sequences; artificial sequences; vectors.
TITL 1 (bases 1 to 4152)
JOURNAL Berendzen, K.W., Breuer, F., Obereschall, A., Schell, J. and Koncz, C.
Direct Submission
Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
FEATURES
source
1. .4152
/organism="Plant expression vector pPES1tb"
/mol_type="other DNA"
/db_xref="taxon:292600"
1. .18
/note="Tth111I, NotI, XhoI, KpnI; MCS promoter"
misc_feature
19. .758
/note="duplicated 35S CamV (Cabb B-J1 isolate); 35S;
overexpression in plants"
promoter
759. .793
/note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
misc_feature
794. .805
/note="N-term strep-tag II"
806. .994
/note="PIV2 optimized; prevents detection of epitope tag
in bacteria"
misc_feature
995. .1009
/note="C-term strep-tag II"
1011. .1036
/note="Sall, BamHI, PstI, EcoRI; MCS downstream"
1037. .1289
/note="polyadenylation signal from nopaline synthase gene
of the Agrobacterium Ti plasmid; NOS terminator"
terminator
1290. .1359
/note="KpnI, SacI, NotI, SacI, T7, SfiI; MCS terminator"
misc_feature
complement(1360. .1588)

/note="LacI"
gene
complement(12530. .3390)
/gene="bla"
CDS
complement(12530. .3390)
/note="bla"
/note="resistance to ampicillin"
/codon_start=1
/product="beta-lactamase"
/protein_id="AAU21234.1"
/db_xref="GI:51969439"
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IEIDNSGKILSFRRPFRPMSTFVILCGAVLSRIDGQEQDQGRIRIHSQNDLVE
YSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGPKELTAFLHNGDVTPL
DRWPELNEAI PNDERDTPVAVATTLRLKLTLSRQQLIDMWEADKVAQPL
LRSA L P G W F I A D S G A G E R S R G I I A A L G P D G K P R I V I Y T T G S Q A T M D E R R R Q I A
EIGASLTIKHW"

Query Match 0.6%; Score 26; DB 11; Length 4152;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTAGGAGCTCG 49
Db 1339 TAATACGACTCATTAGGAGCTCG 1314

RESULT 69
LOCUS AY720438 4152 bp DNA circular SYN 18-SEP-2004
DEFINITION Plant expression vector pMENCHU, complete sequence.
ACCESSION AY720438
VERSION AY720438.1 GI:51969444
KEYWORDS
SOURCE Plant expression vector pMENCHU
ORGANISM Plant expression vector pMENCHU
REFERENCE
AUTHORS other sequences; artificial sequences; vectors.
TITL 1 (bases 1 to 4152)
JOURNALS Ferrando, A., Farrae, R., Jasik, J., Schell, J. and Koncz, C.
Intron-tagged epitope: a tool for facile detection and purification
of proteins expressed in Agrobacterium-transformed plant cells
Plant J. 22 (6), 553-560 (2000)
10886775
2 (bases 1 to 4152)
JOURNALS Berendzen, K.W. and Koncz, C.
Direct Submission
Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
FEATURES
source
1. .4152
/organism="Plant expression vector pMENCHU"
/mol_type="other DNA"
/db_xref="taxon:292603"
1. .18
/note="Tth111I, NotI, XhoI, KpnI; MCS promoter"
misc_feature
19. .758
/note="duplicated 35S CamV (Cabb B-J1 isolate); 35S;
overexpression in plants"
promoter
759. .793
/note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
misc_feature
794. .805
/note="N-term HA epitope"
806. .994
/note="PIV2 optimized; prevents detection of epitope tag
in bacteria"
misc_feature
995. .1009
/note="C-term HA epitope"
1010. .1036
/note="Sall, BamHI, PstI, EcoRI; MCS downstream"
1037. .1289
/note="polyadenylation signal from nopaline synthase gene
of the Agrobacterium Ti plasmid; NOS terminator"
terminator
1290. .1359


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gene      /note="lact"
           complement (2531. .3391)
CDS       /gene="bla"
           complement (2531. .3391)
           /gene="bla"
           /note="resistance to ampicillin"
           /codon_start=1
           /product="beta-lactamase"
           /protein_id="AAU21233.1"
           /db_xref="GI:51989437"
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           YSPVTEKHLLTDGMTVRELCSAATMSDNTANLLITIGPKELTAPLHNGDVATRL
           DRWPELNEAIPInderDTMPVMAATLRKLTLGELLTLASRQQLIDMWEADKVGPL
           LRSLAPGWEIFADKSGAGERSGRTIAALGPDGKPRIVIVITGSOATMDERRRQIA
           EIGASLIKHM"

ORIGIN
Query Match      0.6%; Score 26; DB 11; Length 4153;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      24  TAATACGACTCATTAGGAGCTCG 49
Db      1340 TAATACGACTCATTAGGAGCTCG 1315

RESULT 72
AY720437 4154 bp DNA circular SYN 18-SEP-2004
LOCUS     Plant expression vector pMESH1, complete sequence.
DEFINITION
AY720437
VERSION   AY720437.1 GI:51989442
KEYWORDS
SOURCE    Plant expression vector pMESH1
ORGANISM  Plant expression vector pMESH1
REFERENCE 1 (bases 1 to 4154)
AUTHORS   Ferrando,A., Koncz-Kalman,Z., Farrae,R., Tiburcio,A., Scheil,J. and
           Koncz,C.
TITLE     Detection of in vivo protein interactions between Snf1-related
           kinase subunits with intron-tagged epitope-labelling in plants
           cells
JOURNAL   Nucleic Acids Res. 29 (17), 3685-3693 (2001)
PUBMED    11522840
REFERENCE 2 (bases 1 to 4154)
AUTHORS   Berendzen,K.W. and Koncz,C.
TITLE     Direct Submision
JOURNAL   Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
           Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
           Location/Qualifiers
FEATURES
source
1. .4154
   /organism="Plant expression vector pMESH1"
   /mol_type="other DNA"
   /db_xref="taxon:292602"
misc_feature
1. .18
   /note="Tth1111, NotI, XhoI, KpnI; MCS promoter"
19. .758
   /note="duplicated 35S CaMV (Cabb B-J1 isolate); 35S;
   overexpression in plants"
misc_feature
759. .793
   /note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
794. .808
   /note="N-term c-myc epitope"
809. .997
   /note="PIV2 optimized; prevents detection of epitope tag
   in bacteria"
misc_feature
998. .1012
   /note="C-term c-myc epitope"
1013. .1038
   /note="Sall, BamHI, PstI, EcoRI; MCS downstream"
1039. .1291
   /note="polyadenylation signal from nopaline synthase gene

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misc_feature
1292. .1361
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complement (11362. .1590)
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   complement (2532. .3392)
   /gene="ampR"
   complement (2532. .3392)
   /gene="ampR"
   /note="resistance to ampicillin"
   /codon_start=1
   /product="beta-lactamase"
   /protein_id="AAU21236.1"
   /db_xref="GI:51989443"
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   YSPVTEKHLLTDGMTVRELCSAATMSDNTANLLITIGPKELTAPLHNGDVATRL
   DRWPELNEAIPInderDTMPVMAATLRKLTLGELLTLASRQQLIDMWEADKVGPL
   LRSLAPGWEIFADKSGAGERSGRTIAALGPDGKPRIVIVITGSOATMDERRRQIA
   EIGASLIKHM"

ORIGIN
Query Match      0.6%; Score 26; DB 11; Length 4154;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      24  TAATACGACTCATTAGGAGCTCG 49
Db      1341 TAATACGACTCATTAGGAGCTCG 1316

RESULT 73
AY720439 4156 bp DNA circular SYN 18-SEP-2004
LOCUS     Plant expression vector pLOLA, complete sequence.
DEFINITION
AY720439
VERSION   AY720439.1 GI:51989446
KEYWORDS
SOURCE    Plant expression vector pLOLA
ORGANISM  Plant expression vector pLOLA
REFERENCE 1 (bases 1 to 4156)
AUTHORS   Ferrando,A., Koncz-Kalman,Z., Farrae,R., Tiburcio,A., Scheil,J. and
           Koncz,C.
TITLE     Detection of in vivo protein interactions between Snf1-related
           kinase subunits with intron-tagged epitope-labelling in plants
           cells
JOURNAL   Nucleic Acids Res. 29 (17), 3685-3693 (2001)
PUBMED    11522840
REFERENCE 2 (bases 1 to 4156)
AUTHORS   Berendzen,K.W. and Koncz,C.
TITLE     Direct Submision
JOURNAL   Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
           Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
           Location/Qualifiers
FEATURES
source
1. .4156
   /organism="Plant expression vector pLOLA"
   /mol_type="other DNA"
   /db_xref="taxon:292604"
misc_feature
1. .18
   /note="Tth1111, NotI, XhoI, KpnI; MCS promoter"
19. .758
   /note="duplicated 35S CaMV (Cabb B-J1 isolate); 35S;
   overexpression in plants"
misc_feature
759. .793
   /note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
794. .808
   /note="N-term c-myc epitope"
809. .997
   /note="PIV2 optimized; prevents detection of epitope tag
   in bacteria"
998. .1012
   /note="C-term c-myc epitope"

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misc_feature 1013..1040
/note="SalI, BamHI, PstI, EcoRI; MCS downstream"
terminator 1011..1293
/note="polyadenylation signal from nopaline synthase gene of the Agrobacterium Ti plasmid; NOS terminator"
misc_feature 1294..1363
/note="KpnI, SacI, NotI, SacI, T7, SfiI; MCS terminator"
misc_feature complement(1364..1592)
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/gene="ampR"
CDS complement(2534..3394)
/gene="ampR"
/note="resistance to ampicillin"
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/product="beta-lactamase"
/protein_id="AA021238.1"
/db_xref="GI:51989447"
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IEDLNSGKILDSFRPEERPMWSTFKVLGAVLSRIDGQOLGRIRIHVSQNDLVE
YSPVTEKHLLDGMVRELCSAAITWSDNTANILITIGPKELTAFLHMGDVAIRL
DRWEPELNEAIPNDERDTTPVMAATTLRLTGLLTSLRSQQLIDMMEDAVAGPL
LRSALPAGWPIADKSGAGRGSRGIIAALGPDKPSRIIVITYTTSQATMDENRRQIA
EIGASLIKHW"

ORIGIN

Query Match 0.6%; Score 26; DB 11; Length 4156;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCAGTATAGGAGCTCG 49
Db 1343 TAATACGACTCAGTATAGGAGCTCG 1318

RESULT 74
AY720440 4157 bp DNA circular SYN 18-SEP-2004
LOCUS AY720440
DEFINITION Plant expression vector pGIG1, complete sequence.
ACCESSION AY720440
VERSION AY720440.1 GI:51989448
KEYWORDS
SOURCE .
ORGANISM Plant expression vector pGIG1
REFERENCE
1 (bases 1 to 4157)
other sequences; artificial sequences; vectors.
Ferrando,A., Koncz-Kalman,Z., Farkas,R., Tiburcio,A., Scheil,J. and
Koncz,C.
TITLE Detection of in vivo protein interactions between Snf1-related
kinase subunits with intron-tagged epitope-labelling in plants
cellls
Nucleic Acids Res. 29 (17), 3685-3693 (2001)
JOURNAL
PUBMED 11522840
AUTHORS 2 (bases 1 to 4157)
Berendzen,K.W. and Koncz,C.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
FEATURES
source
1..4157
/organism="Plant expression vector pGIG1"
/mol_type="other DNA"
/db_xref="taxon:292605"
1..18
/note="Tth1111, NotI, XhoI, KpnI; MCS promoter"
19..758
/note="duplicated 35S CaMV (Cabb B-J1 isolate); 35S;
overexpression in plants"
759..793
/note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
794..808
/note="N-term c-myc epitope"
809..997
intron

misc_feature 998..1012
/note="C-term c-myc epitope"
misc_feature 1022..1041
/note="SalI, BamHI, PstI, EcoRI; MCS downstream"
terminator 1042..1294
/note="polyadenylation signal from nopaline synthase gene of the Agrobacterium Ti plasmid; NOS terminator"
misc_feature 1295..1364
/note="KpnI, SacI, NotI, SacI, T7, SfiI; MCS terminator"
misc_feature complement(1365..1593)
/note="LacI"
gene complement(2535..3395)
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LOCUS BD235520
DEFINITION Desaturase gene for modifying lipid profile in corn.
ACCESSION BD235520
VERSION BD235520.1 GI:33045290
KEYWORDS
SOURCE JP 2002517984-A/55.
ORGANISM Zea mays
Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 6337)
Shen,J.B.J.
TITLE Desaturase gene for modifying lipid profile in corn
JOURNAL Patent: JP 2002517984-A 55 25-JUN-2002;
ET DU PONT DE MEMOURS AND CO
COMMENT
OS Zea mays (maize)
PN JP 2002517984-A/55
PD 25-JUN-2002
PR 09-JUN-1999 JP 2000553569
PR 11-JUN-1998 US 60/088987
PI JENNIE BIH JIEN SHEN
PC C12N15/09,A01H5/00,A23D7/00,A23D9/00,C12N5/10,C12N15/00,C12N5/00
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Search completed: February 28, 2006, 00:39:40
 Job time : 13896 secs

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; Sequence 3, Application US/09227421

; Patent No. 6559357

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; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.

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APPLICANT: Mizukami, Yukiko

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling and Enhancing Asexual Reproduction in Plants

FILE REFERENCE: 023070-090700PC

CURRENT APPLICATION NUMBER: US/09/227,421

; CURRENT FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: US 09/227,421

PRIOR FILING DATE: 1999-01-

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; NUMBER OF SEQ ID NOS: 8
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SOFTWABE: PatentIn Ver 3.1

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DOJ FILED:
SEO ID NO. 3

LENGTH: 4228

TYPE: DNA

ORGANISM: *Arabidopsis thaliana* ;

FEATURE:

; NAME/KEY: promoter
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 Db 2461 TCTTCAGCAAAAGCGCCGAGAGGTGTCTTATCTTCAATTAAGCTGGGTGTGGCAG 2520
 Qy 2521 ACATCATAGGGCCCTAAGTATATTTAGCTTTACTGTAGCTTAAGCTTTAACAATCTAGT 2580
 Db 2521 ACATCATAGGGCCCTAAGTATATTTAGCTTTACTGTAGCTTAAGCTTTAACAATCTAGT 2580
 Qy 2581 TAGTCTCACTGTACAAACAAACAAATCCAAATTCGTAACATATATACAAATCTACTA 2640
 Db 2581 TAGTCTCACTGTACAAACAAACAAATCCAAATTCGTAACATATATACAAATCTACTA 2640
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 Db 2701 CAAACTGAAGTGTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCAATTGGG 2760
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 Qy 3181 CGATTAAGAAAGACTCTTTTATTTAATTTGAATTAACCTTTTGTGTAATGACT 3240
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Qy 3541 GAAAGTTATGATGATTGCAAGTTTGCACAGAAATGTCGATGATAGATATCAAAA 3600
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 Db 3721 TATCATATCTTACAAACAAAAAATCTGATGATTAATTAATGTTGCCAATGTTTACA 3780
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 Db 3961 AGATCCCAAGGATTCAAACAGCAAAATTTGTGCTTCTCTCTCTTATATATATC 4020
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 Db 4021 CTCTCAAAACCTCTCTCTATATCTCTTAAAGCCCTCTCTCTCTCTTACCGCAA 4080
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 Db 4141 TTTAGCTTACTCTGAGAGATTATAGAAAGAAAGAGATCATTTATGAAGA 4200
 Qy 4201 AGAAGACAGAAACCAAAAAAGAAACC 4228
 Db 4201 AGAAGACAGAAACCAAAAAAGAAACC 4228

RESULT 2
 US-09-479-855-3
 : Sequence 3, Application US/09479855
 : Patent No. 6639128
 : GENERAL INFORMATION:
 : APPLICANT: Fischer, Robert L.
 : APPLICANT: Mizukami, Yukiko
 : TITLE OF INVENTION: Methods for the University of California
 : TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
 : TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
 : FILE REFERENCE: 023070-090720US
 : CURRENT APPLICATION NUMBER: US/09/479,855
 : NUMBER OF SEQ ID NOS: 8
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 3
 : LENGTH: 4228
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 : FEATURE:
 : OTHER INFORMATION: ANT gene 5' promoter
 US-09-479-855-3

Query Match	100.0%;	Score 4228;	DB 3;	Length 4228;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4228;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GTGACGCTAAGGCTCACTGGCCCTAATTAAGACTCACTAATAGGAGCTGAGAGATCCCTTA	60	
Db	1	GTGACGCTAAGGCTCACTGGCCCTAATTAAGACTCACTAATAGGAGCTGAGAGATCCCTTA	60	
Qy	61	GTTAGAAAAAACTTTCTTTGTACGTCGTGTGTGTGTAAAGTCAATTAATTAAGTCTC	120	
Db	61	GTTAGAAAAAACTTTCTTTGTACGTCGTGTGTGTGTAAAGTCAATTAATTAAGTCTC	120	
Qy	121	ACATGTGATATCAATATATATATATTAATGAATTGGAATTATTCATATTAATGAATTAGAT	180	
Db	121	ACATGTGATATCAATATATATATATTAATGAATTGGAATTATTCATATTAATGAATTAGAT	180	
Qy	181	TAAATATATATAGCTGACATTAACCAACCAAAAGCTTTCGCTTTATGATAGTTCTATAT	240	
Db	181	TAAATATATATAGCTGACATTAACCAACCAAAAGCTTTCGCTTTATGATAGTTCTATAT	240	
Qy	241	GTTCGACCTGATATATAGATATATATATAAACTGGGTTATTTAAATCCGTACCACTAAC	300	
Db	241	GTTCGACCTGATATATAGATATATATATAAACTGGGTTATTTAAATCCGTACCACTAAC	300	
Qy	301	AAAAAGTGACCAAAACGAGATCCAGTGTGTGTGTACTTGTGTGTAAACAGATAT	360	
Db	301	AAAAAGTGACCAAAACGAGATCCAGTGTGTGTGTACTTGTGTGTAAACAGATAT	360	
Qy	361	ATGATATATGGAAGATTAATCTTTACTAATATATAAATTTGGAAGAAAACTTAA	420	
Db	361	ATGATATATGGAAGATTAATCTTTACTAATATATAAATTTGGAAGAAAACTTAA	420	
Qy	421	ATATGTTGAGTGCTTCAGTGTCTCACTGTTCAAGAAATATCTCGTGTATCCTACTTGAA	480	
Db	421	ATATGTTGAGTGCTTCAGTGTCTCACTGTTCAAGAAATATCTCGTGTATCCTACTTGAA	480	
Qy	481	CTAGAAAGTGATATACATATAACGCGTAATTTTAAACGACCGTACATTAACACATGTAT	540	
Db	481	CTAGAAAGTGATATACATATAACGCGTAATTTTAAACGACCGTACATTAACACATGTAT	540	
Qy	541	CGATCAAAATCAAAATTAATATGAGACTAATATCCAAAGATGAGAGATCTTAGCAGATA	600	
Db	541	CGATCAAAATCAAAATTAATATGAGACTAATATCCAAAGATGAGAGATCTTAGCAGATA	600	
Qy	601	TACACAGCTAAGAAATTTGTACAAGAGAGTCGAAAAATAGATTCTATCATTTAAAAAGA	660	
Db	601	TACACAGCTAAGAAATTTGTACAAGAGAGTCGAAAAATAGATTCTATCATTTAAAAAGA	660	
Qy	661	TATGATTTCACTTACGATCGATGATATTTACCATTAACGACAGTAGATACATATATTTT	720	
Db	661	TATGATTTCACTTACGATCGATGATATTTACCATTAACGACAGTAGATACATATATTTT	720	
Qy	721	TGTTTTTGTTTTACCGATATATAGAAATGTTGTGTTAAAAATATTTGTTTACTATA	780	
Db	721	TGTTTTTGTTTTACCGATATATAGAAATGTTGTGTTAAAAATATTTGTTTACTATA	780	
Qy	781	AATCGTTTTATGTTAACTATATATATATATGCTTTCGAGATTAATTAAGAAACAAACTGTAA	840	
Db	781	AATCGTTTTATGTTAACTATATATATATATGCTTTCGAGATTAATTAAGAAACAAACTGTAA	840	
Qy	841	TACAAATTAATGTTAAACCATTCGCAATTAATAAAATCCACGGTAGTAAATCCTCAGAAAT	900	
Db	841	TACAAATTAATGTTAAACCATTCGCAATTAATAAAATCCACGGTAGTAAATCCTCAGAAAT	900	
Qy	901	TATGTTAAGTCAACAAATTTTCTCTTTAGATTATAGATTGAGACAAATTAATATATATA	960	
Db	901	TATGTTAAGTCAACAAATTTTCTCTTTAGATTATAGATTGAGACAAATTAATATATATA	960	
Qy	961	CCTTGACGGGGTATTAAGGTCACTGATATGTGACGCTACGATGAAAGCCAAAGAGTGGTTC	1020	
Db	961	CCTTGACGGGGTATTAAGGTCACTGATATGTGACGCTACGATGAAAGCCAAAGAGTGGTTC	1020	
Qy	1021	TCGTGCTTAAGATATCTACAGCTGGCTTCGCTGTGAATATAGAAATTAATGAATATGATAGA	1080	

Dp	1021	TTGTGCTTAAAGAAATATCTACAGCTGCTTGGCTGTGTAATAGAGAAATTAATGAAATGGA	1080
Qy	1081	GAGATCCCATCTAGCGTTTCACGTTTGCCTGCTCCGTCGCAACTTGGCGGTGTGACT	1140
Dp	1081	GAGATCCCATCTAGCGTTTCACGTTTGCCTGCTCCGTCGCAACTTGGCGGTGTGACT	1140
Qy	1141	TTTTTCTTATGTCGTGTGTGACTTAATTTTCTCAGAGTGGAGTGTATATCAGAAAACT	1200
Dp	1141	TTTTTCTTATGTCGTGTGTGACTTAATTTTCTCAGAGTGGAGTGTATATCAGAAAACT	1200
Qy	1201	AATATTCGAAAAAGAAAAAAGGCAAGAAAACTATTGTCCGAAAAAGCATTAATGAC	1260
Dp	1201	AATATTCGAAAAAGAAAAAAGGCAAGAAAACTATTGTCCGAAAAAGCATTAATGAC	1260
Qy	1261	ACTAAAAATGGATTATTAAAAATGGTATATATGTTTGGTGGATTTTAAATCATTAACCA	1320
Dp	1261	ACTAAAAATGGATTATTAAAAATGGTATATATGTTTGGTGGATTTTAAATCATTAACCA	1320
Qy	1321	AATCAAGAGAGAGAGAGGAGCCTCTTCGTCTTATGATTTTCCCTCTAAACAATGCT	1380
Dp	1321	AATCAAGAGAGAGAGAGGAGCCTCTTCGTCTTATGATTTTCCCTCTAAACAATGCT	1380
Qy	1381	CCCACATCTCTTTTCTTACTTCCAAACAATCATTCACAAGAAAAATCTGTCTCTGTATC	1440
Dp	1381	CCCACATCTCTTTTCTTACTTCCAAACAATCATTCACAAGAAAAATCTGTCTGTATC	1440
Qy	1441	ACTTTCATGCAAAATTTAACTTAATTTTGGATTTTGGATTTTGTCAAGTCTGCTGTTTAA	1500
Dp	1441	ACTTTCATGCAAAATTTAACTTAATTTTGGATTTTGTCAAGTCTGCTGTTTAA	1500
Qy	1501	TCGATTAATTTGGTATATCTATATGTGTGATATACATCCAGCTAATCATTAATGAT	1560
Dp	1501	TCGATTAATTTGGTATATCTATATGTGTGATATACATCCAGCTAATCATTAATGAT	1560
Qy	1561	CTCCTCTGCTTATCATTAATTAACCACTTAAGCTAATCAAGCTAATTAATTAACCA	1620
Dp	1561	CTCCTCTGCTTATCATTAATTAACCACTTAAGCTAATCAAGCTAATTAATTAACCA	1620
Qy	1621	CATTCTCTATCATTTTTTAAATGGTATTAATTAACCAAGCATTAAGGCTACAGATT	1680
Dp	1621	CATTCTCTATCATTTTTTAAATGGTATTAATTAACCAAGCATTAAGGCTACAGATT	1680
Qy	1681	GGTATTAAGGATTAATGCTTCTAGTCGAGAAATTTTGTATGATTAACACTGCTGT	1740
Dp	1681	GGTATTAAGGATTAATGCTTCTAGTCGAGAAATTTTGTATGATTAACACTGCTGT	1740
Qy	1741	GAAAAAAAATCAGCTTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTTAAATCA	1800
Dp	1741	GAAAAAAAATCAGCTTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTTAAATCA	1800
Qy	1801	TTAAAAATTAAGGTTTTTGTCTTTAAAGGTTACCAAGCTTAATTCATTAAGAGAT	1860
Dp	1801	TTAAAAATTAAGGTTTTTGTCTTTAAAGGTTACCAAGCTTAATTCATTAAGAGAT	1860
Qy	1861	ATTAACTTGAATCGAAATTCGAAATTCCTTTTAAACAATAAGAAAAATTTTCAGACTT	1920
Dp	1861	ATTAACTTGAATCGAAATTCGAAATTCCTTTTAAACAATAAGAAAAATTTTCAGACTT	1920
Qy	1921	TTAAATTAAGGGTACATTTATTTGGGTTCAATTAATATGTTTCCAGTAAAGTTTGGAGT	1980
Dp	1921	TTAAATTAAGGGTACATTTATTTGGGTTCAATTAATATGTTTCCAGTAAAGTTTGGAGT	1980
Qy	1981	TTAAACCATGAATATGTTTTTGAATTTAAAAAACAATTAATTTTCTATGATTAACACTT	2040
Dp	1981	TTAAACCATGAATATGTTTTTGAATTTAAAAAACAATTAATTTTCTATGATTAACACTT	2040
Qy	2041	TTTAAACGTCATCGAATGTATTAATGAAGCAATCTGAAAAACATTTTTTTTTTTCTGTG	2100
Dp	2041	TTTAAACGTCATCGAATGTATTAATGAAGCAATCTGAAAAACATTTTTTTTTTTCTGTG	2100
Qy	2101	AATCTGTGTTAAATCTCTCTGCTGCAATCTTGCAAGGCATTTGACCAAGCATTAACATA	2160

Db 2101 AATCTGTTAAATCTCTGCTGATACATTGACGACATTGACCAACGACTATACATA 2160
Qy 2161 TTGAAAGCAAAATATCCACGCGATGATAGGGTTAGATCCCACTTCATATCTTTGT 2220
Db 2161 TTGAAAGCAAAATATCCACGCGATGATAGGGTTAGATCCCACTTCATATCTTTGT 2220
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Db 2221 CTTGTTATTTATGAAAAACAATATTTATGAGGAAAAAAGTTCTCTCTAGTGGTA 2280
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Db 2401 AAAAAATGCAAAAAGAGATATATTTAAGTCAAAATTAATAAGATGATGGTGAT 2460
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Db 4201 AGAGAGCAAGAACCAAAAAAGAAC 4228

RESULT 3
US-09-227-421-1
; Sequence 1, Application US/09227421

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/ Patent No. 6559357
/ GENERAL INFORMATION:
/ APPLICANT: Fischer, Robert L.
/ APPLICANT: Mizukami, Yukiko
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Method for Altering Organ Mass, Controlling Fertility
/ TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
/ FILE REFERENCE: 023070-090700PC
/ CURRENT APPLICATION NUMBER: US/09/227,421
/ PRIOR FILING DATE: 1999-01-08
/ PRIOR APPLICATION NUMBER: US 09/227,421
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 2148
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (269)..(1936)
/ OTHER INFORMATION: AINTEGUMENTA (ANT)
/ NAME/KEY: misc feature
/ LOCATION: (1109)..(1339)
/ OTHER INFORMATION: encodes first AP2 domain
/ NAME/KEY: misc feature
/ LOCATION: (1340)..(1414)
/ OTHER INFORMATION: encodes linker region
/ NAME/KEY: misc feature
/ LOCATION: (1415)..(1621)
/ OTHER INFORMATION: encodes second AP2 domain
/ US-09-227-421-1
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Query Match 6.3%; Score 268; DB 3; Length 2148;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AGATCCCAAGGATTCACAGCAAAATTTGTGCTTCTCTCTTATTAATATC 60
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DB 61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTCTCTTCTTCTACCGCA 120
QY 4081 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTCTCTGTGTAACCAATGATGGGT 4140
DB 121 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTCTGTGTAACCAATGATGGGT 180
QY 4141 TTAGCTTACTCTCGAGAGATTATTAAGAAAGAGGAAATACATTATGAAGA 4200
DB 181 TTAGCTTACTCTCGAGAGATTATTAAGAAAGAGGAAATACATTATGAAGA 240
QY 4201 AGAAGACAGAAACCAAAAAAGAAACC 4228
DB 241 AGAAGACAGAAACCAAAAAAGAAACC 268

RESULT 4
US-09-479-855-1
/ Sequence 1, Application US/09479855
/ Patent No. 6639128
/ GENERAL INFORMATION:
/ APPLICANT: Fischer, Robert L.
/ APPLICANT: Mizukami, Yukiko
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
/ TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
/ FILE REFERENCE: 023070-090720US
/ CURRENT APPLICATION NUMBER: US/09/479,855
/ CURRENT FILING DATE: 2000-01-07
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
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/ SEQ ID NO 1
/ LENGTH: 2148
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ OTHER INFORMATION: AINTEGUMENTA (ANT) cDNA
/ NAME/KEY: CDS
/ LOCATION: (269)..(1936)
/ OTHER INFORMATION: AINTEGUMENTA (ANT)
/ US-09-479-855-1
```

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Query Match 6.3%; Score 268; DB 3; Length 2148;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3961 AGATCCCAAGGATTCACAGCAAAATTTGTGCTTCTCTCTTATTAATATC 4020
DB 1 AGATCCCAAGGATTCACAGCAAAATTTGTGCTTCTCTCTTATTAATATC 60
QY 4021 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTCTCTTCTTCTACCGCA 4080
DB 61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTCTCTTCTTCTACCGCA 120
QY 4081 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTCTCTGTGTAACCAATGATGGGT 4140
DB 121 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTCTGTGTAACCAATGATGGGT 180
QY 4141 TTAGCTTACTCTCGAGAGATTATTAAGAAAGAGGAAATACATTATGAAGA 4200
DB 181 TTAGCTTACTCTCGAGAGATTATTAAGAAAGAGGAAATACATTATGAAGA 240
QY 4201 AGAAGACAGAAACCAAAAAAGAAACC 4228
DB 241 AGAAGACAGAAACCAAAAAAGAAACC 268
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RESULT 5
US-09-806-708B-22
/ Sequence 22, Application US/09806708B
/ Patent No. 6784342
/ GENERAL INFORMATION:
/ APPLICANT: The University of British Columbia
/ TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
/ FILE REFERENCE: 4810-58741
/ CURRENT APPLICATION NUMBER: US-09/806,708B
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: US 60/147,133
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 22
/ LENGTH: 1141
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (1)..(1141)
/ OTHER INFORMATION: consensus sequence of A.c., L.a., and B.n. PAI1 promoters
/ US-09-806-708B-22
```

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Query Match 1.7%; Score 72.4; DB 3; Length 1141;
Best Local Similarity 10.7%; Pred. No. 0.00011;
Matches 107; Conservative 373; Mismatches 511; Indels 6; Gaps 1;
```

```
QY 1459 ACTAATTTTGGATTTTGTCAAGTTGCTGCTTTAAGTGAATTTGGTAATAC 1518
DB 53 MSKSRKWTWARYCKRYRYNNKSRWKMVKYKWBKANNBSBYHABRWKMTAYBM 112
QY 1519 TATATGTGATATACATCAAGCTAATCAATATGATCTCTTCTGCTAATCAAT 1578
DB 113 TWTNKWKGKGMHRVWRMBDVTVDHVTAMNNAMTTMCMWDKDKTRWMMKNNNA 172
QY 1579 AATTAACACCATTAAGCTAATCAAGCTAATTAATTAACACCATCTCTTATCAATTTT 1638
```


Db 173 TCGDDDDTKHMMNNNGBYTMMVRYKTDKDDMSKRNAYGMBWKKMSYDVTYTWWD 232
Qy 1639 TATATGGTATAAATAAACAACCGATAAGCTACAGAGTGGTATTAAGCATTAATG 1698
Db 233 MCRKRVAVRTGRRMRYVAVMBTAHRRYNNQMTBAMA YRATYNNNNNNNAKAMCKRA 292
Qy 1699 CCTTCTAGTGAAGAAATTTTGTATGATACTCGGGGAAAAAATCCAGCTTA 1758
Db 293 KYGMMNABVNSTCTTKSKTKYRTSCWANNCAAGANDHKWKKMSAAGVYNNNNN 352
Qy 1759 ATATGCTATTAAAGATAATGATTAAATGCTTAATCACTAAATAAAGATTTT 1818
Db 353 NMNTYKARBARBDWVHSAKMHAAAYSHKMTBYRKKTVMNNNGTTMKKMA 412
Qy 1819 GCTTTTAAAGGTTACCAACGCTTAATTCATCATAGAGAATAATACTTGAATGAAT 1878
Db 413 WYWMQMDMBGTYNNNNGRTYGYMTKMKMMTYKMKANNCKRAMDHKTCTHNTTW 472
Qy 1879 TCCAAATATCTTTTAAACATTAAGAAATTTTCAGATTTTAAATAAGGTTACAT 1938
Db 473 WKXKTYNNCYKSMITGKSHRBAAYTYWMMWRBYAHANNNDY-----WYRAC 526
Qy 1939 TATGGGTCAATATATATATGTTCCAGTAAGTTGAGGTTTACCAACATGAATGTT 1998
Db 527 WYTKBVCSKMMNYAAYTYSWNTSRYRKMTNNSWRMRSDRSGRANTYABAHYG 586
Qy 1999 TTGATTTAAAAACACATAATTTTCTAGTAATTAACATTTTAAACGTCATCCAGA 2058
Db 587 YKNNTRMBWSHTHBRBAGAAHYMBMWTYBAKCHCKAMWKAKGVAGAGSNNNNNN 646
Qy 2059 TTGTATTAAGTACAATCTGAATAATTTTCTTGAATCTTGTGTTAAATCTC 2118
Db 647 NNNNNNNATCADDYAAASRWYMANAKYUYGBAANNA YTTANNMWGCNNATDTR 706
Qy 2119 TCTGCTGATCTGACGAGCTTGCACACGATTCATATATGAAAGAAAATATCCA 2178
Db 707 TMMKNNNNNAGTKKNNNNNAKASAAKYAAVAAPAKKMMWAKMARGHADA 766
Qy 2179 CCAAGGATGATAGGTTAGATCCACATTCATATCTTTGTCTTGTATTAATGAAA 2238
Db 767 BTDDKRNAGAYTKTTNNNNNTYRGVLTAAABGMMNNNNNNNNNNNGMSDMVTV 826
Qy 2239 ACAATATTTATCAGAAAAACGTTCTCTAGTGTATAGTATAATGATTAAC 2298
Db 827 WAAVANGTNNNNNNNNNAAYAMTNNKYTTDDMRBA YTNNNNNMAYGAYADYAY 886
Qy 2299 AAAATTTAATAGTATGTTATGTTATCTTCAACTTACATCCTTCAACATTA 2358
Db 887 YMSDTCDAMMKWDATKNNNAATTYRGTA MRTNNNNNTMTKTYBHAAMNNNNNGKMC 946
Qy 2359 TATGATCAATTTTATTTTATTTTACTTAACACTTCCATAAATAAGCAAGAGA 2418
Db 947 TATHTWCAKATKTKGCMNCTTTCRKYKNNCTYTTMTTTRITRYAATRKNNATGSM 1006
Qy 2419 GATATATATTTAACTCAAGTAAATTAAGATGATG 2455
Db 1007 TRCNATGKNNNNYTGKTRWTA YRAMTRMKAMWKV 1043

RESULT 6
US-09-806-708B-22/c
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OR INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806, 708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAEI promoters
US-09-806-708B-22

Query Match 1.7%; Score 71.4; DB 3; Length 1141;
Best Local Similarity 12.8%; Pred. No. 0.00016;
Matches 127; Conservative 359; Mismatches 497; Indels 12; Gaps 3;

Qy 1463 AATTGGTATTTTGTGCAAGTCTTGCTGTTAAGCATTAATTTGTAATACATA 1522
Db 1138 WRYTCHGNTTTTKTYKANNNNNNNNNGMGKDMRMDATKMSATGTAMTTHAARGATMC 1079
Qy 1523 TGTGTGATATTAACATCCAGCTAATCAATTAATGATCTCTGCTGCTATCAATAAT 1582
Db 1078 WYWTGTGNRWCRTYAMRTWYRSNANWSCATKBMWMTMKYATYRTAAMWMCAMR 1019
Qy 1583 TACACGATTAAGCTAATCAAGCTAATTAATTAACACAGATTCCTATCAATTTTATA 1642
Db 1018 NNNMWCATNGYASCATNNNAWYATTAAYAAKARMAAGNNRMTGAAAGKMGCMMA 959
Qy 1643 TGTATTAATAAACAACCGATAAGCTACAGAGTGTGTAATTAAGCATTAATGCTT 1702
Db 958 MATTGBMWADTAGMCKNNNNNNNTTVDYRMAAKKNNNNNAWYTA CYNBAATNNKQATH 899
Qy 1703 CTAGTCAGAAATTTTCTT--GTATGATTAACCTGTGGGAAAAAATCCAGCTAAT 1760
Db 898 WMKYTHGASHKRPRHRTCTCRKYNNNNNNAATVYWHAAARMWNAWTRNNNNNN 839
Qy 1761 ATGCTATTAAGGATAATGATTAATGCTTAATCAATTAATAAATAAGTTTTTGC 1820
Db 838 NNNNACATNTTWAABWMSHCNNNNNNNNNNNNNTYCHTTANABECYRANNNNAARM 779
Qy 1821 TTT--TAAAGTTACACCGCTTAATTCATCATTAAGAGAATAATTAATGATGAAA 1877
Db 778 ARCTNNMHAAYTTTHDWCYKTMWNTWYMDWTTTBTNTTNNNNNNNNMWA 719
Qy 1878 TTCAAAATATCTTTTAAACATAGAAAATTTTCAGCATTTTAAATAAAGGTACAT 1937
Db 718 CTNNNNNNMKAAYAHAATNNWGCMMNTDARRTNNITVMMRRWNTNKTMYSTRHHY 659
Qy 1938 TTAATGGGTTCAATTAATATGTTTCCAGTAAAGTTGAGGTTAACACATGATGTT 1997
Db 658 TGAATNNNNNNNNNNNNNNNSCCTTRMTTRMTKGDGNTVRKV-----KRDITC 606
Qy 1998 TTTTGATTTAAAAACAACATAATTTCTAGTATTAACATTTTAAACGTCATCCAG 2057
Db 605 TYVDVWADSVWYANMRCBDYTRNNNTYCKSYAISYVWSNNAWRYRSABNSSM 546
Qy 2058 ATTGTAATAAGTGAACAATCTGAACAATTTTCTTCTGATCTTGTGTTAAATCT 2117
Db 545 ARWTRNNMMWSGBVRWAGTMMWRHMNNNNNTDTRYWMMKRAABITTYVDSMCVAKS 486
Qy 2118 CTCGCTGCAATCTTGACGAGCATTTGACCAACGATTCATCATGTAAGAAAATATCC 2177
Db 485 MMRGNNNRMAKMMWAAANDAGADHTWYMGNTMRRMAKMMWMCRAAYCANNNN 426
Qy 2178 ACCAGGATGATAGGTTAGATCCACATTCATTAATCTTGTGTTATTAATGAAA 2237
Db 425 RACVHHGKMMRWTKWKKMKAACNNNNBKAMYRVAAWNTSRDPTNTDMMWNTDWBH 366
Qy 2238 AACAAATATTTTACAGAAAAACGTTCTCTAGTGTATAGTATAATTAATA 2297
Db 365 YTVDTYMMRAMNNNNNNNNWCKTYSWMMWMDHNTHCTYGNNTWGSAYEMAAISMWAG 306
Qy 2298 CAAATTTAATCTAGTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 2357

Db 305 ASNBVYNNMCBMYNGKMTNNNNNNKAYRTKTVACNNRYYDDTAVTEBKNYKC 246
QY 2358 ATATGATGCAATTTTATTTTCTTAACTACTCCACTAAAATGCAAAAGAG 2417
Db 245 YAYBMYBYBMYGCHHMBRABHRSNNMMVKCRNRYWVSMHYHARBYKMAVGCNN 186
QY 2418 AGATATATATTTTAACTCAAGTAATTAAGATGGA 2452
Db 185 NMDRMAHHHMCATNNNNMMWYAYVMMHMKKGA 151

RESULT 7
US-09-949-016-14164/c
; Sequence 14164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14164
; LENGTH: 18773
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14164

Query Match 1.6%; Score 68.6; DB 3; Length 18773;
Best Local Similarity 43.6%; Pred. No. 0.00088;
Matches 554; Conservative 0; Mismatches 704; Indels 13; Gaps 5;

QY 2628 ACAATPACTAGTACTAGTACGCTACGCTATACATCGCTTTTCGCAATTTCTAAA 2687
Db 18351 AATATTTCTAT 18292
QY 2688 CTAATCATACACAATCTGAATGTTTGTGTAATTAATCTTAAACCAAGTTTGA 2747
Db 18291 AAT 18232
QY 2748 ATTGTCATTTGGAGCTACACTAGTCCCTTTTCCCAAAATATCTCCTTACATC 2807
Db 18231 AAT 18172
QY 2808 GACCGGTTAAAGTAATTAACCAAAATTTAATTTGTTGCTGAAGGTAACAACATGC 2867
Db 18171 TA-----TAT 18117
QY 2868 ACATATATAGAGACAGATGTTTATACAAATAATGTCATGTAATGGAATCAATA 2927
Db 18116 AAT 18057
QY 2928 TAAATACGAATTCGCACTCTGTTTAAATGTTTGAAGATTAATGAATATATAATG 2987
Db 18056 AAT 17997
QY 2988 AATTCAAAGATACAGACTATATATGTCGGGTCAATTAGACCGTGACCAAAAGTTTCG 3047
Db 17996 TAT 17942
QY 3048 TCGTAAATTTCTACGTCGCTCAAGAAATTTTGACTTTTCTCACCCCTTTATGACT 3107
Db 17941 AAT 17882
QY 3108 TCTGTATAGTTTTCGCAATTAATTTGTAATGCTATATATTTTGTTCATATATG 3167

Db 17881 AT 17822
QY 3168 ATACGTAATTCACGTAAGAAAGACTCTTTTATTTATTTGATTTAAACCTTTTGT 3227
Db 17821 TAT 17762
QY 3228 TTTGAAATGACCTACACCAAGTTAAAGTTTATGATGATCCAAATTTTCAAAAATGTTT 3287
Db 17761 TAT-AT 17703
QY 3288 CGAGATGCGTTCGAGTGTCTACACCATCGTACCACTCGTAGGGTTTATATATAGG 3347
Db 17702 AT 17644
QY 3348 TTTTTCCTCTTTTCCAAATGCTTTTAAATTTGAACCACTCTAAATTTCTTTTAAA 3407
Db 17643 TATTTTAAATTAAT 17584
QY 3408 TTAGTTAAGAAATCTGAATTTTCTGTGATTTTAAACCAAGTTTCAATCTCTTAG 3467
Db 17583 TTTAT 17524
QY 3468 CACAAAAAAGGTTTCAATTTTAAAGATCTAAATTTTGTGAGTTCAAGAG 3527
Db 17523 AT 17464
QY 3528 TTTAATGATAGCTGAAAGATTTGAATGATGCAATTTTGAACAGAAAGTGTGATG 3587
Db 17463 ATTGATTAATTAATGATTAAGATATATATATATATATATATATATATATATATAT 17404
QY 3588 TACATATCAAAAAATCATGATCAAAATTAATATATATATATATATATATATATATAT 3647
Db 17403 AAT 17344
QY 3648 TAAACGAACAAATCGTTAAACACTTAAAAATCTTGAATTAATTTTGTAGTAAATTTTC 3707
Db 17343 TAT 17284
QY 3708 TGTAAAGAGAGATCATATCTTACAAAAAATCTCAATTTGAGATTAATATGTTGT 3767
Db 17283 TAT 17225
QY 3768 CCAATGTTACCAAGATGTTTGTGCTCATGATGATGTAATGTAATGCTGCTTACGCC 3827
Db 17224 ACATTTTATATAGAAAT 17165
QY 3828 ATATAGTTCTAAATTTTAAATGTTTCAAGACTTTTACAAAAATTAATATATATAGT 3887
Db 17164 TAT 17105
QY 3888 GGAATTTGAG 3898
Db 17104 AGAAATCTGG 17094

RESULT 8
US-09-806-708B-23
; Sequence 23, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-56741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 23
; LENGTH: 1055
; TYPE: DNA

LENGTH: 32392
TYPE: DNA
ORGANISM: Ambacia moorei entomopoxvirus
US-09-662-254B-27

Query Match 1.6%; Score 66.2; DB 3; Length 32392;
Best Local Similarity 45.3%; Pred. No. 0.0028;
Matches 447; Conservative 0; Mismatches 523; Indels 17; Gaps 5;

Qy 1465 TTTTGTATTTTGTGCAAGTCTGCTGTTTAAAGTCATTAATTTGGTAATACATATATG 1524
Db 8551 TTTCGAATATTTTATCCAAATTTATTTTATTTTAAATTAATTAATTCATTAA 8492
Qy 1525 TGTGATATATACATCCAGATTAATCAATATGATCTCTGCTTATCAATTAATTA 1584
Db 8491 TGTAGAAATATATGATTAATCAACCAATCTATATTAATGTTATTCATATTAATTTT 8432
Qy 1585 CACCAATTAAGCTAATCAAGTAATTAATTAACCAATCTCTATCAATTTTATATG 1644
Db 8431 ATCTGTAGATATATTTTGTATTAATTTTTCATTCATTTTATTTTATATAT 8372
Qy 1645 GTATTAATTAACCAACGACTATAGCTACAGATGCTATTAAGCATTAATTCCTCT 1704
Db 8371 TATTTATATATATACATCTGTATTAATTAATCAATATTAACAAATTAATCAATAT 8312
Qy 1705 AGTCGAAGAATTTTGTATGATTAACCTCTGTGGAATAAATCCAGCTTAATGC 1764
Db 8311 ATCTAAATTTATTAATTTTAAATTAATTAATTCGATGTAAT-----GATTCAT 8260
Qy 1765 TCATTTAAGATTAATGATTAATGCTTAATCATTAATAAATTAAGTTTGTCTTT 1824
Db 8259 TTATATATTTATATTAATTAATTAATTAATTAATTTTCAAAATTAATTAATTA 8200
Qy 1825 AAAGGTACCAACGCTTAATTCATCATTAAGAGATTAATTAATTCGAAATTCGAA 1884
Db 8199 AATTTTATTTTGAATTAATTAATCAATTAATTAATATCATCTATATTAATTAATC---AA 8143
Qy 1885 ATACTTTTATTAACATTAAGAAATTTTCAGCATTTTAAATTAAGGTACATTTATGG 1944
Db 8142 TATTTATTTTAAATTAATCTTAAATTAATTAATCTTTTATATTTATTAATTTAA 8083
Qy 1945 GTTCAATTAATTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTA 2004
Db 8082 TATTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8027
Qy 2005 TTAATAAACAACATTAATTTCTAGTAATTAATTAATTTTAAACGTCATCAGATTTGTA 2064
Db 8026 TTTTATATATATTTTATTTTATTTTAAACATTTTAAAGATTTATATTTATTAATTA 7967
Qy 2065 TTAAGTCAAAATCTGAATAATTTTCTGTAATCTGTTAAATCTCTGCT 2124
Db 7966 TTATTTATCTAAATTAATTCATTAATTTTAAATTTATTTCTATTAATTAATTAATTA 7907
Qy 2125 GCAT-ACCTGAGGATTTGACCAACGATTAATTAATTAAGCAAAATTCACACGAG 2183
Db 7906 ATATCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7847
Qy 2184 GATGATAGGTTAGATCCCAATTCATTAATTTGCTGCTTATTTAATTAAGAAACAA 2243
Db 7846 TTATCTATATGCAATTTTCAATTTTATTAATTAATTAATTAATTTAACTTTAATTAATTA 7787
Qy 2244 TATTTATCAGAAAAAAG-TTTCTCTCTAGTGTATTAAGTATTAAGATTAATTAACAAA 2302
Db 7786 TTTCATCAAAAACGATTTTATTTTATTTATTTATTTATTAATTTCAATTAATTTATA 7727
Qy 2303 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2362
Db 7726 TTTAACAAGTTTAAATTAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7667
Qy 2363 GATCAATTTTATTTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 2422
Db 7666 TGTAAATTCGATGAATTTAATTAATTAATTAATTAATTAATTTATTTATTTAATTAATTA 7607

Qy 2423 TATATTTAGCAAGTATTAATTAAGAT 2449
Db 7606 GATATATTTTATTAATTAATTAATTAAT 7580

RESULT 12

US-09-949-016-13703/C
Sequence 13703, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13703
LENGTH: 67755
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1) -- (67755)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13703

Query Match 1.5%; Score 64; DB 3; Length 67755;
Best Local Similarity 45.1%; Pred. No. 0.0082;
Matches 321; Conservative 0; Mismatches 385; Indels 6; Gaps 2;

Qy 1749 ATCCAGCTATATATGCTCATTTAAAGATTAATGATTTAAATGCTTAATCATTAATA 1808
Db 41201 ATCTAAATAAATAAACAACATCAATTAATTAATTAATTAATTAATTAATTAATTT 41142
Qy 1809 AAAGTTTGTCTTTAAAGTTTACCGCTTAATTAATTAATTAATTAATTAATTAATTA 1868
Db 41141 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 41082
Qy 1869 TGATGAATTTCCAAATTAATTTTAAACATTAAGAAATTTTCAGATTTTAAATTA 1928
Db 41081 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 41022
Qy 1929 AGGTACATTAATTTGGTCAATTAATTAATTTCCAGTAAGTTTGAGGTTTAACAC 1988
Db 41021 ATATATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 40962
Qy 1989 ATGAATGTTTTCATTTAAATAAACAATTAATTTCTAGTAATTAACATTTTAAACG 2048
Db 40961 TATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 40902
Qy 2049 TCATCCAGATTTGTAATTAAGTGAACAAATCGAAACATTTTCTGTAATCTTGT 2108
Db 40901 TATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 40844
Qy 2109 TTAATTTCTCTGCTGATTAATTTGACGAGTTTGACCAACGATTAATTAATTAATTA 2168
Db 40843 ATTAATTAATTTTAAATTAATTAATTAATTTTATTAATTAATTTATTAATTAATTAAT 40784
Qy 2169 AAAATATCCACGAGATTAATTAATTTGATCCCAATTAATTTCTGTTGTTA 2228
Db 40783 ATATATTAATTAATTAATTAATTTAGCTAATTAATTAATTAATTAATTAATTAATTA 40724
Qy 2229 TTAATGAATAAACAATTAATTTATCAGAAAAAAGTTTCTCTGTAATTAATTAATTA 2288
Db 40723 TTAATTAATTAATTAATTAATTTATTAATTAATTTGTTATTAATTAATTAATTAATTA 40664


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QY 3223 TGTGTTTGGAAATGACGTCATACAGAGTTAAAGTTGATGCCAATTACAAA 3282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 403 TTTTATATATTTATATATTTATTTTATTTTATTTTATTTTATTTTATTTT 344
QY 3283 TGTTCAGAGTGGCTCGAGTGTCTACACACATCGACCACTCGAATGGTTATTA 3342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 343 TTTTATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 284
QY 3343 TTAGGTTTTTCTCTTTTCCAAATGCTTTATTAATGAACACCTGAAATTTCTTTT 3402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 TTTATTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 224
QY 3403 TTAATAGGTTAAGAACTTGAATTTCTGTTGATTTTAAACAAGTTTCAATCTT 3462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 TTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 164
QY 3463 CTT 3465
    |||
Db 163 TTT 161

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RESULT 15
US-09-949-016-12378/c
; Sequence 12378, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12378
; LENGTH: 119153
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(119153)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12378

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Query Match 1.5%, Score 61.8; DB 3; Length 119153;
Best Local Similarity 44.4%; Pred. No. 0.023;
Matches 381; Conservative 0; Mismatches 472; Indels 6; Gaps 3;

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QY 3052 AATTTACGCGTCGATAGAAATTTTGACCTTTCTCACCCCTTTATGAATCTTG 3111
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QY 3112 TATAGTTTTGTGCGATTATATATTTTGATTCGATATTTTGTCTATATATGATAC 3171
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Db 86981 TAAATATATATTTAATATATTTTATATATTAATTAATTAATTAATTAAT 86922
QY 3172 GTAAATTCACGATAGAAAGCTTTTATTTTA-ATTGATTTAAACCTTTGTTTT 3230
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Db 86921 TAAATATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 86862
QY 3231 GGAATGACCTATACAGAGTTAAAGTTGATGCTATCCAATTTACAAAATGTTTGA 3290
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Db 86861 ATATATATATATATATATTAATTAATTAATTAATTAATTAATTAATTAAT 86802
QY 3291 GAGTGCCTGAGAGTCTTACACCATGTAACCAACTGTATGGGTTTATATTAAGTTT 3350
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Db 86801 TATCTTATATATATATATATATTAATTAATTAATTAATTAATTAATTAAT 86742

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QY 3351 TTTTCTTTTTCGAATGCTTTATATTTGAACCACTTAATTTCT----TTTTTAA 3406
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QY 3407 ATTAGTTAAGAAATCTGAATTTTCTGTGATTTTAAACAAGTTTCAATCTTCTTA 3466
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QY 3467 GCACAAAAAAGTTTTCATTTTAAAGATCTAAATTTTGTGAGTTCAAGA 3526
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QY 3527 GTTTATGATAGCTGAAAAGTTATGAATGTGCAAGTTTGA-ACGAATGCTGATGT 3585
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Db 86501 GATATATATATATATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 86442
QY 3646 AATTAACGAACATCGTTAACCACTTAAATCTTGAATTTTGTAGTAAATTT 3705
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QY 3886 GTGGAATTTGTAGGCTTA 3904
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 Job time : 504 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 16:39:56 ; Search time 2103 Seconds
(without alignments)
16625.264 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtgcagctctgagcctcactg.....agaacccaagaagaacc 4228

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residue

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4228	100.0	4228	9	US-10-623-477-3
2	4203.4	99.4	4228	6	US-10-059-911-3
3	268	6.3	2148	9	US-10-059-911-1
4	268	6.3	2148	6	US-10-623-477-1
5	147	3.5	8056	8	US-10-473-126-386
6	107.8	2.5	8056	8	US-10-473-126-386
7	106.8	2.5	8056	8	US-10-473-126-240
8	99.4	2.4	8056	8	US-10-473-126-240
9	80.2	1.9	3673778	6	US-10-312-841-2
10	79.4	1.9	3673778	6	US-10-312-841-1
11	77.2	1.8	3673778	6	US-10-312-841-1
12	74.2	1.8	960	5	US-10-198-846-6381
13	73.2	1.7	13573	6	US-10-311-455-1842
14	71.6	1.7	17421	5	US-10-239-676-54
15	71.6	1.7	17421	6	US-10-240-453-56
16	71.4	1.7	115218	8	US-10-278-698-255
17	71.4	1.7	115218	8	US-10-278-698-769
18	70.6	1.7	158001	7	US-10-211-179-11
19	69.8	1.7	6881	6	US-10-311-455-1353
20	69.8	1.7	6881	6	US-10-240-453-123
21	68.6	1.6	15548	6	US-10-311-455-2128
22	68	1.6	17703	7	US-10-257-166-34
23	66.8	1.6	9238	6	US-10-240-453-240

24	66.6	1.6	1105	8	US-10-425-115-173590	Sequence 173590,
25	66.2	1.6	560	7	US-10-021-323-2253	Sequence 2253, Ap
26	66.2	1.6	6106	6	US-10-311-455-1445	Sequence 1445, Ap
27	66.2	1.6	6106	7	US-10-257-166-113	Sequence 113, App
28	66.2	1.6	6106	7	US-10-221-714A-151	Sequence 151, App
29	66.2	1.6	7049	6	US-10-311-455-130	Sequence 130, App
30	66.2	1.6	7049	6	US-10-240-452-6	Sequence 6, Appli
31	66.2	1.6	32392	8	US-10-706-635-27	Sequence 27, Appl
32	66	1.6	6409	7	US-10-221-714A-218	Sequence 218, App
33	65.6	1.6	6145	6	US-10-311-455-945	Sequence 945, App
34	65.6	1.6	8222	9	US-10-486-319A-65	Sequence 65, Appl
35	65.6	1.6	37515	7	US-10-433-793-27	Sequence 27, Appl
36	65.4	1.5	15373	6	US-10-311-455-439	Sequence 439, Appl
37	65.4	1.5	3673778	6	US-10-312-841-2	Sequence 2, Appli
38	65.2	1.5	8873	7	US-10-221-613-82	Sequence 82, Appl
39	65	1.5	17131	6	US-10-311-455-1026	Sequence 1026, Ap
40	64.6	1.5	11976	6	US-10-311-455-567	Sequence 567, App
41	64.4	1.5	6500	7	US-10-311-507-89	Sequence 89, Appl
42	64.4	1.5	17738	6	US-10-311-455-1511	Sequence 1511, Ap
43	64.4	1.5	19087	6	US-10-311-455-765	Sequence 765, App
44	64.2	1.5	1501	8	US-10-473-126-328	Sequence 328, App
45	64.2	1.5	335913	3	US-09-754-853A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-623-477-3
Sequence 3, Application US/10623477
Publication No. US20050132445A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
TITLE OR INVENTION: The Regents of the University of California
TITLE OR INVENTION: Methods for Altering Organ Mass, Controlling Fertility
FILE REFERENCE: 023070-090720US
CURRENT APPLICATION NUMBER: US/10/623, 477
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/09/479, 855
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.1
SRQ ID NO 3
LENGTH: 4228
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURES:
OTHER INFORMATION: ANT gene 5' promoter
US-10-623-477-3
Query Match 100.0%; Score 4228; DB 9; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 3781 AGTATGTTTGTGCTGATCAAGTTGTAATGTAATGTAATGTAATGTAATGTAATGTA 3840
 QY 3841 TTTTAAATGTTTCAAAAGCTTTTCAAAATTAATTAATTAATTAATTAATTAATTAAT 3900
 DB 3841 TTTTAAATGTTTCAAAAGCTTTTCAAAATTAATTAATTAATTAATTAATTAATTAAT 3900
 QY 3901 CTAAAGCCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3960
 DB 3901 CTAAAGCCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3960
 QY 3961 AGATCCCAAGGATTCAAACGCAAAATTTGCTGTTCTCTCTTATTAATTAATTC 4020
 DB 3961 AGATCCCAAGGATTCAAACGCAAAATTTGCTGTTCTCTCTTATTAATTAATTC 4020
 QY 4021 CTCGCAAAACCTCTCTATATCTCTTAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCT 4080
 DB 4021 CTCGCAAAACCTCTCTATATCTCTTAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCT 4080
 QY 4081 CAAAGAAAAACAAAGTTTGAAGAAATGCTGTTCTGTTGTAACCAATGATGGGT 4140
 DB 4081 CAAAGAAAAACAAAGTTTGAAGAAATGCTGTTCTGTTGTAACCAATGATGGGT 4140
 QY 4141 TTTAGCTTACTCTGAGAGATTAATTAAGAAAGAGTAATTAATTAATTAATTAATTAAT 4200
 DB 4141 TTTAGCTTACTCTGAGAGATTAATTAAGAAAGAGTAATTAATTAATTAATTAATTAAT 4200
 QY 4201 AGAAGACAGAAACCAAAAGAAAGAAC 4228
 DB 4201 AGAAGACAGAAACCAAAAGAAAGAAC 4228

RESULT 2
 US-10-059-911-3
 ; Sequence 3, Application US/10059911
 ; Publication No. US20030159180A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer, Robert L.
 ; APPLICANT: Mizukami, Yukiko
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Methods for Altering Organ Mass in Plants
 ; FILE REFERENCE: 023070-090730US
 ; CURRENT APPLICATION NUMBER: US/10/059, 911
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 4228
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: AINTEGUMENTA (ANT) promoter, 5'-upstream sequence
 ; US-10-059-911-3

Query Match 99.4%; Score 4203.4; DB 6; Length 4228;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 4226; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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QY 1 GTGACCTTAGGCTCTACCTGCTTAATACGACTCATATAGGAGCTCGAGATCCTTTA 60
Db 1 GTGACCTTAGGCTCTACCTGCTTAATACGACTCATATAGGAGCTCGAGATCCTTTA 60
QY 61 GTTAGAAAAAATCTTCTTTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 61 GTTAGAAAAAATCTTCTTTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ACATGTATATCAACAATATATATATGAAATGGAAATATATATATATATATATATAT 180
Db 121 ACATGTATATCAACAATATATATATGAAATGGAAATATATATATATATATATATAT 180
QY 181 TAATATATATACGTGATTAACCAACCAATGTTTCTGCTTTATATAGATTTCTATAT 240
Db 181 TAATATATATACGTGATTAACCAACCAATGTTTCTGCTTTATATAGATTTCTATAT 240
QY 241 GTTGACCTTATATATATATATATATATATATATATATATATATATATATATATAT 300
Db 241 GTTGACCTTATATATATATATATATATATATATATATATATATATATATATATAT 300
QY 301 AAAAGTGACCAAAACGAGATCCATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db 301 AAAAGTGACCAAAACGAGATCCATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 ATGATTTATGAAATTAATCTTTTACTTAATATATATATATATATATATATATATAT 420
Db 361 ATGATTTATGAAATTAATCTTTTACTTAATATATATATATATATATATATATATAT 420
QY 421 ATATGTTGAGTGTCTTCACTGCTCACTGCTCAAGAAATATCGTGTATCTTACTTAA 480
Db 421 ATATGTTGAGTGTCTTCACTGCTCACTGCTCAAGAAATATCGTGTATCTTACTTAA 480
QY 481 CTAGAGCTGATATATATATATATATATATATATATATATATATATATATATATAT 540
Db 481 CTAGAGCTGATATATATATATATATATATATATATATATATATATATATATATAT 540
QY 541 CGATCAATATCAAAATTTATATGAGCTAGAAATCCAAATGAGATGCTCTAGCAATA 600
Db 541 CGATCAATATCAAAATTTATATGAGCTAGAAATCCAAATGAGATGCTCTAGCAATA 600
QY 601 TACACGCTAAGATTTGTATGAGATCTAGAAATCCAAATGAGATGCTCTAGCAATA 660
Db 601 TACACGCTAAGATTTGTATGAGATCTAGAAATCCAAATGAGATGCTCTAGCAATA 660
QY 661 TATGATTTTCACTTACGATTTGATTTACATTAACGATTAAGATTAATATATATAT 720
Db 661 TATGATTTTCACTTACGATTTGATTTACATTAACGATTAAGATTAATATATATAT 720
QY 721 TGTGTTTGTGTTTACGATTAATATGAAATGTTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 721 TGTGTTTGTGTTTACGATTAATATGAAATGTTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY 781 AATCGTTTATGTTATCTATATATATATATATATATATATATATATATATATATAT 840
Db 781 AATCGTTTATGTTATCTATATATATATATATATATATATATATATATATATATAT 840
QY 841 TACAAATTTATGTTATGCTTATGCAATTAATAAATCCAGGATTAATATCTCAGAAAT 900
Db 841 TACAAATTTATGTTATGCTTATGCAATTAATAAATCCAGGATTAATATCTCAGAAAT 900
QY 901 TATGTTTATGTTTACAAATTTTCTTTTATGATTAATGTTTGAACAAATTTATGATA 960
Db 901 TATGTTTATGTTTACAAATTTTCTTTTATGATTAATGTTTGAACAAATTTATGATA 960
QY 961 CTTGACGGGTATTAAGGTCATGCAATGTCAGATCAGATTAAGGTCAGATTAAGGTC 1020
Db 961 CTTGACGGGTATTAAGGTCATGCAATGTCAGATCAGATTAAGGTCAGATTAAGGTC 1020
QY 1021 TCTGTCTTAAGATATCTACAGCTGCTTGTGCTGTGATAGAGAAATGATATGA 1080
Db 1021 TCTGTCTTAAGATATCTACAGCTGCTTGTGCTGTGATAGAGAAATGATATGA 1080
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Db 1021 TCTGTCTTAAGATATCTACAGCTGCTTGTGCTGTGATAGAGAAATGATATGA 1080
QY 1081 GAGATCCCATATAGGCTTACAGTTTGCCTTCCGTCGCAACTTTGGCGGTTGTGACT 1140
Db 1081 GAGATCCCATATAGGCTTACAGTTTGCCTTCCGTCGCAACTTTGGCGGTTGTGACT 1140
QY 1141 TTTTCTTATGCTGTGTTTGAATATATATATATATATATATATATATATATATATAT 1200
Db 1141 TTTTCTTATGCTGTGTTTGAATATATATATATATATATATATATATATATATATAT 1200
QY 1201 AATATTCGAAAGAAAGAAAGAAAGCAAGAAATCTATTTGTGAAAGCAATTAATGAC 1260
Db 1201 AATATTCGAAAGAAAGAAAGAAAGCAAGAAATCTATTTGTGAAAGCAATTAATGAC 1260
QY 1261 ACTTAAATGATATTAATAAATGATATATATGTTGTGGAATTTATATATATATATAT 1320
Db 1261 ACTTAAATGATATTAATAAATGATATATATGTTGTGGAATTTATATATATATATAT 1320
QY 1321 AATCAAGGAGAGAGAGAGACCTTCTGCTTATGATTTTCTCTTAAACATGCTCT 1380
Db 1321 AATCAAGGAGAGAGAGAGACCTTCTGCTTATGATTTTCTCTTAAACATGCTCT 1380
QY 1381 CCCACTATCTTTTACTTCCAAACAATCATTCACAGAGAAATCTGTCTGTGATC 1440
Db 1381 CCCACTATCTTTTACTTCCAAACAATCATTCACAGAGAAATCTGTCTGTGATC 1440
QY 1441 ACTTCAATGAAATTAATCTAAATTTGATTTTGTGCAATTTGCTGCTGTTTAAAG 1500
Db 1441 ACTTCAATGAAATTAATCTAAATTTGATTTTGTGCAATTTGCTGCTGTTTAAAG 1500
QY 1501 TCGATATATTTGATATATATATATATATATATATATATATATATATATATATATAT 1560
Db 1501 TCGATATATTTGATATATATATATATATATATATATATATATATATATATATATAT 1560
QY 1561 CTCCTTCTGCTTATCAATTAATTAACACCATTAAGCTTAATTAATTAACCA 1620
Db 1561 CTCCTTCTGCTTATCAATTAATTAACACCATTAAGCTTAATTAATTAACCA 1620
QY 1621 CATTCCTTATCAATTTTATATATATATATATATATATATATATATATATATATAT 1680
Db 1621 CATTCCTTATCAATTTTATATATATATATATATATATATATATATATATATATAT 1680
QY 1681 GGTATTAAGGATTAATGCTTCTTACGAGAAATTTTGTATATATATATATATATAT 1740
Db 1681 GGTATTAAGGATTAATGCTTCTTACGAGAAATTTTGTATATATATATATATATAT 1740
QY 1741 GGAAGAAATCCAGCTTAATATGCTATTAAGATTAATGATTTTATATATATATAT 1800
Db 1741 GGAAGAAATCCAGCTTAATATGCTATTAAGATTAATGATTTTATATATATATAT 1800
QY 1801 TTAATAATTAAGGTTTGTCTTAAAGGTTACACCGCTTATATATATATATATATAT 1860
Db 1801 TTAATAATTAAGGTTTGTCTTAAAGGTTACACCGCTTATATATATATATATATAT 1860
QY 1861 ATTAACCTTATGATTAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC 1920
Db 1861 ATTAACCTTATGATTAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC 1920
QY 1921 TTAATAATTAAGGTTTATATATGCTTCAATTAATATGTTTCAACGTAAGTTTGA 1980
Db 1921 TTAATAATTAAGGTTTATATATGCTTCAATTAATATGTTTCAACGTAAGTTTGA 1980
QY 1981 TTAATAATTAAGGTTTATATATGCTTCAATTAATATGTTTCAACGTAAGTTTGA 2040
Db 1981 TTAATAATTAAGGTTTATATATGCTTCAATTAATATGTTTCAACGTAAGTTTGA 2040
QY 2041 TTTAACCGTTCATCCAGATTTGATTAAGGTCAGAAATCTGAAACATTTTCTTCTTG 2100
Db 2041 TTTAACCGTTCATCCAGATTTGATTAAGGTCAGAAATCTGAAACATTTTCTTCTTG 2100
QY 2101 AATCTGTTTAAATTTCTCTGCTGATATCTTACAGGATTTTGAACCAAGATTAACATA 2160
Db 2101 AATCTGTTTAAATTTCTCTGCTGATATCTTACAGGATTTTGAACCAAGATTAACATA 2160
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QY 2161 TTGAAGCAAAATATCCAGGAGATGATGGGTTAGATCCACATTCAATATCTTTGT 2220
 Db 2161 TTGAAGCAAAATATCCAGGAGATGATGGGTTAGATCCACATTCAATATCTTTGT 2220
 QY 2221 CTTTGTATTTATGAAAAACAATATTTATCAGGAAAAAAACGTTCTTCTAGTGT 2280
 Db 2221 CTTTGTATTTATGAAAAACAATATTTATCAGGAAAAAAACGTTCTTCTAGTGT 2280
 QY 2281 TAAATATAGATATATCAAAATTTAATCTAGTAAATGATTTACTATCTTCAACTT 2340
 Db 2281 TAAATATAGATATATCAAAATTTAATCTAGTAAATGATTTACTATCTTCAACTT 2340
 QY 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTATTTTATCTTCAACTTCACTA 2400
 Db 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTATTTTATCTTCAACTTCACTA 2400
 QY 2401 AAAAAATGCAAAAGAAAGATATATTTAATGCAAAATTAATAAGATGGATGGAT 2460
 Db 2401 AAAAAATGCAAAAGAAAGATATATTTAATGCAAAATTAATAAGATGGATGGAT 2460
 QY 2461 TCTTCAAGCAAAACGGCCCGTAGAGTGTCTTATCTTACATTACAGCTGGGTGGCAG 2520
 Db 2461 TCTTCAAGCAAAACGGCCCGTAGAGTGTCTTATCTTACATTACAGCTGGGTGGCAG 2520
 QY 2521 ACATCATAGGGCCCTATATTTGATCTTACCTTACCTTACCTTACCTTACCTTACCT 2580
 Db 2521 ACATCATAGGGCCCTATATTTGATCTTACCTTACCTTACCTTACCTTACCTTACCT 2580
 QY 2581 TAGTCTCATCTGCAACAACAACAATCCATTCGTAACATATATATCAATCTACTA 2640
 Db 2581 TAGTCTCATCTGCAACAACAACAATCCATTCGTAACATATATATCAATCTACTA 2640
 QY 2641 GTATCATATTAAGCTATGATATCATGCTTTTTCGCAATTTCTAACTAATCTATACA 2700
 Db 2641 GTATCATATTAAGCTATGATATCATGCTTTTTCGCAATTTCTAACTAATCTATACA 2700
 QY 2701 CAAACTGAAATGTTTGTGTGTATTTATCTTAAACCAAGTTTGAATGTGATGGG 2760
 Db 2701 CAAACTGAAATGTTTGTGTGTATTTATCTTAAACCAAGTTTGAATGTGATGGG 2760
 QY 2761 AGCTACACTAGTCCCTTTTTCGCAAAATATATCTTACATGACCGGTTAAAGT 2820
 Db 2761 AGCTACACTAGTCCCTTTTTCGCAAAATATATCTTACATGACCGGTTAAAGT 2820
 QY 2821 ATTTAAACCAACAATTTTATTTGTGTGTAAGTCAAAATCATGTCATATATAGAGA 2880
 Db 2821 ATTTAAACCAACAATTTTATTTGTGTGTAAGTCAAAATCATGTCATATATAGAGA 2880
 QY 2881 CAGCATCTTATATCAAAATATGTTGATGTTATGGAATCAAAATATATAGAAATTA 2940
 Db 2881 CAGCATCTTATATCAAAATATGTTGATGTTATGGAATCAAAATATATAGAAATTA 2940
 QY 2941 GCGACTACTGTTTAAATGTTTGAAGATTAAGAAATTAAGAAATTAAG-AGTA 2999
 Db 2941 GCGACTACTGTTTAAATGTTTGAAGATTAAGAAATTAAGAAATTAAGAAATTAAG-AGTA 2999
 QY 2999 GCGACTACTGTTTAAATGTTTGAAGATTAAGAAATTAAGAAATTAAGAAATTAAG-AGTA 2999
 Db 2999 GCGACTACTGTTTAAATGTTTGAAGATTAAGAAATTAAGAAATTAAGAAATTAAG-AGTA 2999
 QY 3000 ACAGAGCTATATATGCGGCTATTTAGAGCGCTGACCAAAAGTTGCTGTAATTTCTA 3059
 Db 3000 ACAGAGCTATATATGCGGCTATTTAGAGCGCTGACCAAAAGTTGCTGTAATTTCTA 3059
 QY 3059 CCGTGGCTATATAGAAATTTTGAAGCTTTTCTCAACCTTTTATGAACTTCTGTAATTTCT 3119
 Db 3059 CCGTGGCTATATAGAAATTTTGAAGCTTTTCTCAACCTTTTATGAACTTCTGTAATTTCT 3119
 QY 3119 TTTGCGGATTAATATTTGTAATTTGTAATTTTGTCTTAAATATAGATCGTAATTC 3179
 Db 3119 TTTGCGGATTAATATTTGTAATTTGTAATTTTGTCTTAAATATAGATCGTAATTC 3179
 QY 3179 TTTGCGGATTAATATTTGTAATTTGTAATTTTGTCTTAAATATAGATCGTAATTC 3179
 Db 3179 TTTGCGGATTAATATTTGTAATTTGTAATTTTGTCTTAAATATAGATCGTAATTC 3179
 QY 3180 ACGATTAAGAAAGACTCTTTTATTTATTTGATTTAAACTTTTGTGTTTGAAGATGAC 3239
 Db 3180 ACGATTAAGAAAGACTCTTTTATTTATTTGATTTAAACTTTTGTGTTTGAAGATGAC 3239

QY 3240 TCATACAAAGGTTAAAGTTTGAATGATCCAAATTTTCAAAAAATGTTTGAAGTGGCTT 3299
 Db 3240 TCATACAAAGGTTAAAGTTTGAATGATCCAAATTTTCAAAAAATGTTTGAAGTGGCTT 3299
 QY 3300 CAGATGCTTACCAACCATGCTTACCACTGATGAGTTTATATTTAGGTTTTTTCTTCT 3359
 Db 3300 CAGATGCTTACCAACCATGCTTACCACTGATGAGTTTATATTTAGGTTTTTTCTTCT 3359
 QY 3360 TTTTCCAAATGCTTTATATTTGAACCACTTAAATTTCTTTTAAATATAGTTAAGAA 3419
 Db 3360 TTTTCCAAATGCTTTATATTTGAACCACTTAAATTTCTTTTAAATATAGTTAAGAA 3419
 QY 3420 TCTTGAATTTTCTGTTAATTTTAAACCAAGTTTCAATCTTCTGCACAAAAAAAA 3479
 Db 3420 TCTTGAATTTTCTGTTAATTTTAAACCAAGTTTCAATCTTCTGCACAAAAAAAA 3479
 QY 3480 AAAAAATTTTCAATTTATTAAGATCTAAATTTTGAATTCAGATTTAATGATAGC 3539
 Db 3480 AAAAAATTTTCAATTTATTAAGATCTAAATTTTGAATTCAGATTTAATGATAGC 3539
 QY 3540 TGAAGATTTATGATGATTTGCAAGTTTGCACAGATGCTGATGATATCAAAA 3599
 Db 3540 TGAAGATTTATGATGATTTGCAAGTTTGCACAGATGCTGATGATATCAAAA 3599
 QY 3600 ACATGATCAAAATTAATATTTGCTTACAGAGAAAGCATTTGAATTAACAGAACAA 3659
 Db 3600 ACATGATCAAAATTAATATTTGCTTACAGAGAAAGCATTTGAATTAACAGAACAA 3659
 QY 3660 TCGTTAACCACTTAAATATCTTGAATATTTTGTATGATATTTCTGTAAGAGAG 3719
 Db 3660 TCGTTAACCACTTAAATATCTTGAATATTTTGTATGATATTTCTGTAAGAGAG 3719
 QY 3720 GTATCATATCTTACAAAAAAATCTATTTCAATTAATATATGTTTCCATGTTACC 3779
 Db 3720 GTATCATATCTTACAAAAAAATCTATTTCAATTAATATATGTTTCCATGTTACC 3779
 QY 3780 AAGTATGTTTGTGTCATGATGATTTGTAATCTGCTTACGATATATAGTTCTAA 3839
 Db 3780 AAGTATGTTTGTGTCATGATGATTTGTAATCTGCTTACGATATATAGTTCTAA 3839
 QY 3840 GTTTTAAATGTTTCAAAAGCTTTTACAAATTAATTAATATATAGTGAATTTGTAGG 3899
 Db 3840 GTTTTAAATGTTTCAAAAGCTTTTACAAATTAATTAATATATAGTGAATTTGTAGG 3899
 QY 3900 GCTTAAAGCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3959
 Db 3900 GCTTAAAGCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3959
 QY 3960 CAGATCCCAACGATTTCAACAGCAATTTGTGCTTGTCTTCTTATATATATAT 4019
 Db 3960 CAGATCCCAACGATTTCAACAGCAATTTGTGCTTGTCTTCTTATATATATAT 4019
 QY 4020 CCTCTCAAAAACCTCTCTATATCTCTTAAAGCCCTCTCTGTTTCTCTACCGCA 4079
 Db 4020 CCTCTCAAAAACCTCTCTATATCTCTTAAAGCCCTCTCTGTTTCTCTACCGCA 4079
 QY 4080 ACAAGAAAAACAAGATTTGAAGAAATGATGTTGTTGTTGTAACCAATGATGGG 4139
 Db 4080 ACAAGAAAAACAAGATTTGAAGAAATGATGTTGTTGTTGTTGTAACCAATGATGGG 4139
 QY 4140 TTTTATGCTTACTTCTGAGATTTATGAAGAAAGATGTAAGATATATATATATAT 4199
 Db 4140 TTTTATGCTTACTTCTGAGATTTATGAAGAAAGATGTAAGATATATATATATAT 4199
 QY 4200 AAGAGAGCAAGAACCAAAAAAGAAC 4228
 Db 4200 AAGAGAGCAAGAACCAAAAAAGAAC 4228

RESULT 3
 US-10-059-911-1
 ; Sequence 1, Application US/10059911
 ; Publication No. US20030159180A1

GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
TITLE OF INVENTION: Methods of the University of California
FILE REFERENCE: 023070-090730US
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 2148
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: AINTEGUMENTA (ANT) cDNA
NAME/KEY: CDS
LOCATION: (269) ..(1936)
OTHER INFORMATION: Arabidopsis AINTEGUMENTA (ANT)
US-10-059-911-1

Query Match 6.3%; Score 268; DB 6; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3961 AGATCCCAACGAGTTCAGAAAGCAAAATTTGCTTGTCTCTCTTATTAATATC 4020
DB 1 AGATCCCAACGAGTTCAGAAAGCAAAATTTGCTTGTCTCTCTTATTAATATC 60
QY 4021 CTCTCAAAAACCTCTCTCTATCTCTCTTAAAGCCCCCTTCTCTTCTCTACCGCA 4080
DB 61 CTCTCAAAAACCTCTCTCTATCTCTCTTAAAGCCCCCTTCTCTTCTCTACCGCA 120
QY 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTGTAACAATGAGGT 4140
DB 121 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTGTAACAATGAGGT 180
QY 4141 TTGAGCTTACTTCTGAGAGATTATTAAGAAAGAGGAGATTCATTATGAAAGA 4200
DB 181 TTGAGCTTACTTCTGAGAGATTATTAAGAAAGAGGAGATTCATTATGAAAGA 240
QY 4201 AGAGAACGAGAAACCAAAAAAGAAACC 4228
DB 241 AGAGAACGAGAAACCAAAAAAGAAACC 268

RESULT 4
US-10-623-477-1
Sequence 1, Application US/10623477
Publication No. US20050132445A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
TITLE OF INVENTION: Methods of the University of California
FILE REFERENCE: 023070-090720US
CURRENT APPLICATION NUMBER: US/10/623,477
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/09/479,855
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 2148
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (269) ..(1936)
OTHER INFORMATION: AINTEGUMENTA (ANT) cDNA
OTHER INFORMATION: AINTEGUMENTA (ANT)

US-10-623-477-1

Query Match 6.3%; Score 268; DB 9; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3961 AGATCCCAACGAGTTCAGAAAGCAAAATTTGCTTGTCTCTCTTATTAATATC 4020
DB 1 AGATCCCAACGAGTTCAGAAAGCAAAATTTGCTTGTCTCTCTTATTAATATC 60
QY 4021 CTCTCAAAAACCTCTCTCTATCTCTCTTAAAGCCCCCTTCTTGTCTCTACCGCA 4080
DB 61 CTCTCAAAAACCTCTCTCTATCTCTCTTAAAGCCCCCTTCTTGTCTCTACCGCA 120
QY 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTGTAACAATGAGGT 4140
DB 121 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTGTAACAATGAGGT 180
QY 4141 TTGAGCTTACTTCTGAGAGATTATTAAGAAAGAGGAGATTCATTATGAAAGA 4200
DB 181 TTGAGCTTACTTCTGAGAGATTATTAAGAAAGAGGAGATTCATTATGAAAGA 240
QY 4201 AGAGAACGAGAAACCAAAAAAGAAACC 4228
DB 241 AGAGAACGAGAAACCAAAAAAGAAACC 268

RESULT 5
US-10-473-126-386/c
Sequence 386, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Biogenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
FILE REFERENCE: proliferative disorders
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
LENGTH: 8056
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match 3.5%; Score 147; DB 8; Length 8056;
Best Local Similarity 42.8%; Pred. No. 1e-15;
Matches 1674; Conservative 0; Mismatches 2175; Indels 62; Gaps 16;

QY 73 TTTCTTTGACGT 132
DB 3982 TTTCTTTGACGT 3923
QY 133 ACAATATATATATGAATTTGAATTTATCATTTATAGTATGATGATATATATATAC 192
DB 3922 ATTAATTTTCACAATTTTITAAAACATTTAAATTTCAATTTTATTTATCATTTGCA 3863
QY 193 GCTGACATTCACCAACCAATTTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 252
DB 3862 AATCATTTTCAAAATTTTACATTTTCAAAATTTTCAAAATTTTCAAAATTTTCAAAATTTT 3803
QY 253 TATGATCTATTAATAAATCGGTTTATTTAAATCCGATCCATTAACAAATGAGCA 312
DB 3802 AATCATTTTCAAAATTTTATTAATAAATCGGTTTATTTAAATCCGATCCATTTAAATTTTAA 3743
QY 313 AAACGATTCATGTTTGT 372
DB 3742 AATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3683
QY 373 GATTAATCTTCTAATTAATTAATTAATTTGGA--AAACCAACTTAATATGTTGAG 430

QY	1488	TTGCGTTTAAAGTCGATTAATTTGGTATACATATAGTCGGATATACATCCAGCTA	154
DB	2543	TTATTTTAATAATTATTAATTAATTTTTTTTTTTTCAATTAATTTAATTTTAAAA	2488
QY	1548	ATCATTAATGATCTCTTCTGCTATCATTAATAATTACACCACTTACGTATCAAGCTA	1607
DB	2483	CAAAATTAATAAAAAATATATAAATTAATAAAAAATTAATTTTAAATAATAATA	2422
QY	1608	ATTAATTAACACCACTCTCTTATCATTTTATATGATTAATTAACAACGACATAT	1667
DB	2423	ATTATTTTTTTTTTAAATTTTCAAAAAATAAATAATTAATAATTTATTTTAAAAATA	2366
QY	1668	AGGCTACAGATGTGATTTAAGGACATATATGCGCTCTAGTGGAGGAATTTTTTGATAT	1727
DB	2363	AAATTAATTAATTTAAAAATTTAATAAATTTTATTAATACAAAAATTAATAATTAATTTT	2306
QY	1728	GATACACTCGTGGAAAAAAATCCAGCCTAATATGCTCATTTTAAAGATATGATTTTA	1787
DB	2303	AAAAATTAATAAATTAATAAATTTTAAATTTTAAATTTTAAATTTTAAATAATA	2244
QY	1788	AATGCTTTAATCATTAATAATAAGGTTTTTGTCTTTTAAGGTTACCAACCGTTAATTC	1844
DB	2243	A-----TTTATTAATTAATAATAAATTTTTTTTTTTTTTATTTTTTTTCATTTTTTTTA	2190
QY	1848	TCATTAGSAGAAATNTACCTTGATTCGAAATCCAAAATCTTTTTTAAACATATAGAA	1907
DB	2189	AAATTTTAATAATAATTAATAATTTTTTTTTTTTTTATTTTATTAATTAATAATAATAA	2133
QY	1908	AATTTTCAGCATTTTTTAAATAATAAGGATCATTTATTTGGTTCATAATAATATGTTCCAGCT	1967
DB	2129	ATTATTAATAATTAATTAATAATTTTAATAATTAATTAATTAATAATAATTAATAATTTT	2070
QY	1968	AAAGTTTGAAGTTTAAACCATGATGTTTTTGAATTTAAAAAACACATTAATTTCTA	2027
DB	2069	ATTAATAATTTTTTAAAAATAAAAAATAATTAATAATAATTTTAAATTAATTTTAA	2010
QY	2028	GTAATTAACATTTTTTAAACGTCATCCAGATGTGAATTAAGTGAACAATCTGAAAACAT	2087
DB	2009	ATTTTATTAATAATTTTAAATAAAAAATTAATAATTAATTTTAAATAAAAAATTAATTT	1956
QY	2088	TTTTTTTTTCTGGAATCTTGTTAATTTCTCTGCTGACATCTGACGATTTGACCA	2147
DB	1949	TTTTATTAATAATTAATAATTAATTAATTTTTTTTTTAAATTTTATTTTAATAATA	1890
QY	2148	ACGACTATACATATTGAAGCAAAATATCCACGAGATGATAGGTTAGATCCACATTT	2207
DB	1889	AAAAAATTAATAATAATTAATAATAATTTTTTTTTTTTTTTTTTTTTTAAAAACA	1830
QY	2208	CAATATCTTTTGTCTTTGTATTTATATGAANAACAA-----ATAATTAATAG	2253
DB	1829	AAATTTTATTTTATTAATTAATAATAATTAATAATTAATAATTAATTTTAAATTTTAT	1770
QY	2254	GAATAAAAAAGTTTCTCTAGTGTATAGATATAGATATAACAAATTTTAATCTTA	2313
DB	1769	TTAAAAAATTTTTTAAATTTTAAATTTTAAATAATTAATAATAATTAATAATTAAT	1710
QY	2314	GTTAATATGA--TTTACATCTTCAAACTTACATCTTCAACATTAATATGATCAAT	2370
DB	1709	ATTAAATTTAATTTTAAATAATTTTAATAAAAAATAAATTTTATCTAATTAATTAATAAT	1650
QY	2371	TTTATTTTTTTTAACTAAACTACTCCACTAAAAAAATGCAAAAAGAGATATATATTA	2430
DB	1649	TTTTTTTATTTTACAAATTCATTTATTTCAATTTTTTAAATAATTAATAATAATTA	1590
QY	2431	AGTCAAAAGTAATTAAGATGAGTGGTGAATTTCTTACAGCAAAACGCGCCGTAGAGTCTC	2490
DB	1589	AATTAATAAT-ATTAATTTTAAATTAATAATTTTAAATAAAAAATTTTATTTAAATAATTT	1531
QY	2491	TTATCTTACATTAACAGCTGGTGTGTGGACATCATATAGGCCCTATCGTATATTTGAGCTT	2550
DB	1530	TTTAAACATTTTAAATTTTATTAATTAATAATAATTTTAATTAATTAATTTTAAATA	1471


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QY 2551 TACTGACGTAAGCTTTACATATCTAGTTAGTCTCACTGTACAAACAAACAAATC 2610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1470 TAATTTATTTAAAAAATATTTTATTTTAAAAA-----AAAAAATTTAAAAA 1415
QY 2611 CAATTGCTACATATATACAAATACATCTAGTACTAGATTACGCTACATACGCTT 2670
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1414 ATAAAAAATTTAAATATTTATTTTAAAAAATTTAAATTTTAAATTTAAATTTAA 1355
QY 2671 TTTCGAAATTTCTTAACCTATATCAACAACAACTGAAATGTTGTTGTAATTTATC 2730
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1354 AATTTAAATTTATTTTATTTAAAAATTTATATATTTTATTTTATTTATTTATTTTAA 1295
QY 2731 TTAAACCAAGTTTGAATGTCAGTGGAGCTACACTAGTCCCTTTTCCCAA 2790
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1294 AAAAAATTTACATTTTATATATTTAAT-ATATTTACATACATTTTATTTTATTTCAAAA 1236
QY 2791 AATATCTCTTACATCGACCGGTAAAGTATTTAAACCAAAATTTTATTTGTTGCT 2850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1235 AATTTATTTATTA-TTAAAAAATTTAAATTTAAATTTAAATTTTAAATTTAAATTTAA 1177
QY 2851 GAAGTACAAACATGTCACATATATAGACAGCATCGTTTATACAAATTAATGTTGATG 2910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1176 TATATATCAAAATATATATTTATTTTAAATTTTCAAAATATCAAAAAATATTT--AAAAA 1119
QY 2911 TTATTTGAAATCAAAATATATATACGAATTAAGCACTCACTGTTTAAATGTTTGAAGA 2970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1118 CAATATATATACATTTTAAAAACATTTAAAAAATTTAAACAAATTTTAAAAATTTTATTT 1059
QY 2971 TATGAAATTTAAATATGATTTCAAGATACAGACTATATATGCGGCTCATTTAGAGC 3030
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1058 TTACATATTTAAATTTCAAAATTTAAATTTAAATTTTAAATTTTAAATTTATTTT 999
QY 3031 CGTGACCAAAAGTTGCTGCTAATTTCTACGCTCGGTCAATAGAAATTTTGACTTTTCT 3090
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 998 AAAAAATTTATATATATATTTTATTTTCAATTTTAAAAATTTAAATTTATTTTAAA 939
QY 3091 TCACCTTTTATGACCTCTGATAGTTTGTGCGATATATATTTGTAATTCGTATAT 3150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 938 AAAAAATTTATCAAAAAACAAAAATATTTAAATTTTAAATTTTAAATTTACAAAT 879
QY 3151 TTTTGTCTTATATATGATACGTAAATTCAGATTAAGAAAGACTCTCTTTTATTTAATTT 3210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 878 TTTTATATCAATTTAAAAAATTTAAAAAATTTTATTTTAAATTTTAAATTTAAT 819
QY 3211 GATTTAAACCTTTGTTTGGAAATGACTCATACCAAGTTAAAGTTGATGATCC 3270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 818 CATTTATATATTTTAAATATATATATTTTAAATTTTAAATTTTAAATTTTAAATTT 759
QY 3271 AATTTCAAAATATGTTTCGAGTGGCTTCGAGTGTCTACCAACATCGTACCACTCGT 3330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 758 TAAATTTTAAATTTTATATATATATATTTTAAATTTTAAATTTTAAATTTTAAAT 699
QY 3331 ATGGGTTTATATAGTTTCTTTCTTTTTCAAATGCTTTTATATTTGAACCACTCT 3390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 698 AATTTTATATATTTTATTTTATTTTATTTTATTTTAAATTTTAAATTTTAAATTTA 639
QY 3391 AATTTCTTTTAAATTTAGTTAAGTAATCTGAATTTCTGCTGATTTTAAACCAAG 3450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 638 TTTAAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 579
QY 3451 TTTTCAATTTCTTTAGCACAAAAAATTTTCAATTTTCAATTTTAAAGATCTTAA 3510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 578 AATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 519
QY 3511 TTTTGTAGTCAAGGTTTAAATGATAGCTGAAAGTTTAAATGATGCAAGTTTGA 3570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 518 ATATTTAATAT-ATTTTAAATTTTAAATTTTATTTTAAATATATTTTATTTTAAAA 460
QY 3571 CAGAAATGTCATGTATGATATCAAAAAATGATCAAAAAATTTATTCGCTTACG 3630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 459 TTAATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 400
QY 3631 AAGAGAAAGCATTTGAATTAACAGAACATCTTAACTTAAATTTTAAATTTTAA 3690
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Db 399 AATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 340
QY 3691 TTGTAGTAAATTTTCTGTAAAGAGAGATATCATATCTTCAAAAAAATTCATTTTC 3750
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 339 ATTTATTTTATTTTAAATTTTATTTTAAAAATTTTAAATTTTAAAAATTTTATTT 280
QY 3751 AGATTAATTAATGTTGTCATATCTGTTACCAAGTATGTTT--GCGTCAATGATTTA 3807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 279 TATTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 220
QY 3808 TTGTAACTGCTCTTAGCCATATAGTCTTAAGTTTAAATGTTTCAAAAGCTTTACA 3867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 TTTAAATTTATATATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA 160
QY 3868 AATTTAAATTTATATATAGTGAATTTGTAGGCTTAAAGCGAAATTTAAATTTAAAT 3927
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 AAAAAATTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 100
QY 3928 AAAATTAAGAA 3938
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 AATTTATTTAAA 89
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RESULT 6
US-10-473-126-386
; Sequence 386, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; Applicant: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match      2.5%; Score 107.8; DB 8; Length 8056;
Best Local Similarity 43.4%; Pred. No. 9.6e-09;
Matches 1170; Conservative 0; Mismatches 1477; Indels 46; Gaps 13;

QY 1505 TTATTTGTAAATCTATATATGTTGATATATACATCCAAAGCTAATCAATTTGATCTCC 1564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1868 TAATTAATTTATTTTATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTA 1927
QY 1565 TTCTGCTTATCAATTAATTTACACCATTTAGCTAATCAAGCTAATTAATTTACCACTT 1624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1928 TTAATTAATTAATTAATTAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1987
QY 1625 CTCTTATCAATTTTATATGATATTAATTAATTAATTAATTAATTAATTTAGGCTACAGAGTGTGA 1684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1988 TTTATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 2044
QY 1685 TTTAAGCATTTATGCTCTTAGTCGAAGAAATTTTGTGTTATGATATACACTCGTGGAA 1744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2045 ATTTTATTTTATTTTAAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2104
QY 1745 AAAATTCAGCTAATATAGCTCAATTTAAAGATTAATTTGAATTTAAATGCTTTAAATCA 1804
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2105 AATTTATTTATTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2162
QY 1805 AATTAAGATTTTGTGTTTAAAGTTTACACCGCTTAATCATCTTTAGAGAAATATTA 1864
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2163 AAAAAATTTATATTTTATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2222
QY 1865 ACTTTGATCGAAATTCAAATATCTTTTAAACATATAGAAATTTTGCATTTTAA 1924
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[illegible][illegible]


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Db      145 AAAAAAAAAAATATAAAAAATTAAAATAATTAATTTAAATTTTTTAAATTTAAAAATTA   86
QY      3943 CTTTCGAATGAGACAGATCCCAACGGATTCMAAACAGCAAATTTGCCTTGCTT    4002
Ddb     85 AAAAATTAATAAAAAAATAAAAAAATTTTATATTATTAATTAATTAATTAATTAATTT  26

Db      4003 CTCCTCATTATPAA 4016
               |||||
QY      25 TTAGTTATTTTAA 12

RESULT 8
US-10-473-126-240
; Sequence 240, Application US/10473126
; Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
FILE REFERENCE: proliferation disorders
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 240
LENGTH: 8056
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-240
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Oy		2803	CGATGCACGGTTAAGTATTAAACAACAAATTTTAATTTGTCGGAAGGTACAAC	2865
Db		1224	TATTAAAAAATTAAATTAAATTAAATTAAATTTTAAAATAAATTAATTAATATCGAA	11651
Oy		2863	ATGTCACATATATAGACAGCATCGTTTATCAATATATGTCGATGTTATTGGAAATC	29222
Db		1164	ATATATTAAATTTTAAATTTTGSAATATCGAAAAAAATTTTAAAAACG-ATATATTAC	11062
Oy		2923	AAATRTAAATACGAATTAGCCACTCATTGCTTTAATAGTTGGAGAATATGAATATA	29823
Db		1105	TTTTTAAAAAGTTAAAAAAAACGAATTTAAACGAATTTTTTTTATTACGTAATTAA	10463
Oy		2983	AAATGAATCCAAGGATCACAGCTATATATGTCGGATCTTAGAGCCGTGACCAGAA	30424
Db		1045	TTTCGAAATTTAAAAATATATAAAAAATTTTAAAAATATATTTTAAAAAAATTATA	986
Oy		3043	TTTCGCTGAATTTCTACGTCGGTCGATACAGAAATTTTGGACCTTTCTTCACTTAT	31025
Db		985	TATATATTATNTCGTTTAAATTAABAAAAATATAATTTTAAAAAAATTTATTRC	926
Oy		3103	GAACTCTGTATAGTTTTTGTCCGATTATATTTGTAATTCGTATATTTTTGTCTAA	31626
Db		925	GAAAAACGAAAAATTAATTAATAATTTAAATTAATTCGAAATTTTATACGTAA	866
Oy		3163	TATATATACGTAAATTCACGATACAGAAAGCTCTTTTATTTAATTGATTTAAACT	32227
Db		865	AAAAAATTAaaaaaaCGATTTTTTTTAAATAAAATTTTAAATATCGTTATATATT	806
Oy		3223	TTGTTTTTGGAAATGACTACACACAAGSTTAAAGTTGATGSTRATCAAATTTCAAAA	32828
Db		805	ATTTTAAATATATATTAATTAATATATATTTTATATTTTAAATTTTAAATTAATAA	746
Oy		3283	TGTTTCGAGAGTCGGTTCGAGTGTCTTCAACCATCGTACCAACTCGTATGGGTTATTA	33429
Db		745	TTTATATATATATATTAATTTTAAATTTAAATTTTAAATTTTAAATTTTAAAT	686
Oy		3343	TTAGCTTTTTCTCTTTTCCATAGTCTTATATATGAACCACTPAATTTCTTTT	34030
Db		685	TTATATATTTTTTTTTTTTTTAAATTAATTAATTTTAAATTTTAAATTTTAAATTTT	626
Oy		3403	TTAATATAGTTAAGATCTGAATTTCTGTGATTTTAAACAAGTTTCAATCTT	34631
Db		625	AAAAATTATATATATTTTTTTTATATATATATTAATTAATTAATTAATTTTAAATAA	566
Oy		3463	CTTAGCACAAAAAAAAAAAAAAGTTTCAATTTAATAAGATCTAAATTTTGTGAGTTC	35232
Db		565	CGTTATATATATATATATATATTTTAAATTTAATTAATTAATTAATTAATTAAT	506
Oy		3523	AAGAGTTTATATAGTACGTAAGAAAGTTATGAATGATTCGACAGTTGGCAACAGATGCTGA	35823
Db		505	TATAAATTTTATTTTTTTTTTATTTAAATATATTTTAAATTTAAATTTTAAATTTT	446
Oy		3583	TGTATGATCATATCAAAAACATGCATCAAAATTAATATTCGTGCTTAGAAGAGAACAT	36424
Db		445	TTATTTTTTAAAAAAAATTAATAATTAATTAATTAATTAATTAATTAATTTTAAATAT	386
Oy		3643	TGAATATAACAGAACATCGTTAACACTTAAAAATCTTAGAATTAATTTGTAGATTA	37025
Db		385	AAATATTTTATTTTCGTTTTTTTTTTTTTTTAAATTTATTTATTTTATTTTATTA	326
Oy		3703	TTTTCTGTAAAGAGAGGTATCATATCTTACAAAAAAAACCTCATTTTCAGATTAATAT	37626
Db		325	ATTATTTTTTAAAAAATPATTTTTTAAAAAAAATTAATTTTTTTTAAATTAATTT	266
Oy		3763	GTTGTCCAATCGTTACCAAGTATGTTTTTGTCTGATCAGTTGATTTGACTGCTCT	38227
Db		265	TAAAAATTTTAAAAATTTTAAATTTTAAAAATTTTAAATTTTAAATTTATATAT	206
Oy		3823	TAGCCATATAGTCTAAGTTTAAATGTTTTCAAGACTTTACAAAAATTAATATATAT	38828
Db		205	AATATATTTAAATTTATATATTTAAAAAAAATTAATTAATTAATTAATTAATTAATTA	146
Oy		3883	AAGGTGAATTTGTAGGGCTAAAGCGAAAAATATAATAATTAATTAAGTAAAGAACT	39429

	Query Match	2.4%; Score 99.4; DB 8;	Length 8056;
	Best Local Similarity	42.6%; Pred. No. 3e-07;	
	Matches 1195;	Conservative 0; Mismatches 1566;	Indels 46; Gaps 11;
Oy	1138	ACTTTTCTTCATGCGTGTTGACATAATTTCTCAGAGTAGAGTAACAAGAA	1197
Dd	408	AATATATTATTAATTTATTTATTTTTAAAAATATAAAAAAAAAATATATTTAAA	467
Oy	1198	ACTAATATTCGAAGAAGAAAAAGCAGAAAACTTTGTCCGAAGACATAAT	125
Dd	468	AATAAATATATTTAAATAAAAAAATTTAAATTTATATATATATTAATTA	527
Oy	1258	GACACTAAATTTGGATTAATTAATAATGTAATATATGTTGGTGAATTTATCATATAC	131
Dd	528	TATATTAATAATTAATTTATATATATATATATTAAGCTTTATTAATAATATATATAT	587
Oy	1318	CAAAATCAAAGAGAGAGAGGACCTCTTCGTATGATTTCCCTCTTAACAAT	1377
Dd	588	TATATATATATTTATATAAAAAATATATATATTAATTTTAAAAATATATTT	647
Oy	1378	GCTCCCATATCCTTTTCTTACTTCCAACAAATCATTCACACGAGAAATCTGCTCGTG	1433
Dd	648	TAAATATTAATTTTATTAATAAAAAAAAAAAAAATATAAATTAATAAAATTTTATAT	707
Oy	1438	ATCATTTTCATGCANAATTAACATAATTTTGGATTTTTTGTACAGTCTGCGTATTT	1497
Dd	708	TTTAAATTTATTTAAATAATATTTATATATATATTAATTAATTTTAAATTT--TTAAATTTTA	765
Oy	1498	AAGTCGATTAATTTGGTATATCTATATATGATGATATACATCCAGCTATCATATAT	1557
Dd	766	ATTAATATTAATAAATATATATTTAATATATATATTAATAATTAATTAACGATATATTT	825
Oy	1558	GATCTCCTTGCTTATCATATAATATCACACATTTAGCTATCATAGCTAATTAATACA	1617
Dd	826	AAATATATTTTATTAATAAAAAATCGTTTTTTTTTTTTTTTACGTATAAAAATTTCGT	885
Oy	1618	CCACATCTCTATCAATTTTATATATGTAATTAATAAACAACGACTATATAGGTACAGA	1677
Dd	886	AATTAATTAATTAATATATTTTATATTTATTTTCGTCGTTTGTATTAATATTTTATTA	945
Oy	1678	GTGTGTATTAAGCATTAATGCCCTTCATGTCGAAGATTTTTTTTGTATGATTAACATC	1737

Db 946 ATAAATTTTATTTTATTTTAAAGAAATAAATATATTAATTTTAAATAA 1005
Qy 1738 GTGGGAAAAAATCCAGCCATATATGCTCTTTAAAGATTAATGATTTAAAGCTTTAA 1797
Db 1006 ATTAATTTTAAATAATTTTATTTATTTTAAATTTTGAATTTTAATTAATTAATTAATAA 1065
Qy 1798 TCATTAATAATTAAGGTTTTGCTTTTAAAGTTACACCGCTTAATTCATTAAGAG 1857
Db 1066 AAATTTGCTTTAATTCGTTTTTTTTTTTAAAGCTTTTAAAGCTTAATATATCGTTTTTAA 1125
Qy 1858 AATATTAACCTTGATCGAAATTCGAAATATCTTTTAAACATTAAGAAATTTTGAGCA 1917
Db 1126 A-----TATTTTTCGATTCGAAATTTAAATATTAATATTTTCGATTAATTAATA 1180
Qy 1918 TTTTAAATTAAGGATTAATTTGGGTTCAATTAATATGTTCCACGTAAGTTTGA 1977
Db 1181 TTTATTTTAAATTTTAAATTAATTTTAAATTTTAAATTTTAAATTAATTAATTTTTC 1240
Qy 1978 GGT-----TAACCATGATGATGTTTTTGAATTTAAATAACATTAATTTCTAGTAA 2031
Db 1241 GAATTAATAAATAAATCGTTACGTAATTAATTAATTAATTAATAAAGTAATATTTTAAATA 1300
Qy 2032 TTACATATTTTAAACCGTCCATCCAGTTGTAATTAAGTGAATAATCTGAATAATTTTT 2091
Db 1301 TTAATTAATTAATAAATAATTTATTAATTTTAAATTAATAAATAATTTAAATTTTAAT 1360
Qy 2092 TTTTCTGATCTGTTTAAATTTCTCTGCTGCAATCTTGAGGATTTGACCAAGA 2151
Db 1361 TTTTATTAATAAATTTTATTTTAAATAAATAATTAATTAATTTTAAATTTTAAATTTT 1420
Qy 2152 CTATACATATTT-----GAAGCAAAATATCCACAGGATGATGAGGTTAGATCCACATTC 2208
Db 1421 ATTTTTTTTTTTTAAATAAATAAATAATTAATTTTAAATTAATAATTAATAATA 1480
Qy 2209 AATATCTTTTGTCTGTTATTTATGAATAAATAATTTATGAGAAATAAATCGTTCT 2268
Db 1481 ATTAATTAATTAATTAATTAATTAATAATTAATAATTAATAATTAATAATAATTTTAA 1540
Qy 2269 TCTCTAGGTATTAAGTATTAAGTAAATTAACAAATTTTAATCTAGTAAATGATTTACT 2328
Db 1541 AATTAATAATTAATTTTAAATAAATAATTAATTAATAATTTTAAATTTTAAATTTTAA 1600
Qy 2329 ATCTCAACCTTACATCTTCAACATTAATTTGATCAATTTTATTTTAACTTAA 2388
Db 1601 TTTTAATATTTTAAATAAATGAAATTAACGAATCGTAATAATTTAAATAATTTTAAAT 1660
Qy 2389 CTATCTTCCACTTAAATAAATGCAAAAGAGATATATATTTTAAAGTCAAGTAAATTAAGA 2448
Db 1661 TAATACGATTAATAATTTATTTTAAATAATTAATAATTAATAATTAATAATTAATA 1720
Qy 2449 TGAATGGATATCTTCAAGCAAAACGCGCGTGAAGGTCTTAATCTTCAATTAAGCT 2508
Db 1721 TATTTTAAATTTTAAATTTTAAATAAATAATTAATAAATAATTTTAAATTTTAAATAAT 1780
Qy 2509 GGGTTGGGAGACATCATGAGGCTGATATTTTGAAGCTTACCTGAGC-----TAAAGC 2565
Db 1781 AAAATTAATTAAGTATTAATTTATTTTAAATTAATAATAAATTTGTTTTTAAATA 1840
Qy 2566 TTTTAACTATCTAGTTAGTTCTCATGTAACAAACAAATTCGAATTCGTAACATAT 2625
Db 1841 AAAAAAAAAAAAAAAAAAATAATTAATTAATTAATTTTAAATTTTAAATTAATAA 1900
Qy 2626 ATACAATATCTAGTATGATTAAGCTAAGTATACATCGCTTTTCCGAATTTCTA 2685
Db 1901 ATAAAAATTTTAAATAAATAAATAATTAATTAATTAATTAATTAATTAATTAATAA 1953
Qy 2686 AATCAATCTATTAACAACAACCTGAAGTTTGTGTTGAATTTATCTTAAACAAGTTT 2745
Db 1954 TATTAATTTTAAATAAATAAATAATTAATTAATTTTAAATAATTTTAAATAATTTTAA 2013
Qy 2746 GAATGTGCAATGGAGCTACATTAATGCTCCCTTTTCCCAAAATAATCTCTTACA 2805

Db 2014 AATATATTTTAAATAAATAATTAATTTTAAATAATTTTAAATAATTTTAAATAATTTTAA 2073
Qy 2806 TGAACCGGTTAAAGATTTTAAACAACAATTTTAAATTTGTCGTAAGGTACAAACATG 2865
Db 2074 AATATTTTAAATTTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2132
Qy 2866 TCATATTAATTAAGACAGCATCGTTTAAACAATAATGTTGATGTTTGAAT----- 2921
Db 2133 TTAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2192
Qy 2922 -----CAATTAATAATGCAATTTGCGATCTGCTTAAATGTTTGAAGTAAT 2974
Db 2193 AAAAAAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2252
Qy 2975 GAATTAATAAATGAATTCAAAGATACAGAGTATATATGTCGGTCAATTAAGCCGTG 3034
Db 2253 AATATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2312
Qy 3035 ACCAAAGTTTGTGCTGTAATTTCTACGGTCCGTCATTAAGAAATTTTGAATTTTTCAC 3094
Db 2313 TATTAATTTTGTGATTTAAATAATTTTATTTTAAATTTTAAATAATTTTATTTTAA 2372
Qy 3095 CCTTTATGACCTTCTGTAATGTTTGTGCGATTAATATTTGTAATGTAATTTT 3154
Db 2373 TAAATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2432
Qy 3155 GTTTCTATTAATGATACGTAAATTCAGATTAAGAAAGCTCTTTTATTAATTTGAAT 3214
Db 2433 TTTTAAATAATTAATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2490
Qy 3215 TAAACCTTTTGTGTTTGAATAATGCTCATTAACAAGTTTGAATTTTGAATTTTCAAT 3274
Db 2491 ATTAATTAATAATTAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2550
Qy 3275 TACAAAAAGTTTGCAGAGTGGCTTGAAGTCTTCAACATCGTAACCAATCGTATGG 3334
Db 2551 AATTTAAATAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2610
Qy 3335 GTTTATTAATGAGTTTCTCTCTTTTCAATGCTTATTAATTTGAACACTTAAT 3394
Db 2611 AATATTAATTAATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2670
Qy 3395 TTCTTTTAAATTAATGTTAAGATCTGAATTTTCTGTAATTTTAAACAAGTTT 3454
Db 2671 TAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2730
Qy 3455 CAATTTCTTACACAAAAAATAAATAAATAAAGTT-----TCAATTTTAAAGATTTAA 3509
Db 2731 TAAATTAATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2790
Qy 3510 ATTTTGAATTCAGAGTTTAAATGATGCTGAATAAGTTATGAATGATTCAGATTTGCA 3569
Db 2791 ACGAATTTGTTATTAATAATCGTTATTAATTAATAACGATATTTTATTAATAATTTA 2850
Qy 3570 ACAGAAATGTCATGATGATACATATCAAAACAATGATCAAAATAATATTCGCTAG 3629
Db 2851 AAATTCGAAATATTTTACGAAAAAATAATTCGTCGAAAAAATAAATAATTCGAAAAACG 2910
Qy 3630 CAAGAGAAAGATTTGAATTAACAGAAACAATGTTTAAACCTTAAATAATCTTAAATAT 3689
Db 2911 AAAAAAAAAAGTTTAAATTTTACGAAACGTAAATTTTAAACGATTAATTTTAAATAA 2970
Qy 3690 TTTGATGATATTTTCTGTAAGAGAGATATCATATCTTCAAAAAAAATCTCATTT 3749
Db 2971 AATTAATAAATAAATAATTAATAAATAATTAATAAATAAATAAATAAATAAATAAATA 3030
Qy 3750 CAGATTAATAATATGTT-ATCAATCTTTTACCAAGTATGTTTGTGCTCATAGTTGAT 3808
Db 3031 AATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 3090
Qy 3809 TGTAACTCGCTCTTACCAATATAGTTTAAATGTTTAAATGTTTCAAGACTTTTACAA 3868
Db 3091 TTTTACGCGTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 3150

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QY 3869 AATAAAATATATAGGTGAAATTTGGGCTTAAAGCAAAAT 3915
DB 3151 AATGGTTTATATATATTTTAAATATATATTTTATATATAAT 3197

RESULT 9
US-10-312-841-2
; Sequence 2, Application US/10312841
; Publication NO. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/MO
; CURRENT APPLICATION NUMBER: US/10/312, 841
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (379615)
; US-10-312-841-2

Query Match 1.9%; Score 80.2; DB 6; Length 3673778;
Best Local Similarity 43.5%; Pred. No. 0.0096;
Matches 467; Conservative 0; Mismatches 596; Indels 8; Gaps 2;

QY 1386 TATCCTTTTCTCCACAAATCATTCACAGAGAAATCTGCTCGATCACTT 1445
DB 1132183 TATACGTTGTAAGTAGGTTTAAATTTTATTTTAAATTTTATAGTTT 1132242
QY 1446 CAGCAAAATTAATCTAATTTTGGTATTTTGTCAAGTTCTGCTTTAAGTGAT 1505
DB 1132243 TTTTAAATATTAATATATATATATATATATATATATATATATATAT 1132302
QY 1506 TATTTGGTACTATATATGTGTGATATACATCAAGCTAATCAATATGATCT 1565
DB 1132303 GTTTATATTAATATATATATATATATATATATATATATATATATAT 1132362
QY 1566 TCTGCTATCAATATATATATATATATATATATATATATATATATATAT 1625
DB 1132423 TATATATATATATATATATATATATATATATATATATATATATATAT 1132482
QY 1686 TAAAGCATTAATGCTCTATGAGAAATTTTGTATATATATATATATATAT 1745
DB 1132483 TTAATTAATTTTAAAGATATATATATATATATATATATATATATAT 1132542
QY 1746 AATATCAGCTATATATCTCATTTAAAGATATATATATATATATATATAT 1805
DB 1132543 TGAATTTGTATTTGTAAATATATATATATATATATATATATATATAT 1132602
QY 1806 ATTAAGGTTTGTCTTTAAAGGTACACCGCTTAATCATTAAGAAATATTA 1865
DB 1132603 TTTTATAGATATATATATATATATATATATATATATATATATATAT 1132662
QY 1866 CTTTGATGAAATCCAAAATCTTTTAAACATTAAGAAATTTTCAAGATTTT 1925
DB 1132663 TGTATATATATATATATATATATATATATATATATATATATATATAT 1132722
QY 1926 TAAAGGTATCATTTATGGGTCAATTAATATATATATATATATATATAT 1985
DB 1132723 GAAATATATATATATATATATATATATATATATATATATATATATATAT 1132782
QY 1986 CACATGATGTTTGTATATATATATATATATATATATATATATATATAT 2045
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DB 1132783 TTAATTTTGTATATATATATATATATATATATATATATATATATAT 1132842
QY 2046 CCGTCATCCAGATTTGATATATATATATATATATATATATATATATATAT 2105
DB 1132843 TTAATATATATATATATATATATATATATATATATATATATATATAT 1132902
QY 2106 TGTATATATATATATATATATATATATATATATATATATATATATATAT 2160
DB 1132903 TGAATTTATGTTTATATATATATATATATATATATATATATATATAT 1132962
QY 2161 TTGAAGCAAAATATATATATATATATATATATATATATATATATATAT 2220
DB 1132963 TTTGATATATATATATATATATATATATATATATATATATATATATAT 1133022
QY 2221 CTTTGTTATTTATATATATATATATATATATATATATATATATATATAT 2280
DB 1133023 TTTTATATATATATATATATATATATATATATATATATATATATATAT 1133082
QY 2281 TAAATATATATATATATATATATATATATATATATATATATATATATAT 2340
DB 1133083 TTTATTTTATATATATATATATATATATATATATATATATATATAT 1133142
QY 2341 ACATCTCTCAACATTAATATATATATATATATATATATATATATATAT 2400
DB 1133143 ---GTTTAAATATATATATATATATATATATATATATATATATAT 1133199
QY 2401 AAAAAATGCAAAAGATATATATATATATATATATATATATATATATAT 2453
DB 1133200 AATATATATATATATATATATATATATATATATATATATATATAT 1133252

RESULT 10
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication NO. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/MO
; CURRENT APPLICATION NUMBER: US/10/312, 841
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
; US-10-312-841-1

Query Match 1.9%; Score 79.4; DB 6; Length 3673778;
Best Local Similarity 41.6%; Pred. No. 0.013;
Matches 1013; Conservative 0; Mismatches 1401; Indels 23; Gaps 7;

QY 1124 TTTGGCGGTGTGACTTTTCTTATGTCGTTTGTGACTAATTTTTCAGAGTG 1183
DB 1712880 TTTTGGATTTTAAAGTTGGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1712939
QY 1184 GTGTATCAAGAAATATATATATATATATATATATATATATATATATATAT 1243
DB 1712940 TTTGATTTGTATATATATATATATATATATATATATATATATATAT 1712999
QY 1244 GAAATGATATATATATATATATATATATATATATATATATATATATAT 1303
DB 1713000 TTAATATATATATATATATATATATATATATATATATATATATAT 1713059
QY 1304 TTTATATAT -CATTAACAAATCAAGAGAGAGAGGACCTTGTGCTTATG 1362
DB 1713060 TTAATATATATATATATATATATATATATATATATATATATATAT 1713119
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QY 1363 CCTCCCTAAACAAGTCTCCCACTCTCTTTTCTTCAACAAATCATTCACAGAG 1422
DB 1713120 AATATATATATTAAGCATTAATTTATTTGTGTGTGTATATATATTTTATATAT 1713179
QY 1423 AAAATCTGTCTGTATCACTTTCATGCAAAATTAACATAATTTTGTGAT 1482
DB 1713180 AAT 1713239
QY 1483 AGTCTTGTCTGTAT 1542
DB 1713240 TTTAT 1713299
QY 1543 AGCTAAATCAAT 1602
DB 1713300 TTTAT 1713359
QY 1603 AGCTAAATCAAT 1662
DB 1713360 AAT 1713419
QY 1663 ACATATGCTACAGAGTGTATATATATATATATATATATATATATATATATATAT 1722
DB 1713420 TAT 1713479
QY 1723 GTATATGTAACACTCGTGGGAAAAAATCCAGCTAATATGCTCATTTAAAG-GATATAT 1781
DB 1713480 AAT 1713539
QY 1782 GATTTAAATGCTTTAATCAT-----TAAATTAAGGTTTTTGTCTTTAAAGGTAC 1833
DB 1713540 TAT 1713599
QY 1834 CACCGCTTAATCATCTATAGGAATATATATATATATATATATATATATATATATAT 1893
DB 1713600 AATTTAT 1713659
QY 1894 TAACACATAGAAATTTTTCAGACTTTTAAATTAAGGATATATATATATATATATATAT 1953
DB 1713660 AAT 1713719
QY 1954 AATATGTTCCAGTAAGTTTGAGGTTTAAACATGAATGTTTTTGAATTTAAAAAC 2013
DB 1713720 AAT 1713779
QY 2014 ACATTAATTTTCTAGAT 2073
DB 1713780 TAT 1713839
QY 2074 AATCTGAAAAATTTTTTTTTTCTGAAATCTGTTTAAATCTCTGCTGCACTCTG 2133
DB 1713840 TATTTAT 1713899
QY 2134 CAGCAATTTGACCAACGACTATACATATGAAAGCAAAATATCCACGAGGATGATGAGG 2193
DB 1713900 TAT 1713959
QY 2194 TTGATCTCCACATTCATATCTTTTGTCTTTGT-TATTTATGAAAACAAAATTTATCA 2252
DB 1713960 AATTTTAT 1714019
QY 2253 GGAAGAAAAAGTTCTCTCTAGGATATAGTAAAGTAAAGCAAAATTTAAATCTT 2312
DB 1714020 TATTTAT 1714079
QY 2313 AGTTAATGATTTACTATCTTCAAACTTACATC---CTTCAACATTAATTTGATCAAT 2369
DB 1714080 AATTTAT 1714139
QY 2370 TTTTATTTTTTTTACTAACTATCTTCAAAAAAATGCAAAAGAGATATATATAT 2429
DB 1714140 TTTTAT 1714199

QY 2430 AAGTCAAGTAATTAAGATGATGAGGTATCTTTCAGCAAAAAGCGCCGATGAGGTGT 2489
DB 1714200 TAT 1714259
QY 2490 CTATATCTTACATTTACAGCTGGGTTTGCGAGACATCATAGGCGCTACGATATATTTGAGCT 2549
DB 1714260 AATTTTAT 1714319
QY 2550 TTACTGTAGTAAGGCTTTTACATATCTATGTTAGTCTGACTGACAAACAAAT 2609
DB 1714320 AAT 1714379
QY 2610 CCAATTCGTAACATATATCAAAATCTACTAGTACTAGT-----TACGCTAGCTAT 2661
DB 1714380 TAT 1714439
QY 2662 ACATGCTTTTTCGCAATTTCTTAACTATATCAACAAACTTGAATGTTTGTG 2721
DB 1714440 AAT 1714499
QY 2722 TATTTATCTTAAACCAAGTTTGAATTTGTGCAATGGGAGTACACTAGTCCCTT 2781
DB 1714500 TAT 1714559
QY 2782 TTTCCCAAAATATATCTCTTACATGACCGGTTAAAGTATTTAAACCAAAATTTTAA 2841
DB 1714560 ATGAT 1714619
QY 2842 TTTGTTGCTGAAGGTAACAAATGTCATATATATAGACAGCATGCTTATATCAAAATTA 2901
DB 1714620 AAT 1714679
QY 2902 TGTTCGATGTTATGAAATCAAAATTAATTAATGCAATTTAGCGCTGCTGTTTATATAG 2961
DB 1714680 TAT 1714739
QY 2962 TTGGAAGATTAATGAATTAATAAATGAATTAACAAAGATACAGACTATATATATGCGGCTC 3021
DB 1714740 TATTTAT 1714799
QY 3022 AATTAAGCCGTCGACCAAAAGTTTCTGCTGATTTCTAGCGTCGTCATATAGAAATTTTG 3081
DB 1714800 AAT 1714859
QY 3082 GACTTTTCTCACCTTTATATGACTCTGATATATTTTGTGGAATATATATATATATATAT 3141
DB 1714860 TAT 1714919
QY 3142 TCGTAT 3201
DB 1714920 AAT 1714979
QY 3202 AATTA-ATTTGATTTAAACTTTTGTGTTTGAATGACTCATACAAAGTTTAAAGTTT 3260
DB 1714980 AAT 1715039
QY 3261 GATGATATCCAAATTTACAAAATGTTTCGAGAGTGGCTGCAATGTCACCAACATCGT 3320
DB 1715040 AAT 1715099
QY 3321 ACCAATCTGATGAGGTTTAT 3380
DB 1715100 AAT 1715159
QY 3381 GAAACATCTAAATTTCTTTTAAATTAAGTTAAAGATCTTGAATTTTCTGTGATTT 3440
DB 1715160 TTTAT 1715219
QY 3441 TAAACCAAGGTTTCAATCTCTTTCGACACAAAAAAGTTTCAATATATATAT 3500
DB 1715220 TAT 1715279
QY 3501 AGAATCTAAATTTTGTGAGTTCAAGGTTTAAATGATA 3537

Db	1715280	TTTTATATATATTATTTATATATATATTTTATATATA	1715316
		RESULT 11	
		US-10-312-841-1/C	
		/ Sequence 1, Application US/10312841	
		/ Publication No. US20030186277A1	
		/ GENERAL INFORMATION:	
		/ APPLICANT: Epigenome AG	
		/ TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC	
		/ FILE REFERENCE: E01/1208/MO	
		/ CURRENT APPLICATION NUMBER: US/10/312,841	
		/ CURRENT FILING DATE: 2002-12-30	
		/ NUMBER OF SEQ ID NOS: 2	
		/ SEQ ID NO 1	
		/ LENGTH: 3673778	
		/ TYPE: DNA	
		/ ORGANISM: Artificial Sequence	
		/ FEATURE:	
		/ OTHER INFORMATION: chemically created genomic DNA (Homo sapiens)	
		/ FEATURE:	
		/ NAME/KEY: unsure	
		/ LOCATION: (3294164)	
		US-10-312-841-1	
		Query Match	
		Best Local Similarity 41.7%; Pred. No. 0.033;	
		Matches 111; Conservative 0; Mismatches 1528; Indels 27; Gaps 9;	
Qy	1580	AATTACACCACATTAGCTATTCAGACTAATAATTAACCAACATTCTCTATTCATTTTT	1639
Db	1715550	AATCAAATTTTCTAAAAAACAAACCTAATAAATATATATATATATATATATATATAT	1715491
Qy	1640	ATATGCTTAATAATAACAACCGACTATAGGCTACAGGTGGATATAGGCATTATTC	1699
Db	1715480	AT	1715431
Qy	1700	CTTCTAGTCGAAGCATTTTTTGTATGATATACACTCGTGGAATAAAAATCCAGCCTAA	1759
Db	1715430	AAAATATATCATATATAATATATCATATATAATATATATATATATATATATATATATA	1715371
Qy	1760	TATGCTCATTTAAAGATTAATTGATTAAATGCTTAAATCATTAATAAAAGGTTTGG	1819
Db	1715370	TA	1715311
Qy	1820	CTTTTAAAGTGACACGCCGTTAATTCATCATTAGAGATAATTAACCTTGATCGAAT	1879
Db	1715310	TAAATA	1715251
Qy	1880	CCAAATATCTTTTTTAAACATTAAGAAATTTTCGACTTTTAAATPAAGGTATCAT	1939
Db	1715250	AT	1715191
Qy	1940	ATTGGGTCATTAATATATGTTTCCAAGTAAAGTTGAGTTTAAACACATGAATGTTT	1999
Db	1715190	AAAATA	1715131
Qy	2000	TTGATTTTAAAAAACCATTAATTTTCTAGTATATACATTTTTR-ACCGTCATCCAGA	2058
Db	1715130	TA	1715071
Qy	2059	TTGTATATATAGTACAAATCTGAAAAACATTTTTTTTTTCTTGAATCTGTGTTAATCTC	2118
Db	1715070	TA	1715011
Qy	2119	TCTGCTGATATCTTGACAGCATTTTGACCAACGACTATACATATTTGAAAGCAAAATATCA	2178
Db	1715010	TA	1714951
Qy	2179	CCAGGATGATAGGTTATGATCCGACATTCATATCTTTGTCTTGTATATATGAAA	2238
Db	1714950	TATATCAAAATA	1714891

OY	2239	ACAAATTTTTCGCGAAAAAACGTTCTCTCTACGTGGATAGATTAAGATTAATAC	2238
Db	1714890	ATATATATATATATAAATATATATATAAATATATATATAAATATATATATAT	1714831
OY	2299	AAATTTTA-----ATACCTAGTTAAGTATTTCTATCTTCAAACTTACATCCTTCAA	2352
Db	1714890	AAATTTTAAAT	1714771
OY	2353	CATTATATGTATCAATTTTATTTTTTTTCTAACTACTCCATPAAAAATGCAAA	2412
Db	1714770	AAATATCATATATAAAATATATATATATAAATATACATTTAAAAATATATATAC	1714711
OY	2413	AGAAAGATATATATTTTAAGTCAAGTAATTAAGATGAGATGGGTGATCTCGCAAAA	2472
Db	1714710	ATATATAAATATACATATAAATAATACATATAAATAATATAT- --AAATATATATATAA	1714654
OY	2473	CGGCGCGTAGAGGTGCTTATCCTACATTAACGCTGGGTGGCGAGACATCAGGCG	2532
Db	1714653	ATATATATATATAAATATATATATATATAAATATATATATAAATATATATATAAAT	1714594
OY	2533	CTACGATATTTGAGCTTACTGTACGTAAAGCTTTAATATCTAGTACTGCTACTG	2592
Db	1714593	ATATCATAAATATATATATATATAAATATATACATAAAATATATATAATATATATAA	1714534
OY	2593	TACAAACAAAACAAATCAATTCGTACATATATACAAATATACATCTAGTACTAGAT- TA	2651
Db	1714533	AAATATATATATAAATATATATATAAATAATATATATAAATATATATATAAATAATATATA	1714474
OY	2652	CGTACGTATCATCGCTTTTTCGCAATTTCTTAACTATCTATACAAACCTTGAT	2711
Db	1714473	AAATATATATAAATATATATATAAATATATATATAAATAATATATATAAATAATATATATAA	1714414
OY	2712	GTTTGTTTGTAATTATCTTAAACCAAGTTTGAAT- TGTCATTTGGAGCTACCTC	2770
Db	1714413	TATATATATAAATAATATATAAATAATATATATATAAATAATATATATAAATAATATATA	1714354
OY	2771	TAGTCCCTTTTCCCAAAATATATCCCTTACATCGACGCGTTAAAGATTTAAAA	2830
Db	1714353	TAAATATATATATAAATATATATAAATATATATAAATATATATATAAATAATATATAAATA	1714294
OY	2831	ACAAATTTTAATTTGTGCTGAAAGTACAACATGTCAATATATAGACAGCATCGTT	2890
Db	1714293	TATATATAAATAATATATATATAAATAATATATAAATAATATATATAAATAATAT	1714234
OY	2891	TATACAAATATATGTCATGTTATTTGAAATCAATATATAATACGATTTAGCGTCACT	2950
Db	1714233	AAATATATATATAAATATATATATAAATAATATATAAATAATATATAAATAATATATAAAT	1714174
OY	2951	TGTTTATATAGTTTGAAGATTAATGAATATAAATAATGAATTCAAAGATTCAGAGCTATA	3010
Db	1714173	ATATATAATATATATATAAATAATATATATATAAATAATATATATAAATAATATATATAAATA	1714114
OY	3011	TATGTCCGGTCATTTAGACCGGTGACCAAAAGTTTCGTGTAATTTCTACGTCGTCAAT	3070
Db	1714113	TATATATAAATAATATAAATAATATATATAAATAATATATAAATAATATATATAAATAAT	1714054
OY	3071	A-----AGAAATTTTGACCTTTCTTGACCCCTTTATGAACTTCGTATAGTTTGG	3122
Db	1714053	ATATATAAATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATA	1713994
OY	3123	TCCGATATATATTTGATTCGATTCGATTTTTTTTGTCTAATAATGATACGTAAATTCACG	3182
Db	1713993	TATATAATATATATATAAATAATATATAAATAATATATATAAATAATATATAAATAATAT	1713934
OY	3183	ATTAAGAAGACTCTCTTTTATTTTATATTTGATTTAAAACTTTGTTTGGAAAAATGACTCA	3242
Db	1713933	ATATATAAATATATATAAATAATATATATAAATAATATATAAATAATATATAAATAAT	1713874
OY	3243	TACCAAGGTTAAAGTTTGAATGATCCATTTTACAAAATGTTTGGAGAGTGGCTTCGA	3302
Db	1713873	ATATATATATAAATAATATATATATATAAATAATATATAAATAATATATATAAATAATATA	1713814

OY	3817	GTCTTGGCCCTAAGTTC	TAAAGTTTAAAGTTTCAAAAGACTTACAAAAAATAAT	3876
Db	240	ATTTAATTGNNAAAAA	TTATTTAAAAAAATTTATTTATTTAAACNATGTGATAAAAA	181
OY	3877	AATAATAAGTGAATTTGTAGGCGCTAAAGCGCAAAATTAATAATAATAAGTAAG	3936	
Db	180	NNTTAAAAAATAGNATTNTTGAANTTAATAATTTTAAATATCTTTNAATTAATAAANTTAT	121	
OY	3937	AAAGCTCTTTCATATAAGACACAGATCCCAACGGAATTCAAACAGCAAT	3987	
Db	120	TNATTTTAAAAA	AAAAAAAAAAAAAACCGNNGNNGNCNAGATTCNT	70

RESULT 13

```

US-10-311-455-1842
Sequence 1842, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPERBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Cytosine Methylation of Cytosine Methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1842
LENGTH: 13573
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1842

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[illegible]

QY	3462	TCTTAGACCAAAAAAAAAAGGTTTCAATTATTAAGAATCTAAATTTTGAGTT	352
Db	4162	TTTTTTTAGTAGATATATATATTTTGTAGTTTTCATTTAAAGTAGATATATGTGTTT	4222
QY	3522	CAAGATTTAATGATAGCTGAAAAGTTATGCAATGTTGCAAGTTTG	3567
Db	4222	TTGGTTTATTTGAATATTTAGAGGTATTTGAGAGATTTATTAATGG	4267

RESULT 14

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US-10-239-676-54/C
Sequence 54, Application US/10239676
Publication No. US20030082603A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIENSBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIORITY APPLICATION NUMBER: PCT/EP01/03368
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIORITY FILING DATE: 2001-04-06
2000-04-06
2000-04-07
2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 54
LENGTH: 17421

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	ORGANISM:	Artificial Sequence
	FEATURES:	
	OTHER INFORMATION:	chemically treated genomic DNA (Homo sapiens)
	FEATURE:	
	NAME/KEY:	unsure
	LOCATION:	(167, 1832..1833, 1836..1837, 1842, 1848, 1852, 1857, 1859..1860).
	FEATURE:	
	NAME/KEY:	unsure
	LOCATION:	(2953, 4024, 4630, 4733, 4767, 8161, 8189, 8200, 9142..9143)
	FEATURE:	
	NAME/KEY:	unsure
	LOCATION:	(9147, 9153, 9168, 9170, 9173, 10243, 10340, 10394, 11996)
	FEATURE:	
	NAME/KEY:	unsure
	LOCATION:	(12002, 12005, 12012, 12102, 13715, 13717, 16077, 16097, 16907)
	US-10-239-676-54	
	Query Match	1.7%; Score 71.6; DB 5; Length 17421;
	Best Local Similarity	44.9%; Pred. No. 0.036;
	Matches 311; Conservative 0; Mismatches 379; Indels 2; Gaps 1;	
Dy	3271 AATTTCAAAAAATCTTGCAGAGTGCGTTGAGTGTCCACACACTGTAACAATCGT	3330
Db	9128 AAATTCAAAATTACTCCACATAATCTTCAACGCTATTATTATACAACTTTTTAACTTTA	9069
Dy	3331 ATGGCTTATTATTAGGTTTTTTCTCTTTCCATNGCTTTATATATGAACACTCT	3390
Db	9068 ACCATTTTATTAATAATATATATACTTTTAATTTACAACTCTTAAAAACAAATATATTT	9009
Dy	3391 AAATTTCTTTTTTAAATTAAGTTAAGAATCTGAAATTTCTGTGATTTTAAACCAAG	3450
Db	9008 AAATATCTTTATCATATTTCTTACTTAACATTCATACATCTTCTTTTATAAAATATATCTTTC	8949
Dy	3451 TTTTCATTTCTTTCAGCACCACAAAAAAAAAAAAAGTTTCCAATATTAAAGATCTTAA	3510
Db	8948 AAATCATCTATCCACTAAAAAATAAACAAATACATATCTCTATTTATTAACATATAAAA	8889
Dy	3511 TTTTTCAGTTCAAAGACTTTAATGATAGCTGAAAA--GTTATGATCATTTGCAAGTTTGC	3568

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Db 8888 ATTATTTTAAABAACTAAATCTTAATACAAACCTTACCAAAATCTATTTTTC 8829
Qy 3569 AACAGATGTCATGTAGTACATACAAACATGATCAAAATTAATTCGTGCTTA 3628
Db 8828 AATATATTTTCCAAATTTTAAATCTTAATCTTAATCTTAATCTTAATCTTAAT 8769
Qy 3629 GCAGAGAAACGATGAAATTAACAGACAACTTAAACACTTAAATCTTAAATTA 3688
Db 8768 AAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8709
Qy 3689 TTTTGTAGTATATTTTCTGTAGAGAGATATCTTATCTTAAACAAAAATCTAT 3748
Db 8708 AAAATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8649
Qy 3749 TCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3808
Db 8648 TAATTAACCTACAACTTAATTAATTAATTAATTAATTAATTAATTAATTA 8589
Qy 3809 TGTAACTGCTCTTACCATATAGTCTTAAGTTTAAATGTTTCAAGACTTTACA 3868
Db 8588 AAAAAAATCATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8529
Qy 3869 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3928
Db 8528 AATTTATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8469
Qy 3929 AAGTAAAGAAACGCTTTTCTCAATAGAACAC 3960
Db 8468 AATTACCAAACTAATCTCAAAAAATTAATTAAC 8437

RESULT 15
US-10-240-453-56/c
; Sequence 56, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIERENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
; TITLE OF INVENTION: with DNA Transcription
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240.453
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 56
; LENGTH: 17421
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (167, 1832, 1833, 1836, 1837, 1842, 1848, 1852, 1857,
; LOCATION: 1859, 1860)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2953, 4024, 4630, 4733, 4767, 8161, 8189, 8200, 9142, 9143)
; FEATURE:
; NAME/KEY: unsure
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; LOCATION: (9147, 9153, 9168, 9170, 9173, 10243, 10340, 10394, 11996)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12002, 12005, 12012, 12102, 13715, 13717, 16077, 16097, 16907)
US-10-240-453-56
Query Match
1.7%; Score 71.6; DB 6; Length 17421;
Best Local Similarity 44.9%; Pred. No. 0.036;
Matches 311; Conservative 0; Mismatches 379; Indels 2; Gaps 1;
Qy 3271 AATTACAAATATGTTTTCAGAGTGGCTTGCATGCTTACCAACATCGTACCACTCGT 3330
Db 9128 AATTTCAATTTCTCCACATTAATCTTCAACGCTTATTAATTAATCTTTTAACTTTA 9069
Qy 3331 ATGCTTTATTAATAGTTTTCTCTTTTCCAAATGCTTAAATTAATGAACCTCT 3390
Db 9068 ACCATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 9009
Qy 3391 AATTTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3450
Db 9008 AATATCTTATCATATTTCTTACTTAACATTCATCATCTTCTTTTAAATTAATTA 8949
Qy 3451 TTTTCAATCTTCTTACCAAAAAAATTAATTAATTAATTAATTAATTAATTAAT 3510
Db 8948 AATTCATCTATCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8889
Qy 3511 TTTTGTAGTCAAGGTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3568
Db 8888 AATTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8829
Qy 3569 AACAGATGTCATGTAGTACATATCAAAAATCATCATCAAAATTAATTCGTGCTTA 3628
Db 8828 AATATTTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8769
Qy 3629 GCAGAGAAACGATGAAATTAACAGACAACTTAAATCTTAAATTAATTAATTA 3688
Db 8768 AAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8709
Qy 3689 TTTTGTAGTATATTTTCTGTAGAGAGATATCTTAAATTAATTAATTAATTAAT 3748
Db 8708 AAAATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8649
Qy 3749 TCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3808
Db 8648 TAATTAACCTACAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8589
Qy 3809 TGTAACTGCTCTTACCATATAGTCTTAAGTTTAAATGTTTCAAGACTTTACA 3868
Db 8588 AAAAAAATCATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8529
Qy 3869 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3928
Db 8528 AATTTATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8469
Qy 3929 AAGTAAAGAAACGCTTTTCTCAATAGAACAC 3960
Db 8468 AATTACCAAACTAATCTCAAAAAATTAATTAAC 8437
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Search completed: February 27, 2006, 20:09:19
Job time : 2131 secs

C	1	75.4	1.6	171486	12	US-11-121-086-105	Sequence 105, Appl
C	2	69.6	1.6	171486	12	US-11-121-086-105	Sequence 105, Appl
C	3	63.6	1.5	39794	12	US-11-098-666-8737	Sequence 8737, Appl
C	4	62.8	1.5	173602	12	US-11-121-086-25	Sequence 25, Appl
C	5	62.6	1.5	5132	8	US-10-240-708-73	Sequence 73, Appl
C	6	62.6	1.5	173602	12	US-11-121-086-35	Sequence 25, Appl
C	7	60.2	1.4	119036	8	US-10-995-561-13314	Sequence 13314, A
C	8	59.6	1.4	5582	8	US-10-240-708-63	Sequence 13314, A
C	9	58.8	1.4	26772	8	US-10-995-561-13313	Sequence 13313, A
C	10	58.8	1.4	54946	8	US-10-995-561-13479	Sequence 13479, A
C	11	58.2	1.4	139054	12	US-11-121-086-96	Sequence 96, Appl
C	12	58	1.4	5360	8	US-10-240-708-65	Sequence 65, Appl
C	13	58	1.4	139054	12	US-11-121-086-96	Sequence 96, Appl
C	14	57.4	1.3	6499	12	US-11-011-332A-91	Sequence 91, Appl
C	15	56.6	1.3	6070	8	US-10-240-708-10	Sequence 10, Appl
C	16	56.6	1.3	6669	8	US-10-240-708-6	Sequence 6, Appl
C	17	56.4	1.3	5552	8	US-10-240-708-74	Sequence 74, Appl
C	18	56.4	1.3	26772	8	US-10-995-561-13313	Sequence 13313, A
C	19	56.4	1.3	54946	8	US-10-995-561-13479	Sequence 13479, A
C	20	55.8	1.3	6499	12	US-11-011-332A-77	Sequence 77, Appl

C	21	55	1.3	49979	8	US-10-995-561-13445	A	Sequence 1443, A
C	22	54.8	1.3	28636	12	US-11-011-132A-151	A	Sequence 151, A
C	23	54.8	1.3	28636	12	US-11-011-132A-155	A	Sequence 155, A
C	24	54.8	1.3	49979	8	US-10-995-561-13443	A	Sequence 1343, A
C	25	54.8	1.3	194553	12	US-11-098-686-8738	A	Sequence 8738, A
C	26	54.4	1.3	1230	6	US-09-925-065A-17661	A	Sequence 77681, A
C	27	54.4	1.3	1230	6	US-09-925-065A-177662	A	Sequence 77682, A
C	28	53.2	1.3	611	6	US-09-925-065A-1788158	A	Sequence 788158, A
C	29	53.2	1.3	1230	6	US-09-925-065A-17683	A	Sequence 77683, A
C	30	53.2	1.3	1230	6	US-09-925-065A-17684	A	Sequence 77684, A
C	31	53.2	1.3	6106	8	US-10-240-708-49	A	Sequence 13, A
C	32	53.2	1.3	6106	8	US-10-240-708-49	A	Sequence 13, A
C	33	52.8	1.2	582	6	US-09-925-065A-126874	A	Sequence 726874, A
C	34	52.8	1.2	6866	8	US-10-240-708-20	A	Sequence 20, A
C	35	52.6	1.2	6317	8	US-10-240-708-11	A	Sequence 11, A
C	36	52.4	1.2	20317	8	US-10-995-561-13460	A	Sequence 13460, A
C	37	52.2	1.2	11049	8	US-10-240-708-22	A	Sequence 22, A
C	38	52.2	1.2	10550	8	US-10-995-561-13235	A	Sequence 13235, A
C	39	52	1.2	600	8	US-10-750-185-305	A	Sequence 305, A
C	40	52	1.2	600	8	US-10-750-623-305	A	Sequence 305, A
C	41	52	1.2	1528	8	US-10-750-185-50461	A	Sequence 50461, A
C	42	52	1.2	1528	8	US-10-750-623-50461	A	Sequence 50461, A
C	43	52	1.2	6306	8	US-10-240-708-50	A	Sequence 50, A
C	44	51.6	1.2	677	6	US-09-925-065A-667264	A	Sequence 667264, A
C	45	51.6	1.2	10467	8	US-10-240-708-1	A	Sequence 1, A

ALIGNMENTS

```

RESULT 1
US-11-121-086-105
; Sequence 105, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KRISTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138, 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 105
; LENGTH: 171486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-105

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Query Match	1.8%;	Score 75.4;	DB 12;	Length 171486;
Best Local Similarity	43.0%;	Pred. No. 0.039;		
Matches 894; Conservative	0;	Mismatches 1161;	Indels 22;	Gaps 10;

QY	1785	TTAAATGCTTAAATCATATTAATAAAGTTTTGCTTTAAAGTTACACCGCTTAAT	1844
Db	15684	TAAATTTAAATGTTATATATATATATATATATATATATATATATATATATAT	15748
QY	1845	TCATCATTTAGAGAAATATTAACCTTTGATCGAAATTCGAAATTAAGCTTTTAAACATAAG	1904
Db	15744	ATGTAAAT	15808
QY	1905	AAATTTTCAGCATTTTAAATATAAGGATCAATTTATGGTTCGAATTAATATGTTTCA	1964
Db	15804	ATATTAACATTAATATATTTATATTAATTAATATATATATATATATATATATATATAT	15868
QY	1965	CGTAAAGTTTGAGGCTTTAACCAATGAAGCTTTTGAATTTAAATAAACACATATAATTT	2024
Db	15860	CATATATTTTATATATTAATTAATATATATATATATATATATATATATATATATATAT	15924
QY	2025	CTAGTAAATTAACATTTTTAAACGTCATCCAGATTTGAATTAAGTGACAAATCTGAAAC	2084

Db	15920	ATAATATTAAATTAATTAATAATAATAATTAATTTGATATATTATTAATAATTAATAATAA	15979
Qy	2085	ATTTTTTTTTCTTGAATCTTGTTAAATTCCTCTGCTGCACACTTCGAGCAATTTGA	2144
Db	15980	TAAATATTAAATATTTTATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT	16039
Qy	2145	CCAAAGCACTATAC-ATATTGAAAAGCAAAATATCCACAGGAGATAGAGGTTAGATCCA	2203
Db	16040	CAGCCCACTACACTCCAGCCTGGGTGCAGAGCAAGACTCTGCTCTTAATATTAATATA	16099
Qy	2204	CATTCAATATCTTTTGTCTTGTATTAATTAAGAAAAACAAATATTTATCGAAAAAAACG	2263
Db	16100	TATATATATTAATTAATTAATTTGTATTAATAATATTAATTAATTAATTAATTAATTA	16159
Qy	2264	TTCTCTCTAGAGGTAAAGTATAGATATAACAAATTTAATACCTTAGTAATGAT	2323
Db	16160	TCTATATATTAATTAATTAATTAATTAAGATATATATTAATATATGATATATTAATATAT	16219
Qy	2324	TTACTATCTTCAAACTTACCATCTTCAACATTTATTTGATATCAATTTTATTTTTTTTA	2383
Db	16220	AATATATTAATTAATTAATTAATTTATTAATTAAGTTATTAATTAATTAATTAATTA	16279
Qy	2384	CTAAACTACTTCCACTAAAAAAATGCAAAAGAGATATATTTTAAGTCAAGAAATTT	2443
Db	16280	TATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16339
Qy	2444	AAAGATGATGGGTGATTCCTTCAGCAAAACGGCGGTAGAGGTGCTTATCTCATTA	2503
Db	16340	TATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16395
Qy	2504	CAGCTGGGTGTGGCAACATCATAGGCGCTACGTATATTGAGCTTACTGTAGATAA	2563
Db	16396	TATTTGATTAATTT--ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16452
Qy	2564	GCTTAACATATCTAGTAGTCTGCTCACTGTATCAACAAACAAATCCAAATTCGATACAT	2623
Db	16453	TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16512
Qy	2624	ATATATCAAAATACACTAGTACTAGATTAACGCTACGTATACATCGCTTTTTCGCAATTTTC	2683
Db	16513	ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16572
Qy	2684	TAAACTATCTATACAAACAACCTTGAATGTTTGTGTATTTATCTTAAACCAAGTT	2743
Db	16573	ATATATTAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16631
Qy	2744	TTGAATTTGTGATGGAGCTACACTCTACTCCCTTTTCCCACAAATATATCTCCTTA	2803
Db	16632	TATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16691
Qy	2804	CATCGACCGGTAAAGTATTTAAACCAACAAATTTTAATTTTGTGTGAGGTACAAACA	2863
Db	16692	TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	16751
Qy	2864	TGTCACTATATAGAGACAGCATCGTTTATACAAATTAATGTTGATGTTATTGAAATCA	2923
Db	16752	TATATATGCTTAAATTAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTA	16811
Qy	2924	AATTAATTAATGCAATTAAGCACTCATGTTGTTTAATTAATTTGGAAGATATGAATTA	2983
Db	16812	TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16871
Qy	2984	AATGAATTTCAAAGGATACAGAGCTATATATGTCGGGCTCAATTAAGCCGTGACCAAAAGT	3043
Db	16872	ATACATTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	16931
Qy	3044	TTGCTGTAATTTCTACGCTGC-GTCATAAGAAATTTGGACTTTTCTTCACTTTAT	3102
Db	16932	TAGATATATTAATTAATTAATTTGTATATTTATTAATGATGATATATTAATTAATTAATTTGT	16991
Qy	3103	GAACTTCTGTATAGTTTTTGTGGATTAATTAATTTGTATTTGTAATTTTTTGTCTTAA	3162
Db	16992	ATATTTTAATTAATGATATTAATTAATTTGTATTTTAAATTAATTAATTAATTAATTAAT	17051

QY	3165	TAAATGATACGTAATTCACACATTAAGAAAGCTCTTTTATTTAAATTTGATTTAAAGCTT	3222
Db	17052	ATTATATATATTTATAGATATATATATTAATTTTATATATTTATATATATTAAGATATATATTAAT	17111
QY	3223	TTGTTTTTGGAAATATGACTACATACACAAGGTTAAAGTTGATGGTATCCAAATTTACAAAAA	3282
Db	17112	ATATTATATATTTATATATATTTATAGATATATATATATATTAATATTTATATATATATAG	17177
QY	3283	TGTTTCAGAGTGGCTTCAGAGTCTCTACACACATGTACCAACTGTATGGTTATTA	3342
Db	17172	ATATATATTAATATATTTATATATTTATATATATTAATATATATATATATATATATTTATATA	17231
QY	3343	TTAGTTTTTTTTCTCTTTTCCAAATGCTTTTAAATATGAAACACTCTAAATTTCTTTT	3402
Db	17232	TTTATATATATATAGATATATATATATATATTTATAT -ATTATATATTTATAGATATATATA	17299
QY	3403	TTAAATATAGTTAAGAACTCTGGAATTTCTGTGATTTTAAACCAAGTTTCAATCTT	3462
Db	17291	ATATATTTATATATTTTATATTTTATGTAATATATTAATATTTATATATTTATATATTA	17358
QY	3463	CTTGACCAAAAAAAGGTTTCAATATTTAAGA-----ATCTAAATTTTGG	3517
Db	17351	TGATATATATTAATATATTTATTAAGATTATATATTTATAGATATATATATATATATTTAT	17411
QY	3518	AGTTCAAGAGTTTAAATGATAGCTGAAAAGTTATGAATGATTCGAACTTTCACAACAGATG	3577
Db	17411	AGATTTATATATTAATATAGATATATATTAATATTTATAGTTTATATATATATATATATAT	17470
QY	3578	GTGCATGTATACATATCAAAAACATGCAATCAAAATTAATATTCGCTGCATGACAAAGAA	3637
Db	17471	ATTAATATTA -TTTATATGATTTATATATTTATAGATATATATTAATATATATTTATATAGATTTAT	17522
QY	3638	ACGATTTGAAATTAACAGAACAAATCGTTAACCTTTAAATCTTGA -ATAATTTGTAG	3696
Db	17530	ATATTATAGATATATATTAATATATTTATATGATTTATATATATATATATATATATATATAT	17589
QY	3697	TGATATATTTCTGTAAGAGAGAGGTATCATATCTTACAAAAAAAACATTTACAGATTA	3756
Db	17590	ATTATATATATATATATATATATATTAATATTTATATATTTATATATATATATATATATAT	17643
QY	3757	AATATATTTGCAATCGTTACCAAGATGTTTTCTGTCATCACTGTAATTTGTAACTC	3816
Db	17650	ATTAATATATTTATATATTTATATATATTTATATATATATATTAAGATATATTAACAATATATATATTTAT	17709
QY	3817	GTCCTTACCAATATAGTTCTAAAGTTTAAAGTTTT	3853
Db	17710	ATATTATAGATATATTAATATATTTTATATATTTATAT	17746

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RESULT 2
US-11-121-086-105/C
; Sequence 105, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138, 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105
; LENGTH: 171486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-105

Query Match      1.6%; Score 69.6; DB 12; Length 171486;
Best Local Similarity 43.3%; Pred. No. 0.3;

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Qy	2589	ACTGTACAAACAAAACAAATCCAATTGCTACATATATACAAATATCTACTACTGAC	2648
Db	16675	TATATTATATATGTAAT	16616
Qy	2649	TTAGCGTACGATACATCGCTTTTGGCAATTTCTTAACTATCTATACAAACCTGG	2708
Db	16615	ATTAT	16555
Qy	2709	AATGTTTGGTTTGGTATATTTATCTTAAACCAAAAGTTTGAATGTGCATTGGAGCTACAC	2768
Db	16555	ATATTATGATATATATATATATATATGTTTAAATATATATAT - ATAAATATATATTAATA	16495
Qy	2769	TCTAGTCCCTTTTTCGCCAAATATCTCTTACATGACCGGTAAAGTATTTAAAC	2828
Db	16497	TGTAT	16433
Qy	2829	CAACAAATTTTATTTTGTGCTGAGGTACAAACATGTCATATATATAGACAGATCG	2888
Db	16437	ATTAT	16373
Qy	2889	TTTATACAAATTAATGTCGATGTAATGGAATCAATATATATATATATATATATATAT	2948
Db	16378	ATTAT	16313
Qy	2949	CTTGCTTAAATAGTTTGGAAATATGAAATATATATATATATATATATATATATAT	2986
Db	16318	ATATGTTAT	16281

RESULT 3

US-11-098-686-8737/c

Sequence 8737, Application US/11098686

Publication No. US2006024696A1

GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

TITLE OF INVENTION: FROM LAMSONIA INTRACELLULARIS AND METHODS OF USING

FILE REFERENCE: 09531-12801

CURRENT APPLICATION NUMBER: US/11/098, 686

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: PCT/US03/31318

PRIOR FILING DATE: 2003-10-01

PRIOR APPLICATION NUMBER: US 60/416,395

PRIOR FILING DATE: 2002-10-04

NUMBER OF SEQ. ID NOS: 11433

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8737

LENGTH: 39794

TYPE: DNA

ORGANISM: *Lamsonia intracellularis*

US-11-098-686-8737

Qy	2881	CAGCATGTTTATATCAATATATGTTGCAGTATTGGAATCAATATATATATATATAT	2940
Db	33848	CAGATTTCTTTTGTATATATATATATCAAAAAGCATTTGTATATACATATATATATATAT	33789
Qy	2941	GGCAGCTACTTGGTTTATATGTTTGGAAAGTATATGAATATATATATATATATATAT	3000
Db	33788	TAGAT	33728
Qy	3001	CAGAGCTATATATATGCGGTCATTTAGAGCCGTACCAAAAGTTTGTGATATTTCTAC	3060
Db	33728	TATATGTAT	33669
Qy	3061	GGTGGCAT	3120
Db	33668	TCAAT	33609

Query Match 1.5%; Score 63.6; DB 12; Length 39794;

Best Local Similarity 45.1%; Pred. No. 1.8;

Matches 399; Conservative 0; Mismatches 474; Indels 11; Gaps 4;

Qy	3121	TCGCGATTATATATTTGGTATGTAATTTTGTGTTCTAAATAAGATACGTAATAATCA	3180
Db	33608	T-----TGTATATCTTAATATATAGATTAAATTAGTAGATTAAATAAATAAGTTTAA	33553
Qy	3181	CGATTAAAGAAAGACTCTCTTTTAAATTAATTTGATTTAAAATTCTTTGTTTGGAAAAATGACT	3240
Db	33552	CTATCGTTAAAAAGCTCTCTCTCTCTTCTTCTAAAAAGAAAGAAAGATATATATTTCTTAG	33493
Qy	3341	CATACACAGGTTAAAGTTTGATGATGATCCATTTCAAAAATGTTTCGAGAGTGGCTTC	3300
Db	33492	GTCGCTATTTTATTTAAATTTAG-TGTATACAAAAAGCAAAAAAACTATCTCACTAGCTTAG	33434
Qy	3301	GAGTGTCCTAACCACTCGTACCAACTCGATAGGGTTTATATAGTCTTTTCTCTT	3360
Db	33433	CTAGTTAAGTATTTAACTCTGTTTGGTGTGCAAGTTTACTAGTTACTCTAGTGGCTGT	33374
Qy	3361	TTTCCAAATGCTCTTATATATGAAACCACTCAAAATTCCTTTTAAATTAGGTTAAGAT	3420
Db	33373	TAAAGATTTTATTTATGCTAGTAAGTAATTAATAATATCAATATATATATATTAATCT	33314
Qy	3421	CTTGAATTTTCTGTGATTTTAAACCAAGGTTTCAATCTCTTA--GCAAAAAAAA	3478
Db	33313	TATTAAGTCAATATATACATATATATTAATAATATGCAATAGCTATCTTTGAATAACTAGAA	33254
Qy	3479	AAAAAGGTTTTCATATATTAAGAACTAAATTTTGTAGTTCAGAGGTTTAAATGATAG	3538
Db	33553	AGTATATTAACAACCTATTTATATATAGTAACTATTTAATCTATTAATAACAATTAATAA	33194
Qy	3539	CTGAAAAGTATGATGATTTGCCAAGTTTGCAACGAATGGTCGATGTAGTACATCAAA	3598
Db	33193	ATTATATCAAAAAGCAATTAAGTGTGTAGATAACAGTATGTATTTATTCAAAAGTTAAA	33134
Qy	3599	----AACATGATCAAAATAATATTCGTGCTTAGCAAGAAAGCATTTGAATAAACAAG	3654
Db	33133	TATATAAATTTATACATATATATATTTTATTTTGCTTATTTATGCAATTTCAACTTATAAA	33074
Qy	3655	AACATCGTTAACCACTTAAAAATCTTAGATATATTTGTAGTGAATATTTCTGTAGAA	3714
Db	33073	GATATATTAACAAGTATTTATTAACCGTTAGATTAACCTTATAGTATATATTTATATTAGT	33014
Qy	3715	GAGAGGATATCATATCTTACAAAAAAAACATCTTCAGATTAATA	3758
Db	33013	TTTATATATACGTTAAATCATATATATTTAGTTTATATATA	32970

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RESULT 4
US-11-121-086-25/c
; Sequence 25 Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 173602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-25

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	Query Match	Similarity	1.5*	Score 62.8	DB 12	Length 173602
Best Local	489	Conservative	42.9%	Pred. No. 3.3	637	Indels 14
						Gaps 3
Qy	2150	GACTATACATATTGAAAGCAAAATATCCACCGAGATGATGGGTAGATCCACATTC				2209
Db	137337	GAAAT				137278

[illegible][illegible]

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RESULT 5
US-10-240-708-73/c
/ Sequence 73, Application US/10240708
/ Publication No. US20050282157A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIRENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
/ FILE REFERENCE: 5013.1012
/ CURRENT APPLICATION NUMBER: US/10/240,708
/ CURRENT FILING DATE: 2002-10-03
/ PRIOR APPLICATION NUMBER: PCT/EP01/03971
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: DE 10019058.8
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 98
/ SEQ ID NO 73
/ LENGTH: 5152
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-73

Query Match      1.5%; Score 62.6; DB 8; Length 5152;
Best Local Similarity 43.5%; Pred. No. 1.6;
Matches 399; Conservative 0; Mismatches 504; Indels 13; Gaps 2;

QY 3052 AATTTCACGGTCGGTCAATGAAGAATTTGGACCTTTCTCCACCCTTTATGAACCTTCG 3111
DB 3973 AATTACAACGCCATCATATATCTATTTATATATATTAATTAATAAATTAATTAATTTT 3914
QY 3112 TATAGTTTGTGGATTTATATTTGATTCGATATTTTGTTCCTATATATGATAC 3121
DB 3913 TTTATTTTATTTTATTTTATTTTAAATTTTAACTTATTTAAATCAAAAAATATATAT 3854
QY 3172 GTAAATTCAGATTAAGAAGACTCTTTTATTTATTTGATTTAAACCTTTGTTTTG 3231
DB 3853 ACAATTTTATTCACGAAACATTAATCAATTTCTTTAACACCTTAATTTAAATTA 3794
QY 3232 GAATGACCTCATACACAAGTTAAAGTTGATGATTCATTTACAAAATGTTTCGAG 3291
DB 3793 AATATATTTTCAATTAATTTCTTTTAAACAATCTTTAATTTAATAAATTTTCCC 3724
QY 3292 AGTGCCTTCAGTCTCTACACCATCGTACCACTCGTATGGGTTATTTATGTTTT 3351
DB 3733 ATT--TTTAAAAAAATTTCTTAAATATCTTAAATATTTAAAAACAATTAACATA 3676
QY 3352 TTTCTCTTTTCCATGCTTTTAAATGTAACACTTAATTTCTTTTAAATTTAG 3411
DB 3675 TTTCTATTTCTTACAACTATTTTACTTATTTCTTTACATTTACAAAAATCAAAAT 3616
QY 3412 GTTAAATCTTGAATTTTCTGTGATTTTAAACCAAGTTTCAATTTCTTTAGACA 3471
DB 3615 TTTTAAACGATTTATTTCCAACTTTATTTTAAATTAATTAATTAATCTCTTAAACT 3556
QY 3472 AAAAAAAGTTTGAATTTTCAATTTATTAAGATCTTAATTTTGTGCTCAAGTTTA 3531
DB 3555 AAAAAAATATAAAACACTTATTTCTTAATTAACATATATTAATTTAAATTAACCTT 3496
QY 3532 ATGATACCTGAAGTATGATGCAAGTTTGCAAGATGCGATGATGATGCA 3591
DB 3495 AAAAAATCCTTTATTTACTTATTTCTTTT-----TTCTTTTCTTAAT 3447
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QY 3592 TATCAAAAACATGATCAAAAATATAATTCGTCTAGCAAGAAACGATGAATTA 3651
DB 3446 ACTAAAAATTAATCGTAAAAATTAACCTTTATTAATTAACGAAATTAATTAAT 3387
QY 3652 CAGAACATCGTTAACACCTTAATAATCTTGAATTAATTTGTGATTAATTTTCTGTA 3711
DB 3386 TACACAAAATATTTTAAATATTAATTAACATTAATTTTCAAAACATTAATCAATA 3327
QY 3712 AGAGAGAGTATCATCTTACAAAAAAATCAATTCAGATTAATTAATGTTGTCGA 3771
DB 3326 ACTTAAAAATTAATTTATTAATAAACTATCAAAACATTTATTAACCTTCAATTA 3267
QY 3772 TCGTACCAAGTATGTTTGTCTGTCATCACTGTTATTTGTAATGATCGCTCTACCAT 3831
DB 3366 ATCTTCAAAATTTTATCTCTGACAAATTTATCTGATTCATTTCTATTTATTTATCT 3207
QY 3832 AGTTCTAAGTTTAAATGTTTTCAAAGACTTAAACAAAATTAATTAATTAAGTGA 3891
DB 3206 AAACAAACATTTTAAATTTCTTCAAAAAAAATTTATCTCCATTTTAAACCTTA 3147
QY 3892 TTTGTAGGCTTAAAGGAAAAATTAATAATTAATAAAGTAAGAAACGCTTTCTCA 3951
DB 3146 TATCTAATATTAATTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 3087
QY 3952 TAAGAACACGATCC 3966
DB 3086 AATATTAATTAATTC 3072

RESULT 6
US-11-121-086-25
/ Sequence 25, Application US/11121086
/ Publication No. US20050266459A1
/ GENERAL INFORMATION:
/ APPLICANT: POULSEN, TIM S.
/ APPLICANT: NIELSEN, KIRSTEN V.
/ TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
/ FILE REFERENCE: 09138.6000-00000
/ CURRENT APPLICATION NUMBER: US/11/121,086
/ PRIOR FILING DATE: 2005-05-04
/ PRIOR APPLICATION NUMBER: 60/567,570
/ PRIOR FILING DATE: 2004-05-04
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 25
/ LENGTH: 173602
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-121-086-25

Query Match      1.5%; Score 62.2; DB 12; Length 173602;
Best Local Similarity 43.4%; Pred. No. 4.1;
Matches 540; Conservative 0; Mismatches 688; Indels 15; Gaps 5;

QY 2525 CATGAGGCTTACGATATTTGAGCTTACTGTACGTAAAGCTTTAAACATATCTAGT 2584
DB 136040 CATACATTTTACATATTTTATATATATATATATATATATATATATATATAT 136099
QY 2585 TCTCAGTGTCAAAACAAACAAATCCAAATTCGTA-----ACATATATACAAATACT 2639
DB 136100 TATTTTATATATATATATATATATATATATATATATATATATATATATAT 136159
QY 2640 AGTACTAGATTAAGCTACGATACATGCTTTTTCGAAATTTCTAACTAATCTATACA 2699
DB 136160 ATATAGATATATATATATATATATATATATATATATATATATATATATATA 136219
QY 2700 ACAAACTTGATGTTGTTTGTATATTAATCTTAACCAAGTTTGAATTTGCAATGG 2759
DB 136220 AATATATATATATATATATATATATATATATATATATATATATATATATAT 136279
QY 2760 GAGCTACACTGATGCTCCCTTTTCCCAAAATTAATCTCTTAATCATGACCGGTTAAG 2819
DB 136280 TATATATATATATATATATATATATATATATATATATATATATATATATAT 136338
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QY 2820 TATTTAAACCAAAATTTTAAATTTGCTGAAGGTAACAACATGTCACATATATAGAG 2879
    |||||
DB 136339 TATTTATATATATATATATATATATATATATATATATATATATATATATATAT 136398
QY 2880 ACAGCATCGTTTATACAAATATATGT-TCGATGTTATGGAAATCAATATATATACGAT 2938
    |||||
DB 136399 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 136458
QY 2939 TAGCGACTCCTGGTTTATAGTTTGAAGATATGAATATAAAAATGAAATCAAGGA 2998
    |||||
DB 136459 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 136518
QY 2999 TACAGAGCTATATATGCGGGTCATTAGACCGTGACCAAAAGTTTCGTCGTAATTC 3058
    |||||
DB 136519 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 136571
QY 3059 ACGGTGCGTCATTAAGAAATTTTGACCTTTTCAACCTTTTATGAACCTTCGTATAGTT 3118
    |||||
DB 136572 AAATATATATATATATATATATATATATATATATATATATATATATATATATAT 136631
QY 3119 TTTGTGCGATTAATATATTTGATTCGTAATTTTGTGTTCTTAATATAGTAAAT 3178
    |||||
DB 136632 TGTATATATATATATATATATATATATATATATATATATATATATATATATAT 136691
QY 3179 CACGATAGAAGAAAGCTCTTTTATTTTAAATTTGAAACCTTTGTTTGGAAATGA 3238
    |||||
DB 136692 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 136751
QY 3239 CTCATACACAAAGTTAAAGTTGATCAATTTACAAAAAGTTTCGAGAGTGCCT 3298
    |||||
DB 136752 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 136811
QY 3299 TCGAGTGCTACACACATGTCACCACTGTAAGGTTATATATAGTTTCTTC 3358
    |||||
DB 136812 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 136871
QY 3359 TTTTTCGAATGCTCTTATATATATGACACCTCAATTTCTTTTAAATTTAGGTTAAGA 3418
    |||||
DB 136872 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 136931
QY 3419 ATCTGGAATTTCTGTGATTTTAAACCAAGTTTCAATCTCTTACACAAAAAAA 3478
    |||||
DB 136932 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 136991
QY 3479 AAAAAAGTTTCAATATATTAAGAACTCAATTTTGTGAGTTCAAGAGTTTAATGATAG 3538
    |||||
DB 136992 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 137051
QY 3539 CTGAAAAAGTTAT-GAATGATTGCAAGTTTGCAACAGAAAGTGTGATGATACATATCA 3597
    |||||
DB 137052 GTATATATATATATATATATATATATATATATATATATATATATATATATAT 137111
QY 3598 AAACATGCAATCAAAATATATATTCGTGCTTACAGAGAAACATGGAATTAACAGAAC 3657
    |||||
DB 137112 CATATATATATATATATATATATATATATATATATATATATATATATATATAT 137171
QY 3658 AATCGTTAACCACTTAAAAATCTTGAATATATTTGAGTGATATATTTCTGTAAGAGAG 3717
    |||||
DB 137172 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 137231
QY 3718 AGGTATCATCTTACAAAAAAAACCTCATTTGAGATTAATA 3760
    |||||
DB 137232 TATGTAATATATATATATATATATATATATATATATATATATATATATATATAT 137274

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RESULT 7

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US-10-995-561-13314
; Sequence 13314, Application US/10995561
; Publication No. US20050272054AI
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

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; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DEFLECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13314
; LENGTH: 119036
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(119036)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-995-561-13314

Query Match 1.4%; Score 60.2; DB 8; Length 119036;
Best Local Similarity 43.8%; Pred. No. 7,6;
Matches 263; Conservative 0; Mismatches 338; Indels 0; Gaps 0;

QY 3331 ATGGGTTTATATATAGTTTCTTCTTCTTCCATGCTTTATATATGAACCACTCT 3390
    |||||
DB 31272 ATGGCTGATTAATAGATTTATATATATATATATATATATATATATATATATATATAT 31331
QY 3391 AAATTTCTTTTAAATATAGTTAAGATCTGAATTTTCTGTGATTTTAAACCAAG 3450
    |||||
DB 31332 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 31391
QY 3451 TTTTCAATCTCTTACACAAAAAAAAGTTTTCATTTATTAAGATCTTAA 3510
    |||||
DB 31392 TTTTATATATATATATATATATATATATATATATATATATATATATATATATAT 31451
QY 3511 TTTTGTAGTCAAGGTTTATATGATGCTGAAGAAATTTATGATGATTTGCCA 3570
    |||||
DB 31452 AAATTAAGATTTTATATATATATATATATATATATATATATATATATATATATAT 31511
QY 3571 CAGAATGTCGATGTCATATCAATCAAAAACATGCATCAAAATATATATTCGTGCTTACG 3630
    |||||
DB 31512 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 31571
QY 3631 AAGAGAAAGATTTGAATTAACAGAAACAATCGTTAACACTTAATAATCTTACAAATATAT 3690
    |||||
DB 31572 AAATTAAGATTTTATATATATATATATATATATATATATATATATATATATATAT 31631
QY 3691 TTGTATGATTAATTTTCTGTAGAGAGATATCATATCTTACAAAAAAAATCTCATTTTC 3750
    |||||
DB 31632 AAATTAAGATTTTATATATATATATATATATATATATATATATATATATATATAT 31691
QY 3751 AGATTAATATATATGTTGCCAATCGTTACCAAGTATATGTTTGTGCTGTCATCATGTTGATTG 3810
    |||||
DB 31692 TATTAATATATATATATATATATATATATATATATATATATATATATATATATAT 31751
QY 3811 TAACGTGCTCTTACCATATAGTTCTAAAGTTTAAATGTTTCAAGACTTTTACAAAA 3870
    |||||
DB 31752 GATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 31811
QY 3871 TAAATATATATATATATATATATATATATATATATATATATATATATATATATAT 3930
    |||||
DB 31812 AGATTAATCTTAATATATATATATATATATATATATATATATATATATATATATAT 31871
QY 3931 G 3931
    |||||
DB 31872 G 31872

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RESULT 8

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US-10-240-708-63
; Sequence 63, Application US/10240708
; Publication No. US20050282157AI
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian

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/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13479
/ LENGTH: 54946
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-13479

Query Match 1.4%; Score 58.8; DB 8; Length 54946;
Best Local Similarity 43.5%; Pred. No. 10;
Matches 354; Conservative 4; Mismatches 446; Indels 10; Gaps 2;

QY 157 TTATTCATTTAATGAGTTCATTAATATATATACGCTGACATTCACCAACCAATGTTT 216
DB 2585 WTAT 2644
QY 217 CTGCTTTTATGATGATGCTTATATGTTGCACTTGATTATAGATA--CTATATAAA 273
DB 2645 AATAA 2704
QY 274 GGTATTTTAAATCCGTACCCATACAAAGTGACCAAAAGAGATCCATGGTTTGT 333
DB 2705 ATATATATATGAAATCTATATATATATATATATATATATATATATATATATAT 2764
QY 334 GTTATCTTGTGGTTAACAGATATATATATATATATATATATATATATATATATAT 393
DB 2765 AT 2824
QY 394 TAAATATATTTGGAACCAACCTTAATATATGTTGAGTGTCTTCACTGCTCACTGTTCA 453
DB 2825 AT 2884
QY 454 GAATATCTGCTGTTATCTTACTTGAACCTGAAAGTTGATATACATTAACCGTGAATAT 513
DB 2885 TATATATATATATATATCTTATACATTAATCAATATATATATATATATATATAT 2944
QY 514 TTAAACGCGTACATTAACAGATGATCGATCAATCAATCAATATATATATATATATAT 573
DB 2945 TTTTAT 3004
QY 574 CAAGATGAGATGACTCTACAGATATATACACAGCTTAAGATTTGTCACAGAGATCGAA 633
DB 3005 TAT 3064
QY 634 AATATGATTTCTAATCAT-----TTAAAAAGATATGATTTCAAGTTACGATGATAT 686
DB 3065 ATATTAATAATTAAT 3124
QY 687 TACCATTCAGCAGTATGATACATACATATATTTTGTGTTTACCGATATATGAAT 746
DB 3125 AT 3184
QY 747 GAAATATGTTGTAAATAATATGTTTATCTAAATCTGTTTATGTTTAACTATATATAT 806
DB 3185 TAAAT 3244
QY 807 GTCTTCCGATGTAATGAAACAAACCTGTAATACAAATATGTTAAGCCATTCGAT 866
DB 3245 TAT 3304
QY 867 TAAAAATCCACGGGTATGTAATCCCTCAGAAATATATGTTAAGCTTCAATATTTGCTT 926
DB 3305 ATATTTTAT 3364
QY 927 TAGATTTAGTAAAGTTTGAGACAAATATATATATATATATATATATATATATATAT 960
DB 3365 AAT 3398

RESULT 11
US-11-121-086-96/c
; Sequence 96, Application US/11121086

/ Publication No. US20050266459A1
/ GENERAL INFORMATION:
/ APPLICANT: POULSEN, TIM S.
/ APPLICANT: NIELSEN, KIRSTEN V.
/ TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
/ FILE REFERENCE: 09138.6000-00000
/ CURRENT APPLICATION NUMBER: US/11/121,086
/ CURRENT FILING DATE: 2005-05-04
/ PRIOR APPLICATION NUMBER: 60/567,570
/ PRIOR FILING DATE: 2004-05-04
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 96
/ LENGTH: 139054
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-121-086-96

Query Match 1.4%; Score 58.2; DB 12; Length 139054;
Best Local Similarity 43.6%; Pred. No. 16;
Matches 402; Conservative 0; Mismatches 513; Indels 6; Gaps 3;

QY 1536 ACATCCAGCTAATCAATATATGATCTCTGCTTATCATTAATATACACCACTTAG 1595
DB 44338 AATGATATGACATGAAAGTTGAGTCCAGTATGATTAATTAATTAATTAATCC 44279
QY 1596 CTATGCAAGCTAATAATTAACCAACATCTCTTATCATATTTTATATGATATATATA 1655
DB 44278 CCTATTTTCAAT 44219
QY 1656 ACAACGACTATATGCTACAGAGTTGTTATTAAGCATTAATGCTCTTA--GTGCAAG 1712
DB 44218 TAAACATATTAAT 44159
QY 1713 GAATTTTTTGTATGATTAACCTGCTGGAACCAATCAAGCTTAATATGCTCATTTAA 1772
DB 44158 AATATATTTAT 44099
QY 1773 AGATATATGATTTAATGCTTTAATCATTAATAATTAAGTTTGTCTTTAAGTTTA 1832
DB 44098 TATATTAATGTAATTAATTAACATGATTAATTAATTAATTAATTAATTAATTA 44039
QY 1833 CCACGCTTAATTCATCATTTAGAGAGATATTAACCTTGAATGCAATTCGCAATTA 1892
DB 44038 AATATGTTTAAT 43979
QY 1893 TTAAACATTAAGAAATTTTCAGATTTTAAATTAAGGTAATTAATGCTTCAATA 1952
DB 43978 AATTAATATATATATTAACGATTAATTAATTAATTAATTAATTAATTAATTA 43920
QY 1953 AATATGTTCCAGSTAAAGTTTGAGGTTTAAACATGAAATGTTTGTATTTAAAAA 2012
DB 43919 ATTAATATATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 43860
QY 2013 CACATTAATTTTCTAGTAATTAACATTTTAAACGTCATCCAGATGTAATTAAGTAC 2072
DB 43859 CATATATATATATATATATATATTAACGTAATTAATTAATTAATTAATTAATTA 43800
QY 2073 AATCTGAAAAACATTTTTTTTCTGTAATCTGTTTAAATCTCTGCTGCAATCTT 2132
DB 43799 TATGTT--ATATATATATATATATATATATTAATTAATTAATTAATTAATTA 43742
QY 2133 GCAGGATTTGACCAACGATATATATGAAAGCAAAATATCCACGAGGATGATAG 2192
DB 43741 ATATATATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43682
QY 2193 GTTAGATCCCACTCAATATCTTTGCTGTTATATGAAAAACAAATATTTATCA 2252
DB 43681 TAT 43622
QY 2253 GGAACAAAAACGTTTCTCTCTAGTGTATATAGATATATATATATATATATATAT 2312
DB 43621 TAT 43562

Qy 2313 AGTAAATGATATTTACTATCTTCAAACTTACCATCTTCAACATTAAATATGATCAATTT 2372
Db 43561 TTTAATTAATACTATATCTTCAATTTTAAATTAATTTAAATTAATGATTAATAATA 43502
Qy 2373 TATTTTCTTACTAACTACTTCCATTAATAAATGCAAAAGAGATATATATTAAG 2432
Db 43501 TAAATTAATATGATGATTAATTAATTAATAAGTAATGGAATGTAATTAATTAATATAT 43442
Qy 2433 TCAAAAGTAATTAAGATGAT 2453
Db 43441 TTTATATATTTTAAATTAATCAT 43421

RESULT 12
US-10-240-708-65
Sequence 65, Application US/10240708
Publication No. US20050282157A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PISENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 65
LENGTH: 5360
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-65

Query Match 1.4%; Score 58; DB 8; Length 5360;
Best Local Similarity 50.6%; Pred. No. 8.4; Indels 5; Gaps 1;
Matches 169; Conservative 0; Mismatches 160; Indels 5; Gaps 1;
Qy 3071 AAGAAATTTTGACCTTTCTTCAACCTTTTATGAAGTTCTGTAATGTTTGTGCGAATTA 3130
Db 1580 AAGAAATTTTTTGTGTTTATGATATTTTGTGTTTATTAATTAATGATGA 1639
Qy 3131 TAAATTTGATTCGTAATTTTGTGTTCTAATAATGATACGTAATTCACGATAGAAA 3190
Db 1640 GATATGCTATTTTGTGTTTGTGTTTGTGTTAAGAAAGTAAATTTGATGATA 1699
Qy 3191 GACTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3250
Db 1700 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1759
Qy 3251 GTTAAAGTTGATGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3310
Db 1760 TATGAGATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1814
Qy 3311 CCACCATGTAACCACTGTAATGTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 3370
Db 1815 GTGCTGATTTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1874
Qy 3371 CTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3404
Db 1875 TGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1908

RESULT 13
US-11-121-086-96
Sequence 96, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 96
LENGTH: 139054
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-96

Query Match 1.4%; Score 58; DB 12; Length 139054;
Best Local Similarity 43.4%; Pred. No. 17; Indels 12; Gaps 3;
Matches 424; Conservative 0; Mismatches 540; Indels 12; Gaps 3;
Qy 2833 AATTTTAATTTTGTGCTGAAGTACAAAGTACATATATAGACAGCATCGTTTA 2892
Db 43405 AATTTAATAAATTTAATGATATTAATAATTAATAATTAATAATTAATAATTAATAATTA 43464
Qy 2893 TACAAATTAATGTCATGATTTTGAATCAATATTAATTAATTAATTAATTAATTAATTA 2952
Db 43465 CATATCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43524
Qy 2953 GTTAAATGTTTGAAGATATGAATAAATAAATTAATTAATTAATTAATTAATTAATTA 3012
Db 43525 TTAATTTAATAAATGAAGATATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 43584
Qy 3013 TGTGCGCATTTAGACCGGTGACCAAAAGTTTGTGTAATTTCTACGTCGTCATTA 3072
Db 43585 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43644
Qy 3073 GAAATTTTGACCTTTCTTCAACCTTTTATGAAGTTCTGTAATGTTTGTGCGATTAATA 3132
Db 43645 TAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 43704
Qy 3133 TATTTGATTCGTAATTTTGTGTTCTAATAATGAATTAATTAATTAATTAATTAATTAATTA 3192
Db 43705 TATGATATA--ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43761
Qy 3193 CTTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3252
Db 43762 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43821
Qy 3253 TAAAGTTGATGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3312
Db 43822 CATATTAATGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43881
Qy 3313 ACCATGTAACCACTGTAATGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3372
Db 43882 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43941
Qy 3373 TTAATTAATGAACCACTTAATTTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTTCT 3432
Db 43942 TTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43996
Qy 3433 GTTGAATTTAACCAGGTTTCAATTTCTTTGCACAAAAAAAGGTTTCA 3492
Db 43997 ATAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 44056
Qy 3493 ATTATTAAGATTAATTAATTTTGAAGTTCAAGGTTTAATTAATTAATTAATTAATTAATTAATTA 3552

Db 44057 TTTAAATTAATAATTTAATACATGTTAATATACATTAATATTAATTAATATAATAA 44116
Qy 3553 ATGATTCAGAGTTTGCACAGAAATGCGATGTAGTACATGCAAAAGCATGCAAAA 3612
Db 44117 ATATATATTTTACATGAATATTTTAAATATAAAATATTTATATAAAATTAATAATA 44176
Qy 3613 TAAATATTCGTGCTTAGCAGAGAAACGATTTGAAATTAACAGAAATCGTTAACCACTT 3672
Db 44177 TATATTTATATATTTTAAATATATATATATTTT---TAAATNGTTTATTTGTATATATAT 44232
Qy 3673 AAAAATCTAGATATATTTTGTATGTATTAATTTCTGTAAAGAGAGATTCATATCTTA 3732
Db 44233 TTATACACAGAAATATCTGTGTGTATACATATATGTAAATATAGGGATTTTATTTGTT 44292
Qy 3733 CAAAAAATCTGATTTGCAATATAATATGTTGTCCAAATCGTTACCAAGTATGTTTGG 3792
Db 44293 TAAATATATTTTCTACTGACGAACTCAAACTCATGTCATATTTAAATTTATATTTTA 44352
Qy 3793 CTGTATCATGTTGTAT 3808
Db 44353 CTGTGAATTTTACTAT 44368

RESULT 14

US-11-011-332A-91
; Sequence 91, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foeckens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimrich, Inko
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitz, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dima
; APPLICANT: Mueller, Volkmar
; APPLICANT: Klueth, Antje
; APPLICANT: Schwope, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR SURVIVAL
; TITLE OF INVENTION: BREAST CELL PROLIFERATIVE DISORDER PATIENTS
; FILE REFERENCE: 47675-99
; CURRENT APPLICATION NUMBER: US/11/011.332A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 10/517,741
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP2004/014170
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: EP 03090432.0
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 04090041.7
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: EP 04090380.9
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: EP 04090127.4
; PRIOR FILING DATE: 2004-04-01
; Remaining Ofseq Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 91
; LENGTH: 6499

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-91

Query Match 1.4%; Score 57.4; DB 12; Length 6499;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 256; Conservative 0; Mismatches 311; Indels 2; Gaps 1;

Qy 3054 TTCTACGGTGGTCAATGAAGAAATTTTGACCTTTCTTCAACCTTTTATGACCTTCTGTA 3113
Db 4263 TTTTAAAGATTTGAATTTGAATTTTGTGAGTTTATGTTGTTGTGATTTG 4322
Qy 3114 TACTTTTGTGCGATTTATATTTTGTATTCGTATATTTTGTGTTTCTAATATGATACGT 3173
Db 4323 TTGATTTAAGTTATATATTTTATTTTATTTTGAATTTTATTTTGTGTTAATTTTAT 4382
Qy 3174 AAATTCAGTAAAGAAAGCTCTTTTATTTTATTTTGAATTTTAAACCTTTTGTGTTTGA 3233
Db 4383 AGATGATGATTTGTATTTTATTTATTTATGATGATTTATTTTAAATGTAATTTT 4442
Qy 3234 AATGACTCATACCAAGTTAAAGTTGATGATTCATTAACAAATGTTTCGAGAG 3293
Db 4443 TATTTTGTGTTTGTATTTATTTATAGATTTATTTGTTATTTATTTATGATTTATTTAT 4502
Qy 3294 TGGCTTCAGTCCACACCACTGACCACTGATGCGTTATTTATAGTTT 3353
Db 4503 ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4562
Qy 3354 TCTTCTTTTCCAAAT--GCTTTATTAATTGAACCACTTAATTTCTTTTAAATTTAG 3411
Db 4563 ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4622
Qy 3412 GTTAAGATCTGAATTTCTGTGATTTTAAACCAAGTTTCAATCTTCTTACACA 3471
Db 4623 TTATATATTTTGTATTTAATTAATTTTAAATTTTAAAGTTTATTTTATTTTATTTAGG 4682
Qy 3472 AAAAAAAGTTTCAATTTAATTAAGATCTAATTTTATTTAGTTCAAGAGTTTA 3531
Db 4683 TGTATATATTTTATTTTGTATTTAGTGAAGGTTAAGTTGATTTGTTGTTT 4742
Qy 3532 ATGATAGCTGAAGATTAATGATTTGCAAGTTTCCACAGATGCGATGATGATGACA 3591
Db 4743 ATTAGAGATGAGATTTGTTATGATTTGTTATTTTGTTTTATGATATGATATGATGAGG 4802
Qy 3592 TATCAAAAACAGCATCAAAATTAATTT 3620
Db 4803 TTTTAAAGGTTTAAATTAATTT 4831

RESULT 15
US-10-240-708-10/c
; Sequence 10, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 16:24:53 : Search time 10413 Seconds
(without alignments)
18960.585 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228

Sequence: 1 gtgcagctctgtgcctcactc.....agaacccaataaagaacc 4228

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hlc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_g881:*

10: gb_g882:*

11: gb_g883:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590.4	14.0	652	9	B62389
2	551.4	13.0	581	10	BX290871 Arabidops
3	394	9.3	437	9	CC056828 SALK_1112
4	387.8	9.2	415	9	BZ379137
5	276.4	6.5	323	9	CC797115 SALK_1129
6	252	6.0	276	11	CR402298 Arabidops
7	249	5.9	300	11	CR402297 Arabidops
8	240.4	5.7	2106	4	CNS0A4GJ
9	226	5.3	418	10	AL769556 Arabidops
10	214	5.1	2315	4	CNS0A2BQ
11	212	5.0	796	9	BH510257 Arabidops
12	200.8	4.7	268	10	AL756782 Arabidops
13	193	4.6	234	10	AL936239 Arabidops
14	157.2	3.7	162	10	AL759737 Arabidops
15	156.4	3.7	192	10	AL759736 Arabidops
16	147.2	3.5	698	9	BH936859 Arabidops
17	142.6	3.4	381	9	BH481919 Arabidops
18	142.4	3.4	673	9	BH676371 Arabidops
19	134.6	3.2	424	3	BP561373 Arabidops
20	124.2	2.9	594	6	CB260786 Arabidops
21	112	2.6	112	9	CC455690 Arabidops
22	110.8	2.6	694	9	BH934314 Arabidops

23	107	2.5	793	9	BH510250
24	104	2.5	318	8	BH451271
25	102.4	2.4	1007	8	DN566957
26	102	2.4	969	10	CL484870
27	98.6	2.3	1101	10	CNS00EVL
28	97.4	2.3	418	10	AL769556 Arabidops
29	97	2.3	1896	10	CG753083
30	93.8	2.2	110	10	AL769557 Arabidops
31	93.8	2.2	1112	1	AJ926321
32	93.2	2.2	1101	10	CNS00EVL
33	92.2	2.2	1101	10	CNS017V2
34	91.6	2.2	1092	10	CNS020K7
35	91	2.2	92	10	AL769520 Arabidops
36	89.8	2.1	1896	10	CG753083
37	87.8	2.1	92	10	AL754990 Arabidops
38	87	2.1	1101	10	CNS0039G
39	86.6	2.0	1103	1	AJ926366
40	85.6	2.0	1103	1	AJ926366
41	85.4	2.0	1007	8	DN566957
42	85.2	2.0	1214	10	CL646783
43	85	2.0	1101	10	CNS00EVL
44	84.8	2.0	96	10	AL754991 Arabidops
45	84.6	2.0	1201	10	CNS0167M

ALIGNMENTS

RESULT 1
LOCUS B62389/c 652 bp DNA linear GSS 21-NOV-1997
DEFINITION T21110TR T21110TR Arabidopsis thaliana genomic clone T21110, genomic survey sequence.
ACCESSION B62389
VERSION B62389.1 GI:2629151
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 652)
REFERENCE Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Linher, K., Golden, K., Berry, K., Granger, D., Sun, E., Wible, C., Adams, M.D. and Venter, J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: T21110TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 652.
FEATURES
source
Location/Qualifiers
1..652
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="T21110"
/sex="hermaphrodite"
/clone_id="TAMU"
/note="Vector: BelobAC11; Site 1: HindIII; Site 2: HindIII; Produced by Rod Wing"
ORIGIN
Query Match 14.0%; Score 590.4; DB 9; Length 652;

Best Local Similarity 97.7%; Pred. No. 3.7e-92;
Matches 643; Conservative 0; Mismatches 6; Indels 9; Gaps 4;

QY 1907 AATTTCAGATTTTAAATAAGGACATTT-ATTGGTCAATAAATTTTCCAC 1965
DB 652 ATTTTCAGATTTTAAATAAGGAAACATTTAAAGGGTTCAATAAATTTTCCAC 593
QY 1966 GTAAAGTTGGAGGTTTAA-CCACATGAATGTTTTTGAATTTAAACACATAAATTTT 2024
DB 592 GTAAAGTTGGAGGTTTAAACCCACATGAATGTTTGAATTTAAACACATAAATTTT 533
QY 2025 C-TAGTAATTACACATTTTAAACCGTCCATCCAGATTGTAATAAGTACAAATCTGAAA 2083
DB 532 CTAGTAATATACATTTTAAACCGTCCATCCAGATTGTAATAAGTACAAATCTGAAA 473
QY 2084 CATTTTCTTTCTGTAATCTTTGAATTTCTCTGCTGCAATCTTGACAGCATTTG 2143
DB 472 CATTTTCTTTCTGTAATCTTTGAATTTCTCTGCTGCAATCTTGACAGCATTTG 413
QY 2144 ACCAAGACTATACATATTGAAAGCAAAATATCCACAGGAGATAGAGGTTAGATCCCA 2203
DB 412 ACCAAGACTATACATATTGAAAGCAAAATATCCACAGGAGATAGAGGTTAGATCCCA 353
QY 2204 CATTCATATCTTTTGTCTTTGTTATTTATGAAAAAATAATTTTACAGAAAAAAACG 2263
DB 352 CATTCATATCTTTTGTCTTTGTTATTTATGAAAAAATAATTTTACAGAAAAAAACG 293
QY 2264 TTTTCTTCTAGTGTATAGTATTAAGTATTAACAAATTTTAATCTTAATGATAT 2323
DB 292 TTTTCTTCTAGTGTATAGTATTAAGTATTAACAAATTTTAATCTTAATGATAT 239
QY 2324 TTACTATCTTCAACTTACATCTTCAACATTAATTTGATTAATTTTATTTTATTA 2383
DB 238 TTACTATCTTCAACTTACATCTTCAACATTAATTTGATTAATTTTATTTTATTA 179
QY 2384 CTAAACTACTTCCATTAATAAATAAGCAAAAGAGATATATTTTAAGTCAAGTAAAT 2443
DB 178 CTAAACTACTTCCATTAATAAATAAGCAAAAGAGATATATTTTAAGTCAAGTAAAT 119
QY 2444 AAAGATGATGGGTATTTCTTCAGCAAAACGCGCGGTAGAGGTGTTATCTCAATTA 2503
DB 118 AAAGATGATGGGTATTTCTTCAGCAAAACGCGCGGTAGAGGTGTTATCTCAATTA 59
QY 2504 CAGCTGGGTTGGGAGACATCATAGGGCTAGATATTTGAGCTTTACTGTAAGTA 2561
DB 58 CAGCTGGGTTGGGAGACATCATAGGGCTAGATATTTGAGCTTTACTGTAAGTA 1

RESULT 2
BX290871/c 581 bp DNA linear GSS 02-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-440605-018216,
genomic survey sequence.
ACCESSION BX290871
VERSION BX290871.1 GI:28889867
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL PUMED 12874060
REFERENCE 2
Rosso, M.G., Li, Y., Strizhov, N., Reis, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUMED 14756321
REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
JOURNAL PUMED 14682050
REFERENCE 4 (bases 1 to 581)
AUTHORS Strizhov, N., Li, Y., Rosso, M.G. and Weisshaar, B.
TITLE Direct Substitution
COMMENT Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T28119. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
Location/Qualifiers
1. 581
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-440605-018216"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (Genbank accession number: M537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

Query Match 13.0%; Score 551.4; DB 10; Length 581;
Best Local Similarity 99.5%; Pred. No. 2.2e-85;
Matches 563; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1095 CGTTTACGTTTGGTCCGTCGCGCACTTTGGGAGTTTGTGACTTTTCTTAATGC 1154
DB 581 CGTTTACGTTTGGTCCGTCGCGCACTTTGGGAGTTTGTGACTTTTCTTAATGC 522
QY 1155 GTTGTGACTAATTTTCTCAGATGAGAGTGAATCAAGAAAATTAATTTGAAAAAGA 1214
DB 521 GTTGTGACTAATTTTCTCAGATGAGAGTGAATCAAGAAAATTAATTTGAAAAAGA 462
QY 1215 AAGAAAAAAGGCAAGAAAACATATTGTGCAAAAGCATTAATGACATTAATTTGGATT 1274
DB 461 AAGAAAAAAGGCAAGAAAACATATTGTGCAAAAGCATTAATGACATTAATTTGGATT 402
QY 1275 ATTAATAAATGATATATGTTGGTGAATTTATATCTTACCAAAATTAAGAAAGA 1334
DB 401 ATTAATAAATGATATATGTTGGTGAATTTATATCTTACCAAAATTAAGAAAGA 342
QY 1335 GAGAGGAGCCTCTGCTGTTATGATTTCCCTCTAAACAAGCTCCGACTATCTTTT 1394
DB 341 GAGAGGAGCCTCTGCTGTTATGATTTCCCTCTAAACAAGCTCCGACTATCTTTT 282
QY 1395 TTACTTCAACAAATCATTCACAGAGAAATCTGTCGTGATCATTTTCAGAAA 1454
DB 281 TTACTTCAACAAATCATTCACAGAGAAATCTGTCGTGATCATTTTCAGAAA 222
QY 1455 TTAACTAAATTTTGGTATTTTGTCAAGTTCTTGCTGTTTAATGCTAATTTGGTA 1514
DB 221 TTAACTAAATTTTGGTATTTTGTCAAGTTCTTGCTGTTTAATGCTAATTTGGTA 162
QY 1515 ATACTATATGATGATATACATCAAGCTAATCAATTAATGATCTCTTGCTTAT 1574

Db 161 ATACTATATGTGTGATATACATCCAGTAATCAATAATGATCTCTTCT-CTTAT 103

Qy 1575 CAATAAATTACACCACTTACTATCAAGTAATAATTACACACATTTCTTATCA 1634

Db 102 CAATAAATTACACCACTTACTATCAAGTAATAATTACACCACTTCTTATCA 43

Qy 1635 TTTTATATGTGTATTAATAAACAAC 1660

Db 42 TTTTATATGTGTATTAATAAACAAC 17

RESULT 3
CC056828 437 bp DNA linear GSS 02-APR-2003
LOCUS SALK_111232.51.45.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_111232.51.45.x, genomic survey sequence.

ACCESSION CC056828
VERSION CC056828.1 GI:29476492
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 437)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES
Location/Qualifiers
1..437
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_111232.51.45.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN
Query Match 9.3%; Score 394; DB 9; Length 437;
Best Local Similarity 95.4%; Pred. No. 4.3e-58;
Matches 417; Conservative 0; Mismatches 16; Indels 4; Gaps 1;

Qy 2334 CAACCTTACATCTTCAACATTAATATGATCAATTTTATTTTACTAACTACT 2393

Db 1 CAACCTTACATCTTCAACATTAATATGATCAATTTTATTTTACTAACTACT 60

Qy 2394 TCCACTTAAAAATGCAAAAGAGATATATTAATGCAAGTAATTAAGATGAT 2453

Db 61 TCCACTTAAAAATGCAAAAGAGATATATTAATGCAAGTAATTAAGATGAT 120

Qy 2454 GGGGATTTCTTACAAAGCGGCGTAGAGGTCTTATCCATTAAGCTGGGTT 2513

Db 121 GGGGATTTCTTACAAAGCGGCGTAGAGGTCTTATCCATTAAGCTGGGTT 180

Qy 2514 GTGCGACATCATAGGGCCCTACGTATATTGAGCTTACTGATGAAGCTTAACAT 2573

Db 181 GTGCGACATCATAGGGCCCTACGTATATTGAGCTTACTGATGAAGCTTAACAT 240

Qy 2574 ----ATCTAGTTAGTTCTACCTGACAAACAAACAAATTCATTTGTAACATATATAC 2629

Db 241 TGCAGAGTTTAAAGCAACACTGTACAAACAAACAAATTCATTTGTAACATATATAC 300

Qy 2630 AAATACTACTAGTACTGATTAAGTACGTAACATGCTTTTGGCAAAATTTCTAACT 2689

Db 301 AAATACTACTAGTACTGATTAAGTACGTAACATGCTTTTGGCAAAATTTCTAACT 360

Qy 2690 AATCTATACAAACAACTGAAATGTTGTTGTTGTAATTTATCTTAACCAAGTTTGAT 2749

Db 361 AATCTATACAAACAACTGAAATGTTGTTGTTGTAATTTATCTTAACCAAGTTTGAT 420

Qy 2750 TGTGCAATTTGGAGCTAC 2766

Db 421 TGTGCAATTTGGAGCTAC 437

RESULT 4
B2379137 415 bp DNA linear GSS 26-NOV-2002
LOCUS SALK_112909.37.05.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_112909.37.05.x, genomic survey sequence.

ACCESSION B2379137
VERSION B2379137.1 GI:25470664
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 415)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES
Location/Qualifiers
1..415
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_112909.37.05.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN
Query Match 9.2%; Score 387.8; DB 9; Length 415;
Best Local Similarity 96.9%; Pred. No. 5.2e-57;
Matches 408; Conservative 0; Mismatches 7; Indels 6; Gaps 1;

Oy	2146	AAAGACATATCATATTGAAAGCAAAAATATCCACGAGGATGATRGGTTAGATCCACA	2205
Db	1	CAAGGACATATCATATTGAAAGCAAAAATATCCACGAGGATGATRGGTTAGATCCACA	60
Oy	2206	TTCAATATCTTTTGCTTTGTTATTTATGAAAAACAATATTTATTCAGGAAAAAAGCGTT	2265
Db	61	TTCAATATCTTTTGCTTTGTTATTTATGAAAAACAATATTTATTCAGGAAAAAAGCGTT	120
Oy	2266	TCTTCTCTAGTGTATATAGTATATTAACAAATTTTAATCTTAGTTAGTAAATTT	2325
Db	121	TCTTCTCTAGTGTATATAGTATATTAACAAATTTTAATCTTAGTTAGTAAATTT	174
Oy	2326	ACTATCTTCAAACTTACCATCTCTTCAACATTAATTTATGCAATTTTATTTTTTACT	2385
Db	175	ACTATCTTCAAACTTACCATCTCTTCAACATTAATTTATGCAATTTTATTTTTTACT	234
Oy	2386	AAACTACTTCCATTAATAAAAAATGCAAAAGAGATATATTTTAAGTCAAAAGTATTTAA	2445
Db	235	AAACTACTTCCATTAATAAAAAATGCAAAAGAGATATATTTTAAGTCAAAAGTATTTAA	294
Oy	2446	AGATGTATGGGTGATTTCTTCAGCAAAAACGGGGCGGTAAAGTGTCTTATCTCAATTACA	2505
Db	295	AGATGTATGGGTGATTTCTTCAGCAAAAACGGGGCGGTAAAGTGTCTTATCTCAATTACA	354
Oy	2506	GCTGGGTTGTGGACAGATCATATAGGGCGCTTACGTATATTGAGCTTTACGTACGTAAGC	2565
Db	355	GCTGGGTTGTGGACAGATCATATAGGGCGCTTACGTATATTGAGCTTTACGTACGTAAGC	414
Oy	2566	T 2566	
Db	415	T 415	

RESULT 5

LOCUS	CC/97115	323 bp	DNA	linear	GSS 01-JUL-2003
DEFINITION	SALK_144490.54.40.x Arabidopsis thaliana TDNA insertion lines				
DEFINITION	Arabidopsis thaliana genomic clone SALK_144490.54.40.x, genomic survey sequence.				

ACCESSION	CC797115
VERSION	CC797115.1
KEYWORDS	GSS.
SOURCE	<i>Arabidopsis thaliana</i> (chale cress)
ORGANISM	<i>Arabidopsis thaliana</i>

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 323)	Alonso, J.M., Leisase, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab, C., Jeske, A., Karner, M., Kim, C.J., Parker, H., Prednis, L., Shih, P., Zimmerman, J. and Ecker, J.R.	A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL
COMMENT
Aradiopsis genome
Unpublished (2001)
Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10310 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel.: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckere@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

```

FEATURES
    source
        1. 323
            location/Qualifiers
                /organism="Arabidopsis thaliana"
                /mol_type="Genomic DNA"
                /ecotype="Col-0"
                /db_xref="taxon:3702"
                /clone_id="SALK_144390.54.40.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines"

```

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html

Query Match	Best Local Similarity	6.5% 89.5%	Score 276.4	DB 9	Length 323
Matches 289	Conservative	0	Mismatches 34	Indels 0	Gaps 0
Qy	2524	TCATAGGGCCCTACGTAATATTGAGCTTTACTGTACGTAAAGCTTTTAACATATCTAGTTAG	2583		
Db	1	TCATAGGGCCCTACGTAATATTGAGCTTTACTGTACGTAAAGCTTGACGCCGACCCGTCAA	60		
Qy	2584	TTCTCACTGTACCAACAAAACAAAATTCGAATTGGTAACATATATACAAATACTACTAGTA	2643		
Db	61	CCAACANTGTACNAACAAANANNATCCAAATTCGTAAACATATATACCACTACTACTANTTA	120		
Qy	2644	CTAGATTACGCTACGTATACATGCGCTTTTCCGAAATTTCTAAACCTAACTCTATACAA	2703		
Db	121	CTAATATTACCCCTACNTATATCTTCCTTTTCCNAAAATTTCTAAACCTAATCTATACAA	180		
Qy	2704	ACTGAATGTTTGTGTTTGTATATTAATCTTAACCAAAAGTTTGAATTGTGCATTGGGAGC	2763		
Db	181	ACTTGAATGTTTGTGTTTGTATATTAATCTTAACCAAAANTTTGAAATTTGTGCATTGGGAGC	240		
Qy	2764	TACACTCTAGTCCCTTTTTCGCCAAATTAATCTCCTTACATCGACCGGTTAAAGTATT	2823		
Db	241	TACACTCTAGTCCCTTTTTCGCCAAATTAATCTCCTTACATCGACCGGTTAAAGTATT	300		
Qy	2824	TAAACCAACAAATTTTAATTTGT	2846		
Db	301	TAAACCAACAAATTTTAATTTGT	323		

[illegible]

JOURNAL Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
Location/Qualifiers
1..276
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-853H05-025845"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 6.04; Score 252; DB 11; Length 276;
Best Local Similarity 96.1%; Pred. No. 1.9e-33;
Matches 271; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 2075 ATCGAAGAACTTTTCTTCTGAACTCTGTTAAATCTCTGCTGCATACCTTGC 2134
Db 276 ATCGAAGAACTTTTCTTCTGAACTCTGTTAAATCTCTGCTGCATACCTTGC 217

Qy 2135 AGGCAATTGACCAAGCACTATACATTAATGAAGCAAAATATCCACGAGATGATGGGT 2194
Db 216 AGGCAATTGACCAAGCACTATACATTAATGAAGCAAAATATCCACGAGATGATGGGT 157

Qy 2195 TAGATCCCACTCAATATCTCTTGTCTTGTATTTATGAAAAACAATATTTATCAGG 2254
Db 156 TAGATCCCACTCAATATCTCTTGTCTTGTATTTATGAAAAACAATATTTATCAGG 97

Qy 2255 AAAAAACGTTTCTTCTTCTGATGATTAAGTAAATACAAATTTAATCTTAG 2314
Db 96 AAAAAACGTTTCTTCTTCTGATG-----GTATTAAGTAAATACAAATTTAATCTTAG 43

Qy 2315 TTATGATTTATCTATCTTCAAACTTACCATCTTCAACATT 2356
Db 42 TTATGATTTATCTATCTTCAAACTTACCATCTTCAACATT 1

RESULT 7
CR402297/c 300 bp DNA linear GSS 02-MAY-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-853H05-025756,
DEFINITION genomic survey sequence.
ACCESSION CR402297
VERSION CR402297.1 GI:46943025
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3

REFERENCE
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 300)
AUTHORS Li, Y., Rosso, M.G., Strizhov, N. and Weishaar, B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
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/mol_type="genomic DNA"
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/clone="GK-853H05-025756"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 5.98; Score 249; DB 11; Length 300;
Best Local Similarity 96.1%; Pred. No. 6.2e-33;
Matches 268; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 2082 AACATTTTCTTCTTCTGAACTCTGTTAAATCTCTGCTGCATACCTTGCAGGATT 2141
Db 300 AACATTTTCTTCTTCTGAACTCTGTTAAATCTCTGCTGCATACCTTGCAGGATT 241

Qy 2142 TGACCAAGCACTATACATTAATGAAGCAAAATATCCACGAGATGATGGGTAGATCC 2201
Db 240 TGACCAAGCACTATACATTAATGAAGCAAAATATCCACGAGATGATGGGTAGATCC 181

Qy 2202 CACATTCATATCTTCTTGTCTTGTATTTATGAAAAACAATATTTATCAGGAAAAAA 2261
Db 180 CACATTCATATCTTCTTGTCTTGTATTTATGAAAAACAATATTTATCAGGAAAAAA 121

Qy 2262 CGTTTCTTCTTCTGATGATTAAGTAAATTAACAAATTTAATCTTAGTATGT 2321
Db 120 CGTTTCTTCTTCTGATG-----GTATTAAGTAAATTAACAAATTTAATCTTAGTATGT 67

Qy 2322 ATTACTATCTTCAAACTTACCATCTTCAACATTATA 2360
Db 66 ATTACTATCTTCAAACTTACCATCTTCAACATTAGA 28

RESULT 8
CNS044GJ 2106 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA complete sequence from clone GSLTFB372E02 of flowers and buds of strain col-0 of Arabidopsis

thaliana (thale cress) .
 BX826541
 VERSION BX826541.1 GI:42462514
 KEYWORDS HTC; GSUT cDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 1 (bases 1 to 2106)
 Castell, V., Aury, J.M., Jallou, O., Wincker, P., Clepet, C., Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2106)
 Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 131 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castell V., Aury J.M., Jallou O., Wincker P., Menard M., Craud C., Schachter V., Weissenbach J., Salanoubat M. URV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Barque_Projet_FullLength
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.location/Qualifiers
 FEATURES
 source
 1. 2106
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 /db_xref="taxon:3702"
 /clone="GSUTFB37ZE02"
 /cisue_type="flowers and buds"
 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"
 1. 2106
 /gene="At4g37750"
 gene
 /gene="At4g37750"
 ORIGIN
 Query Match 5.7%; Score 240.4; DB 4; Length 2106;
 Best Local Similarity 97.3%; Pred. No. 1.6e-31;
 Matches 255; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
 Oy 3968 AACGATTCAACAGCAAAATTTGCTTCTCTCTCTATATATATCTCTCA 4027
 Db 1 AAGGATTCAACAGCAAAATTTGCTTCTCTCTCTATATATATCTCTCA 60
 Oy 4028 AAACCTCTCTATATCTCTTAAGCCCCCTTCTTTTCTTAACCGACAAGAA 4087
 Db 61 AAACCTCTCTATATCTCTTAAGCCCCCTTCTTTTCTTAACCGACAAGAA 120
 Oy 4088 AAAACAAATTTGAGAAAATG-GTGTGTTGTTGTTAACAATATTTGGGTTTAC 4146
 Db 121 AAAACAAATTTGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
 Oy 4147 TTACTACTGAGAGATTATAGAAAGAGTGAAGATACATTATAGAAAGAGAA 4206
 Db 181 TTACTACTGAGAGATTATAGAAAGAGTGAAGATACATTATAGAAAGAGAA 240
 Oy 4207 GCAGAAACCAAAAAGAAAC 4228
 Db 241 GCAGAAACCAAAAAGAAAC 262

RESULT 9
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 LOCUS AL769556
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-087D01-012260.
 ACCESSION AL769556
 VERSION AL769556.1 GI:21531758
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 1
 Li, Y., Rosso, M.G., Strizhov, N., Viehsever, P., and Weishaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 REFERENCE 12874060
 PUBMED
 JOURNAL
 REFERENCE
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 PUBMED 14756321
 REFERENCE
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehsever, P., Dekker, K.A. and Weishaar, B.
 TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050
 REFERENCE
 AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the lines are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpi-z-koeln.mpg.de/GABI-Kat/.location/Qualifiers
 FEATURES
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 1. 418
 /organism="Arabidopsis thaliana"
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 /db_xref="taxon:3702"
 /clone="GK-087D01-012260"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: A0537514). The lines contain one or more T-DNA insertions. The DNA fragment (8) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
 ORIGIN
 Query Match 5.3%; Score 226; DB 10; Length 418;
 Best Local Similarity 77.6%; Pred. No. 5.9e-29;
 Matches 250; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 Oy 1717 TTTTGTATGATACATCTGCGGAAAAATCCAGCTATATGCTATTAAAGA 1776
 Db 418 TTTTGTATGATGTTACCTCGTGTGAAAAATCCGCTATATGTTCTTAAAGA 359

QY 1777 TAATGATTAATGCTTAAATCAATTAATAAAGGTTTTGCTTTAAAGGTTACAC 1836
 DB 358 AATGATTTTAAAGCTTTTATCTTAAATTAAGTTTTGTTTAAAGGTTCCCC 299
 QY 1837 CGCTTAATCATCATTAAGAGAAATTAATCTTATGCAATTCGAAATTAATCTTTTAA 1896
 DB 298 CGGTTATTTATCTTGGGGAATATTAACTTTGGTGGAAATCCCAAAATCTTTTTTA 239
 QY 1897 CACTAAGAAAATTTTCAAGCTTTTAAATTAAGGTCATTTTGGGTTCAATAATA 1956
 DB 238 CCAATAAGAAAATTTTCAAGCTTTTAAATTAAGGTCATTTTGGGTCATAATA 179
 QY 1957 TGTTCACGTAAGATTGAGGTTTAAACCATGAATGTTTTGATTTAAAAAACA 2016
 DB 178 TGTTCCTCCGTAAGTTTGGGGGTTTACCCCAAGAAATGTTTTGTTTTNNNNNNNN 119
 QY 2017 TAAATTTCTAGTAATTAACACA 2038
 DB 118 NNNNNNNNNNNNNNNNNNNNTA 97

RESULT 10
 CNS0A2BQ 2315 bp mRNA linear HTC 06-FEB-2004
 LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 DEFINITION GSLTUS90C06 of Adult vegetative tissue of strain col-0 of
 Arabidopsis thaliana (thale cress).
 BX827650.1 GI:42459424
 HTC; GSLT cDNA.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2315)
 Castell, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C.,
 Menard, M., Crnaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
 Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
 Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
 A Combined Approach to Evaluate and Improve Arabidopsis Genome
 Annotation
 Unpublished
 2 (bases 1 to 2315)
 Genoscope.
 Direct Submission
 Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 Web : www.genoscope.cns.fr)
 The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castell
 V., Aury J.M., Jallion O., Wincker P., Menard M., Crnaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet, C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich information center for Protein
 Sequences). 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
 Location/Qualifiers
 1. .2315
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="GSLTUS90C06"
 /tissue_type="Adult vegetative tissue"
 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"
 1. .2315
 /gene="At4g37750"

FEATURES
 SOURCE
 gene

ORIGIN
 Query Match 5.1%; Score 214; DB 4; Length 2315;
 Best Local Similarity 95.7%; Pred. No. 6.1e-27;
 Matches 220; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 3999 TCTTCTCTTAATATATATATCCCTCAAAACCCCTCCATATCTCTTAAGCCCC 4058
 DB 1 TCTTCTCTTAATATATATATCTCTCAAAACCCCTCTCTATATCTCTTAAGCCCC 60
 QY 4059 CTTCCTGTTTCTCTACCGCAACAAAGAAAAAAGTTTGAAGAAATGTTGTTTC 4118
 DB 61 CTTCCTGTTTCTCTACCGCAACAAAGAAAAAAGTTTGAAGAAATGTTGTTTC 120
 QY 4119 GTTGTGAACCAATGATTGGGTTTACCTTACTTCTGAGAGATTATTAAGAAAGA 4178
 DB 121 GTTGTGAACCAATGATTGGGTTTACCTTACTTCTGAGAGATTATGAGAGAGA 180

QY 4179 GTGAGATACATTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4228
 DB 181 GTGAGATACATTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 230

RESULT 11
 LOCUS BH510257/c 796 bp DNA linear GSS 13-DEC-2001
 DEFINITION BOHKU78T BOHK Brassica oleracea genomic clone BOHKU78, genomic
 survey sequence.
 ACCESSION BH510257
 VERSION BH510257.1 GI:17718347
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 Brassica oleracea
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 796)
 Ayle, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
 Utechtack, T.R., Wortman, V.R., White, O.R. and Town, C.D.
 Whole genome shotgun sequencing of Brassica oleracea and its
 application to gene discovery and annotation in Arabidopsis
 Genome Res. 15 (4), 487-495 (2005)
 15805490
 JOURNAL PUBMED
 COMMENT Other GSSs: BOHKU78TF
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.
 Location/Qualifiers
 1. .796
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000H3"
 /db_xref="taxon:3712"
 /clone="BOHKU78"
 /note="Vector: pHOSt; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOSt using BstXI linkers"

ORIGIN
 Query Match 5.0%; Score 212; DB 9; Length 796;
 Best Local Similarity 76.1%; Pred. No. 1.5e-26;
 Matches 303; Conservative 0; Mismatches 85; Indels 10; Gaps 3;
 QY 2822 TTTAAACCAACAATTTATTTGTTGTAAGTACAAACATGTCATATATAGAGAC 2881
 DB 677 TATTAACCTTGAAATCAATGTCTTCTGGAAGTACAAACATGTCATATATAGAGAC 618

OY		2882	AGCATCGTTTATAC-AAATTANGTCGATGGTATTGGAAATCAAAATAAATAAGCAATTA	2940
Db		617	AGCATTGTCTGACGATATATTGTTTGATGTATTCGGAATCAAAATATAATATAC-MAcTA	559
OY		2941	GCGACTCACCTGGTTTAACTAGTTTGGAGAATATGATAATAAAAATGAATTCAAAGATA	3000
Db		558	GCGACAGATTAGTTTTAAAATTTGGAAAGTTACAATAAAAAATGAAATTCAAAGATG	499
OY		3001	CAGAGCTATATATGTCGGGTCAATTAAGCCGTACCAAAGTTTCGTGTAATTTTAC	3066
Db		498	CAGAGCTAACATATGTCGGGTCAATTAAGCCGTACCAAAGTTTCATCTTAATTTGCAC	439
OY		3061	GGTCGGTCATAGAAATTTTGGACCTTCTTCACCCCTTTATGAACTCTGATAGTTT	3120
Db		438	GGTCGGTCATAGGAATTTTGGAGTTTCTTCACCCTTTTGTGACCTCTGTATATGTTT	379
OY		3121	TGTCGGATTATATATTGTTATTCGTAT-----ATTGTTTGTTCTTAATATGATACG	3172
Db		378	TGTGGGTCTATAGTTTGTATTCGTATCCACTTGTGTTTTTTTGTGCTGTAAAGATACG	319
OY		3173	TAAATTCAGATTAAGAAAGACTCTCTTTATTTAATTT	3210
Db		318	TACTTACGATTAGAACACAGTTTCAATTCCAATTTT	281
RESULT_12				
AL756782				
LOCUS			268 bp DNA linear GSS 01-APR-2004	
DEFINITION			Arabidopsis thaliana T-DNA flanking sequence GK-113A12-012505,	
			genomic survey sequence.	
ACCESSION			AL756782	
VERSION			AL756782.1 GI:21489280	
KEYWORDS			GSS.	
SOURCE			Arabidopsis thaliana (chale cress)	
ORGANISM			Arabidopsis thaliana	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;	
			rosidae; euroside II; Brassicales; Brassicaceae; Arabidopsids.	
REFERENCE				
AUTHORS			Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.	
TITLE			GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for	
			the identification of T-DNA insertion mutants in Arabidopsis	
			thaliana	
JOURNAL			Bioinformatics 19 (11), 1441-1442 (2003)	
PUBMED			12874060	
REFERENCE				
AUTHORS			Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and	
			Weisshaar,B.	
TITLE			An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for	
			flanking sequence tag-based reverse genetics	
JOURNAL			Plant Mol. Biol. 53 (1-2), 247-259 (2003)	
PUBMED			14756321	
REFERENCE				
AUTHORS			Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and	
			Weisshaar,B.	
TITLE			High-throughput generation of sequence indexes from T-DNA	
			mutagenized Arabidopsis thaliana lines	
JOURNAL			Biotechniques 35 (6), 1164-1168 (2003)	
PUBMED			14682050	
REFERENCE				
AUTHORS			Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.	
TITLE			Direct Submission	
JOURNAL			Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer	
			Zuchtingforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany	
			This sequence has been recovered from the left border of the T-DNA.	
			It indicates an insertion within the locus defined by Bac clone	
			TB8119. Details on the protocols used for generation of the	
			sequence are described in References 1-3. The sequences are	
			generated at the MPI for Plant Breeding Research in the context of	
			the GABI-Kat project. GABI-Kat is part of the German plant genomic	
			program designated 'GABI'. Information on line availability can be	
			found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ .	
FEATURES			Location/Qualifiers	

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source
1. .268
/organism="Arabidopsis thaliana"
/mo_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-13A12-012505"
/location_1kb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (Genbank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match      4.7%; Score 200.8; DB 10; Length 268;
Best Local Similarity 84.3%; Pred. No. 1.4e-24;
Matches 226; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY      1998 TTTTGATTTAAAAAACCATTAATTTCTCTAGTAATTACACATTTTAAACGTCATCCAG 205T
      |||||
Dp      1 TTTTGATTTAAAAAACCATTAATTTCTCTAGTAATTACACATTTTAAACGTCATCCAG 60

QY      2058 ATTGTAAATTAAGTCACAAATCGAATACTTTTCTTCTGAACTGTGTTAAATCT 211T
      |||||
Dp      61 ATTGTAAATTAAGTCACAAATCTGAATACTTTTCTTCTGAACTGTGTTAAATCT 120

QY      2118 CTCTGCTGCATCTACTTTCGAGGCAATTTGACCAACGACTATACATATTGAAAGCAAAATATCC 217T
      |||||
Dp      121 CTTCGCGGCATACCTGGCGGGCTTTGGACCAACGACTTCTTCTTGGAAAGCAAAATTTTCC 180

QY      2178 ACCAGGGATGATAGGGTTAGATTCCCACTTCAATATCTTTGTCTTTGTTATTATGAA 223T
      |||||
Dp      181 CCCAGGGATGATAGGGGTTAAACCCCACTTCAATATCTTTGGCCCTGTATTATGAGAA 240

QY      2238 AACAAATATTATTACAGAAAAAAACGTT 226S
      |||||
Dp      241 AACAAATTTTTCAGAAAAAACCGTT 268

RESULT 13
AL336239/c 234 bp DNA linear GSS 01-APR-2004
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-047A09-016076,
genomic survey sequence.
ACCESSION
AL336239
VERSION
AL336239.1 GI:24367864
KEYWORDS
GSS.
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE
AUTHORS
Ll.Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
2
JOURNAL
PUBMED
12874060
AUTHORS
Rosso,M.G., Ll.Y., Strizhov,N., Reis,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
3
JOURNAL
PUBMED
14756321
AUTHORS
Strizhov,N., Ll.Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

```

JOURNAL PUBMED	Biotechniques 35 (6), 1164-1168 (2003)
REFERENCE	4 (bases 1 to 234)
AUTHORS	L.I.Y., Strizhov,N., Rosso,M.G. and Weishaar,B.
TITLE JOURNAL	Direct Submision Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT	This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T2B13. Details on the protocols used for generation of the sequences are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-kat project. GABI-Kat is part of the German Plant Genomic program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ .
FEATURES	location/Qualifiers
source	1..234 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="GK-047A09-016076" /c1one="Idb="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Col-0" /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
ORIGIN	
Query Match	4.6%; Score 193; DB 10; Length 234;
Best Local Similarity	100.0%; Pred. No. 3.2e-23;
Matches 193; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1092 TAGCGTTTCACGGTTGCCTTCGCGCAACTTTGGCGGTGTGACTTTTTCTTAT 1151
Dd	213 TAGCGTTTCACGGTTGCCTTCGCGCAACTTTGGCGGTGTGACTTTTTCTTAT 154
QY	1152 GTCCGTGTTGACATAATTCTTCAGAGGAGAAGCTATCAAAGAACTTAATATTCGAA 1211
Dd	153 GTCCGTGTTGACATAATTCTTCAGAGGAGAAGCTATCAAAGAACTTAATATTCGAA 94
QY	1212 AGAAGAAAAAAAAGGCAAGAAAATCATTTGTCGAAAAAGACATAATGACACTAAATTTGG 1271
Dd	93 AGAAGAAAAAAAAGGCAAGAAAATCATTTGTCGAAAAAGACATAATGACACTAAATTTGG 34
QY	1272 ATTATTTAAAAATG 1284
Dd	33 ATTATTTAAAAATG 21
RESULT 14	
LOCUS	AL759737 162 bp DNA linear GSS 01-APR-2004
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK-190B10-014641,
ACCESSION	AL759737 genomic survey sequence.
VERSION	AL759737.1 GI:21498085
KEYWORDS	GSS.
SOURCE	Arabidopsis thaliana (chale crese)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsi.
AUTHORS	1 L.I.Y., Rosso,M.G., Strizhov,N., Vliehoever,P. and Weishaar,B.
TITLE	GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL PUBMED	Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED	12874060

[illegible]

REFERENCE
AUTHORS
TITLE

1 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL
PUBMED
AUTHORS

2 12874060
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.

TITLE
JOURNAL
PUBMED

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

REFERENCE
AUTHORS

3 14756321
Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weisshaar,B.

TITLE

High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL
PUBMED

4 14682050
(bases 1 to 192)

REFERENCE
AUTHORS
TITLE
JOURNAL

Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsfoerhung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany.
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T28119. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

COMMENT

FEATURES
source

1..192
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-190B10-014640"
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/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (rt) which were transformed with the T-DNA from
vector pAC161 (Genbank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 3.7%; Score 156.4; DB 10; Length 192;
Best Local Similarity 96.4%; Pred. No. 7.3e-17;
Matches 160; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2113 ATTCTCTCTGTCATCTTGCAGGCACTTTGACCAAGCACTATACATTTGAAAGCAAAA 2172
DB 21 ACTTTCTCTCTGTCATCTTGCAGGCACTTTGACCAAGCACTATACATTTGAAAGCAAAA 80
QY 2173 TATCCACCAAGGATGATAGGATTAGATCCACATTCATATCTTTGTTGTTATTTA 2232
DB 81 TATCCACCAAGGATGATAGGATTAGATCCACATTCATATCTTTGTTGTTATTTA 140
QY 2233 TGAAGAAACAAATATTTATCAGAGAAAAACGTTTCTTCTAGTGG 2278
DB 141 TGAAGAAACAAATATTTATCAGAGAAAAACGTTTCTTCTAGTGG 186

Search completed: February 27, 2006, 19:33:40
Job time : 10438 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 BioCeleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: February 27, 2006, 07:56:28 ; Search time 2341 Seconds
(without alignments)
12036.873 Million cell updates/sec

Title: US-10-623-477-3
4228
Perfect score: 1 gtcgactcagcctcactg.....agaaacccaaaaaagaacc 4228
Sequence: 1 gtcgactcagcctcactg.....agaaacccaaaaaagaacc 4228

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 496997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_21: *
2: geneseqn1980s: *
3: geneseqn1990s: *
4: geneseqn2000s: *
5: geneseqn2001s: *
6: geneseqn2002s: *
7: geneseqn2003s: *
8: geneseqn2004s: *
9: geneseqn2005s: *
10: geneseqn2006s: *
11: geneseqn2007s: *
12: geneseqn2008s: *
13: geneseqn2009s: *
14: geneseqn2010s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4228	100.0	4228	10	ADG25137 Thalecres
2	4228	100.0	4228	14	AEAT7182 A. thalia
3	4216	99.7	4227	3	AAAS9221 Promoter
4	4203.4	99.4	4228	10	ADG88432 Arabidops
5	268	6.3	2148	8	AAAS9220 CDNA enco
6	268	6.3	2148	8	ABX13437 A. thalia
7	268	6.3	2148	10	ADG25135 Thalecres
8	268	6.3	2148	10	ADG88430 Arabidops
9	268	6.3	2148	14	AEAT7180 A. thalia
10	147	3.5	8056	8	ABZ10246 Haematopo
11	107.8	2.5	8056	8	ABZ10246 Haematopo
12	106.8	2.5	8056	8	ABZ10246 Haematopo
13	99.4	2.4	8056	8	ABZ10100 Haematopo
14	96.6	2.3	2482	14	ADZ71091 Human chr
15	92.6	2.2	7306	6	ABN80291 Human chr
16	88.2	2.1	2131	14	ADZ71009 Human chr
17	84.6	2.0	2482	14	ADZ71091 Human chr
18	81.4	1.9	2131	14	ADZ71009 Human chr
19	77.4	1.8	4660	14	ADZ70902 Human chr

C	20	77.2	1.8	1524	14	ADZ70897	Adz70897 Human mat
C	21	75	1.8	1554	14	ADZ70999	Adz70999 Human chr
C	22	74.2	1.8	883	4	ABL15210	Ab115210 Human bre
C	23	74.2	1.8	960	11	ACN85231	Acn85231 Breast ca
C	24	73.2	1.7	1428	14	ADZ70899	Adz70899 Human mat
C	25	73.2	1.7	13573	6	ABL33869	Ab133869 Human chr
C	26	72	1.7	5286	13	ADS89278	Ad89278 Human chr
C	27	72	1.7	5286	13	ADS89552	Ad89552 Human chr
C	28	71.6	1.7	1524	14	ADZ70897	Adz70897 Human chr
C	29	71.6	1.7	4660	14	ADZ70902	Adz70902 Human chr
C	30	71.6	1.7	17421	4	AA545349	Aa545349 Chemical1
C	31	71.6	1.7	17421	6	ABK28182	Abk28182 DNA trans
C	32	71.4	1.7	115218	8	ACA64845	Ac64845 Human chr
C	33	70.8	1.7	1340	14	ADZ71035	Adz71035 Human chr
C	34	70.6	1.7	158001	12	ADL17884	Adl17884 Human chr
C	35	69.8	1.7	6881	6	ABL33380	Ab133380 Human chr
C	36	69.8	1.7	6881	6	ABK28249	Abk28249 DNA trans
C	37	69.2	1.6	2000	11	ACL35887	Ac135887 Rice stre
C	38	69.2	1.6	110000	13	ABD32968_6	Abd32968_6 Human chr
C	39	69	1.6	1554	14	ADZ70999	Adz70999 Human chr
C	40	68.8	1.6	679	14	ADZ70988	Adz70988 Human chr
C	41	68.6	1.6	4590	1	AAM60472	Aam60472 Sequence
C	42	68.6	1.6	15548	6	ABL34155	Ab134155 Human chr
C	43	68.4	1.6	110000	13	ABD32968_6	Abd32968_6 Human chr
C	44	68.2	1.6	5286	13	ADS89551	Ad89551 Human chr
C	45	68	1.6	17703	6	ABK39953	Abk39953 Human chr

ALIGNMENTS

RESULT 1	ADG25137	ADG25137 standard; DNA; 4228 BP.
ID	ADG25137	
AC	ADG25137;	
XX		
DT	26-FEB-2004 (first entry)	
XX		
DE	Thalecress Aintegumenta, ANT, gene promoter.	
XX		
KM	Thalecress; ds; promoter; Aintegumenta; ANT; AP2 domain; plant;	
KW	seed mass; asexual reproduction; reduced fertility.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	US6639128-B1.	
XX		
PD	28-OCT-2003.	
XX		
XX		
PF	07-JAN-2000; 2000US-00479855.	
XX		
PR	08-JAN-1999; 99US-00227421.	
XX		
PA	(NASC-) NAT SCI FOUND.	
XX		
PI	Fischer RL, Mizukami Y;	
XX		
DR	WPI; 2003-842795/78.	
XX		
PT	New nucleic acid, useful in conferring desired traits on plants, such as	
PT	increased seed mass, asexual reproduction or reduced fertility.	
XX		
PS	Disclosure; SEQ ID NO 3; 25pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid comprising a	
CC	polynucleotide encoding a polypeptide having at least 90% identity with a	
CC	Canola Aintegumenta, ANT, (appearing as ADG25137) as determined using a	
CC	BLAST algorithm and comprising two AP2 domains. Also included are an	
CC	expression cassette comprising a plant promoter operably linked to a	
CC	heterologous polynucleotide encoding the polypeptide, a vector comprising	
CC	the expression cassette, a plant comprising the plant promoter operably	
CC	linked to the heterologous polynucleotide, a method of asexually	

reproducing a plant and a method of reducing fertility in a plant. The nucleic acid is useful in conferring desired traits on plants, such as increased seed mass, asexual reproduction or reduced fertility. The present sequence is the promoter region of the *Thalassia* *Ainmegueta*, CC ANT, gene.

Sequence 4228 BP; 1489 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;

Query Match 100.0%; Score 4228; DB 10; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCTGAGGCTGACCTGACCTAATGACACTCATATGAGGAGCTCGAGATCCCTTA 60
DB 1 GTGACCTGAGGCTGACCTGACCTAATGACACTCATATGAGGAGCTCGAGATCCCTTA 60
QY 61 GTTGAAGAAAACTTCTTTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 GTTGAAGAAAACTTCTTTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ACATGTGATTCACATATATATATGAAATTTGAAATTTATCATTTAATGAGTTAGCAT 180
DB 121 ACATGTGATTCACATATATATATGAAATTTGAAATTTAATGAGTTAGCAT 180
QY 181 TAATATATATAGCTGACATTAACAACCAATGTTCTGCTTTATGAGATTTCTATAT 240
DB 181 TAATATATATAGCTGACATTAACAACCAATGTTCTGCTTTATGAGATTTCTATAT 240
QY 241 GTTGACCTGATTAAGAT 300
DB 241 GTTGACCTGATTAAGAT 300
QY 301 AAAAGTGACCAAAAGAGATCCATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 AAAAGTGACCAAAAGAGATCCATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 ATGATTAATGAGATTAAT 420
DB 361 ATGATTAATGAGATTAAT 420
QY 421 ATATGTGAGTGTCTTCACTGCTCACTGCTCAAGAAATATCTGCTTATCTTACCTTGA 480
DB 421 ATATGTGAGTGTCTTCACTGCTCACTGCTCAAGAAATATCTGCTTATCTTACCTTGA 480
QY 481 CTGAAAGTTGATATACATAACACGTAATTTTAAACGCGTACATTAACCATGTAT 540
DB 481 CTGAAAGTTGATATACATAACACGTAATTTTAAACGCGTACATTAACCATGTAT 540
QY 541 CGATCAAAATCAAAATTTATATGAGACTAGAAATCAAGATGAGGATCTAGACAGATA 600
DB 541 CGATCAAAATCAAAATTTATATGAGACTAGAAATCAAGATGAGGATCTAGACAGATA 600
QY 601 TACAGAGCTAAGATTTTGAACAAGAGTCAAAAATAGATTTCAATCAATTTAAAAAGA 660
DB 601 TACAGAGCTAAGATTTTGAACAAGAGTCAAAAATAGATTTCAATCAATTTAAAAAGA 660
QY 661 TATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 720
DB 661 TATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 720
QY 721 TGTGTTTGTGTTTCCGATTAATGAAATGTTGTGTTAAATTTGTTTAACTTA 780
DB 721 TGTGTTTGTGTTTCCGATTAATGAAATGTTGTGTTAAATTTGTTTAACTTA 780
QY 781 AACTGCTTTATGTTAAT 840
DB 781 AACTGCTTTATGTTAAT 840
QY 841 TACAAATTAATGTTAAGCATTTGCAATTAATAATCCACGGGTGATTAATCTCGAAGAT 900
DB 841 TACAAATTAATGTTAAGCATTTGCAATTAATAATCCACGGGTGATTAATCTCGAAGAT 900
QY 901 TATGTTAAGTCAAAATTTTCTTGTATGATTAAGTTGAGAAATTAATATATATA 960

DB 901 TATGTTAATGTTAAGCATTTTCTTGTATATGATTAAGTTGAGAAATTAATATATA 960
QY 961 CCTTGACGGGATTAAGGATCTGATATGATGACACTGACATGAAGCCAAAGATCTTC 1020
DB 961 CCTTGACGGGATTAAGGATCTGATATGATGACACTGACATGAAGCCAAAGATCTTC 1020
QY 1021 TGTGCTTAAGATATCTACAGCTGCTTCCCTGCTGATATGAGAAATTTGATATGA 1080
DB 1021 TGTGCTTAAGATATCTACAGCTGCTTCCCTGCTGATATGAGAAATTTGATATGA 1080
QY 1081 GAGATCCCATTAAGCTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTT 1140
DB 1081 GAGATCCCATTAAGCTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTT 1140
QY 1141 TTTTGTCTTATGCTGTTGTTTGAATTTTCTCAGAGTGAAGTGAATCAAGAAATCT 1200
DB 1141 TTTTGTCTTATGCTGTTGTTTGAATTTTCTCAGAGTGAAGTGAATCAAGAAATCT 1200
QY 1201 AATATTCGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1260
DB 1201 AATATTCGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1260
QY 1261 ACTAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
DB 1261 ACTAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
QY 1321 AATCAAG 1380
DB 1321 AATCAAG 1380
QY 1381 CCACATATCTTTTACTTCCAAAGAAATCAATTCACAGAGAAATCTGCTGATGATC 1440
DB 1381 CCACATATCTTTTACTTCCAAAGAAATCAATTCACAGAGAAATCTGCTGATGATC 1440
QY 1441 ACTTTCATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
DB 1441 ACTTTCATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
QY 1501 TCGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
DB 1501 TCGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
QY 1561 CTCCTTCTGCTTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
DB 1561 CTCCTTCTGCTTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
QY 1621 CATTCCTTATCAATTTTAT 1680
DB 1621 CATTCCTTATCAATTTTAT 1680
QY 1681 GGTATTAAGGATTAATTTGCTTCACTGATCAAGAAATTTTGTATGATTAACCTGCTG 1740
DB 1681 GGTATTAAGGATTAATTTGCTTCACTGATCAAGAAATTTTGTATGATTAACCTGCTG 1740
QY 1741 GGAAGAAAGAAAGGCTTAATATATATATATATATATATATATATATATATATATAT 1800
DB 1741 GGAAGAAAGAAAGGCTTAATATATATATATATATATATATATATATATATATATAT 1800
QY 1801 TTAATAATTAAGGTTTGTGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAA 1860
DB 1801 TTAATAATTAAGGTTTGTGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAA 1860
QY 1861 ATTAACCTTTGATGGAATTCAAAATTAATTTTAAACATTAAGAAATTTTGAAGATTT 1920
DB 1861 ATTAACCTTTGATGGAATTCAAAATTAATTTTAAACATTAAGAAATTTTGAAGATTT 1920
QY 1921 TTAATAATTAAGGATTAATTTGCTTCAATTAATTAATTTGCTTCAATTAATTTGCTTCA 1980
DB 1921 TTAATAATTAAGGATTAATTTGCTTCAATTAATTAATTTGCTTCAATTAATTTGCTTCA 1980
QY 1981 TTAACCAATGATGTTTGTGTTTAAAGAAACATTAATTTTCAATTAATTAATTAATTA 2040

Dh 1981 TTAACACATGATGTTTGTGATTTAAACACATTAATTTCTAGTAATACACTT 2040
Qy 2041 TTTAACCGTCATTCAGATTGTATTAAGTGACAAATCGAAAACAATTTTTTTCTTG 2100
Db 2041 TTTAACCGTCATTCAGATTGTATTAAGTGACAAATCGAAAACAATTTTTTTCTTG 2100
Qy 2101 AATCTGTTTAAATTTCTGCTGCTGACACTTGACGAGCATTTGACAAACGATATTA 2160
Db 2101 AATCTGTTTAAATTTCTGCTGCTGACACTTGACGAGCATTTGACAAACGATATTA 2160
Qy 2161 TTGAAGCAAAATATCCACGAGGATGATAGGTTAGATCCCACTTCAATATCTTTGT 2220
Db 2161 TTGAAGCAAAATATCCACGAGGATGATAGGTTAGATCCCACTTCAATATCTTTGT 2220
Qy 2221 CTTTGTATTTATGAAAAAACAATATTTATAGGAAAAAAGTTTCTTCTGATGGTA 2280
Db 2221 CTTTGTATTTATGAAAAAACAATATTTATAGGAAAAAAGTTTCTTCTGATGGTA 2280
Qy 2281 TAAATATAGTAAATTAACAAATTTAATTAATTAATTAATTAATTAATTAATTAAT 2340
Db 2281 TAAATATAGTAAATTAACAAATTTAATTAATTAATTAATTAATTAATTAATTAAT 2340
Qy 2341 ACCATCTTCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2400
Db 2341 ACCATCTTCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2400
Qy 2401 AAAAAATGCAAAAGAGATATATATTAAGTCAAAAGTAAATTAAGATGATGGTAT 2460
Db 2401 AAAAAATGCAAAAGAGATATATATTAAGTCAAAAGTAAATTAAGATGATGGTAT 2460
Qy 2461 TCTTACAGAAAAAGGCGCCGAGAGGTCTTAATCCATCAATTAAGCTGGTTGGCAG 2520
Db 2461 TCTTACAGAAAAAGGCGCCGAGAGGTCTTAATCCATCAATTAAGCTGGTTGGCAG 2520
Qy 2521 ACATCATAGGCGCTACGTATATTTAGACTTACGTAGCTTAACATATCTAGT 2580
Db 2521 ACATCATAGGCGCTACGTATATTTAGACTTACGTAGCTTAACATATCTAGT 2580
Qy 2581 TAGTCTCACTGTAACAAACAAACAAATCCAAATGCTAAATATTAATTAATTAAT 2640
Db 2581 TAGTCTCACTGTAACAAACAAACAAATCCAAATGCTAAATATTAATTAATTAAT 2640
Qy 2641 GTACTAGATTAACGTAGTATACATGCTTTTGGCAATTTCTAAACTATCTATCA 2700
Db 2641 GTACTAGATTAACGTAGTATACATGCTTTTGGCAATTTCTAAACTATCTATCA 2700
Qy 2701 CAAACTGAATGTTTGTGTAATTAATCTTAACCAAAAGTTTGAATGTGCAATGGG 2760
Db 2701 CAAACTGAATGTTTGTGTAATTAATCTTAACCAAAAGTTTGAATGTGCAATGGG 2760
Qy 2761 AGCTACACTGTAAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTTAAAGT 2820
Db 2761 AGCTACACTGTAAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTTAAAGT 2820
Qy 2821 AATTTAAACCAACAAATTTTAATTTGCTGAGAGTACAAACATGTCAATATTAAGA 2880
Db 2821 AATTTAAACCAACAAATTTTAATTTGCTGAGAGTACAAACATGTCAATATTAAGA 2880
Qy 2881 CAGCATGTTATTAACAAATATGTTGATGTTATGGAATCAAAATTAATTAATTAAT 2940
Db 2881 CAGCATGTTATTAACAAATATGTTGATGTTATGGAATCAAAATTAATTAATTAAT 2940
Qy 2941 GCGACTCACTGTTTAAATGTTTGAAGATTAATGAATTAATTAATTAATTAATTAAT 3000
Db 2941 GCGACTCACTGTTTAAATGTTTGAAGATTAATGAATTAATTAATTAATTAATTAAT 3000
Qy 3001 CAGAAGCTATATATGTCGGGTCAATTAAGCGGTGACCAAAAGTTTCTGTAATTTCTAC 3060
Db 3001 CAGAAGCTATATATGTCGGGTCAATTAAGCGGTGACCAAAAGTTTCTGTAATTTCTAC 3060
Qy 3061 GGTCGGCTATTAAGAAATTTTGAATTTTCTTCAACCTTTTATGAATCTTGTATAGTTT 3120
Db 3061 GGTCGGCTATTAAGAAATTTTGAATTTTCTTCAACCTTTTATGAATCTTGTATAGTTT 3120

Qy 3121 TGTGGATTAATTAATTTGATATGATATTTTGTCTTAATTAAGATACGTAATTC 3180
Db 3121 TGTGGATTAATTAATTTGATATGATATTTTGTCTTAATTAAGATACGTAATTC 3180
Qy 3181 CGATTAAGAAAGACTTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 3240
Db 3181 CGATTAAGAAAGACTTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 3240
Qy 3241 CATACAAAGTTTAAAGTTTGAATGATTCGAATTTTACAAAAATGTTTGAAGTGGTTC 3300
Db 3241 CATACAAAGTTTAAAGTTTGAATGATTCGAATTTTACAAAAATGTTTGAAGTGGTTC 3300
Qy 3301 GAGTGTCTTACCAACATCGTACCAACGTGATGGGTTATTAATTAATTTTCTTCTT 3360
Db 3301 GAGTGTCTTACCAACATCGTACCAACGTGATGGGTTATTAATTAATTTTCTTCTT 3360
Qy 3361 TTTCCAAATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3420
Db 3361 TTTCCAAATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3420
Qy 3421 CTTGAATTTTCTGTTGATTTTAAACCAAGTTTCAATCTTCTTACCACAAAAAA 3480
Db 3421 CTTGAATTTTCTGTTGATTTTAAACCAAGTTTCAATCTTCTTACCACAAAAAA 3480
Qy 3481 AAAAGTTTCAATTAATTAATTAATTAATTTTGAATTTTGAATTTTGAATTTTGAAT 3540
Db 3481 AAAAGTTTCAATTAATTAATTAATTAATTTTGAATTTTGAATTTTGAATTTTGAAT 3540
Qy 3541 GAAAGTTATGAATGATTAAGTGAAGTTTGAACAGAAATGTTGATGATTAATTAATTAAT 3600
Db 3541 GAAAGTTATGAATGATTAAGTGAAGTTTGAACAGAAATGTTGATGATTAATTAATTAAT 3600
Qy 3601 CATGATCAAAATTAATTAATTTCTGTTAGCAAGAAACGATTAATTAATTAATTAAT 3660
Db 3601 CATGATCAAAATTAATTAATTTCTGTTAGCAAGAAACGATTAATTAATTAATTAATTAAT 3660
Qy 3661 CGTTAACCTTAATTAATTTAGATTAATTTTGTGATTAATTTTCTGTAAGAGAGG 3720
Db 3661 CGTTAACCTTAATTAATTTAGATTAATTTTGTGATTAATTTTCTGTAAGAGAGG 3720
Qy 3721 TATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3780
Db 3721 TATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3780
Qy 3781 AGTATGTTTGTGCTGATCAATGTTATTAATCTGCTCTTAAGCAATTAATTAATTAAT 3840
Db 3781 AGTATGTTTGTGCTGATCAATGTTATTAATCTGCTCTTAAGCAATTAATTAATTAATTAAT 3840
Qy 3841 TTTTAAATGTTTCAAAAGCTTTTACAAAAATTAATTAATTAATTAATTAATTAATTAAT 3900
Db 3841 TTTTAAATGTTTCAAAAGCTTTTACAAAAATTAATTAATTAATTAATTAATTAATTAAT 3900
Qy 3901 CTTAAAGCGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3960
Db 3901 CTTAAAGCGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3960
Qy 3961 AGATCCCAACGATTAACAAACGAAATTTGCTGTTGCTCTTCTCTTAATTAATTAAT 4020
Db 3961 AGATCCCAACGATTAACAAACGAAATTTGCTGTTGCTCTTCTCTTAATTAATTAATTAAT 4020
Qy 4021 CTCTCAAAAAACCTCTCTTAATCTCTTAATGACCCCTCTCTGTTTCTTAACGCA 4080
Db 4021 CTCTCAAAAAACCTCTCTTAATCTCTTAATGACCCCTCTCTGTTTCTTAACGCA 4080
Qy 4081 CAAAGAAAAAACAAGTTTGAAGAAATGTTGTTCTGTTGTTAACAATGATGGGT 4140
Db 4081 CAAAGAAAAAACAAGTTTGAAGAAATGTTGTTCTGTTGTTAACAATGATGGGT 4140
Qy 4141 TTTAGCTTACTTGAAGATTTATTAAGAAAGAAAGATTAATTAATTAATTAATTAATTAAT 4200
Db 4141 TTTAGCTTACTTGAAGATTTATTAAGAAAGAAAGATTAATTAATTAATTAATTAATTAAT 4200

QY 1381 CCCAGTATCTTTTCTTCTCAACAAATCATTCACACGAGAAATCTGTCTGTATC 1440
DB 1381 CCCAGTATCTTTTCTTCTCAACAAATCATTCACACGAGAAATCTGTCTGTATC 1440
QY 1441 ACTTCATGCAAAATTAACATAATTTGGTATTTTGTCAAGTTCTGTGTTTTAG 1500
DB 1441 ACTTCATGCAAAATTAACATAATTTGGTATTTTGTCAAGTTCTGTGTTTTAG 1500
QY 1501 TCGATTATTTGGTAATCTATATGTGTGATATACATCCAGCTAATCAATATTGAT 1560
DB 1501 TCGATTATTTGGTAATCTATATGTGTGATATACATCCAGCTAATCAATATTGAT 1560
QY 1561 CTCCTTGTGCTATCAATTAATTAACACACATTCAGTCAATCAATTAATTAACCA 1620
DB 1561 CTCCTTGTGCTATCAATTAATTAACACACATTCAGTCAATCAATTAATTAACCA 1620
QY 1621 CATTCCTTATCAATTTTATATGTATTAATAAACAACGACTAATAGGCTACAGATT 1680
DB 1621 CATTCCTTATCAATTTTATATGTATTAATAAACAACGACTAATAGGCTACAGATT 1680
QY 1681 GGTATTAAGCATTAATGCTCTAGTCGAAAGAAATTTTGTATGATPACATCGTG 1740
DB 1681 GGTATTAAGCATTAATGCTCTAGTCGAAAGAAATTTTGTATGATPACATCGTG 1740
QY 1741 GGAATAAAATCCAGCCTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTATCA 1800
DB 1741 GGAATAAAATCCAGCCTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTATCA 1800
QY 1801 TTAATAATAAAGTTTGTCTTTAAAGTTTACACGCTTAATTCATCATTAAGAGAAAT 1860
DB 1801 TTAATAATAAAGTTTGTCTTTAAAGTTTACACGCTTAATTCATCATTAAGAGAAAT 1860
QY 1861 ATTAACCTTGATCGAAATTCGAAATATCTTTTAAACATPAGAAATTTTCAGCATTT 1920
DB 1861 ATTAACCTTGATCGAAATTCGAAATATCTTTTAAACATPAGAAATTTTCAGCATTT 1920
QY 1921 TTAATAATAAAGGTATTAATGCTTCATTAATATGTTTCCAGTAATTTGGAGGT 1980
DB 1921 TTAATAATAAAGGTATTAATGCTTCATTAATATGTTTCCAGTAATTTGGAGGT 1980
QY 1981 TTAACACATGAATGTTTGTGATTTTAAACACATTAATTTCTAGTATTAACATTT 2040
DB 1981 TTAACACATGAATGTTTGTGATTTTAAACACATTAATTTCTAGTATTAACATTT 2040
QY 2041 TTTAACCGTCATTCAGATTTGTAATAGTGAACAAATCTGAAACATTTTCTG 2100
DB 2041 TTTAACCGTCATTCAGATTTGTAATAGTGAACAAATCTGAAACATTTTCTG 2100
QY 2101 AATCTGTTTAATTTCTCTGCTGCACTCTTGACAGCATTTGACACATATCTTATCA 2160
DB 2101 AATCTGTTTAATTTCTCTGCTGCACTCTTGACAGCATTTGACACATATCTTATCA 2160
QY 2161 TTTGAAAGCAAAATATCCACAGGAGTATAGGTTAGTCCACATTCATATCTTTGT 2220
DB 2161 TTTGAAAGCAAAATATCCACAGGAGTATAGGTTAGTCCACATTCATATCTTTGT 2220
QY 2221 CTTTGTATTTATGAAAAAATAATTTTATCAGGAAAAAAACGTTCTCTAGTGTA 2280
DB 2221 CTTTGTATTTATGAAAAAATAATTTTATCAGGAAAAAAACGTTCTCTAGTGTA 2280
QY 2281 TAAAGTATAGATTAATAAATAATTTAATCTAGTAAATGATTAATCTTCAAACTT 2340
DB 2281 TAAAGTATAGATTAATAAATAATTTAATCTAGTAAATGATTAATCTTCAAACTT 2340
QY 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTCTAATAACTATCTCACTA 2400
DB 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTCTAATAACTATCTCACTA 2400
QY 2401 AAAAAATGCAAAAGAGATATATATTTAAGTCAAAATTAATTAAGATGGATGGAT 2460
DB 2401 AAAAAATGCAAAAGAGATATATATTTAAGTCAAAATTAATTAAGATGGATGGAT 2460

QY 2461 TCTTCAGCAAAACGGCGCCGTAGAGGTGTCCTTATCCATTAACAGTGGGTTGTGAG 2520
DB 2461 TCTTCAGCAAAACGGCGCCGTAGAGGTGTCCTTATCCATTAACAGTGGGTTGTGAG 2520
QY 2521 ACATCATAGGGCTACGTATATTTGAGCTTTACTGTATCGTAAGCTTTAATCATATCTAGT 2580
DB 2521 ACATCATAGGGCTACGTATATTTGAGCTTTACTGTATCGTAAGCTTTAATCATATCTAGT 2580
QY 2581 TAGTTCTCATGTATCAAAACAAACAAATTCGTAACATATATTAACAAATCTA 2640
DB 2581 TAGTTCTCATGTATCAAAACAAACAAATTCGTAACATATATTAACAAATCTA 2640
QY 2641 GTACTAGATTAACGCTACGTATACATCGCTTTTTCGCAATTTCTAATCTATCAAA 2700
DB 2641 GTACTAGATTAACGCTACGTATACATCGCTTTTTCGCAATTTCTAATCTATCAAA 2700
QY 2701 CAAACTGAAATGTTTGTGTAATTTATCTTAAACCAAGTTTGAATGTGCAATGGG 2760
DB 2701 CAAACTGAAATGTTTGTGTAATTTATCTTAAACCAAGTTTGAATGTGCAATGGG 2760
QY 2761 AGCTACATCTAGTCCCTTTTCCGCAAAATATATCTCTTACATGACCGGTTAAAGT 2820
DB 2761 AGCTACATCTAGTCCCTTTTCCGCAAAATATATCTCTTACATGACCGGTTAAAGT 2820
QY 2821 ATTTAAACCAACAAATTTTAAATTTGTGCTGAAGGTACAAACATGTCATATATAGA 2880
DB 2821 ATTTAAACCAACAAATTTTAAATTTGTGCTGAAGGTACAAACATGTCATATATAGA 2880
QY 2881 CAGCATCGTTATATCAAAATATATGTCATGTTATGGAATTCAAATTAATAGAAATTA 2940
DB 2881 CAGCATCGTTATATCAAAATATATGTCATGTTATGGAATTCAAATTAATAGAAATTA 2940
QY 2941 GCGATCACTGTGTTATATGTTTGAAGATTAATGAATTAATAAATGAATTCAGAGATA 3000
DB 2941 GCGATCACTGTGTTATATGTTTGAAGATTAATGAATTAATAAATGAATTCAGAGATA 3000
QY 3001 CAGAGCTATATATGTCGGGTCAATTTAGAGCGTGAACCAAAAGTTTGTGCTAATTTCTAC 3060
DB 3001 CAGAGCTATATATGTCGGGTCAATTTAGAGCGTGAACCAAAAGTTTGTGCTAATTTCTAC 3060
QY 3061 GGTGCGTCATTAAGAAATTTTGAACCTTTCTTCAACCTTTTATGAACTTCTGTATAGTTT 3120
DB 3061 GGTGCGTCATTAAGAAATTTTGAACCTTTCTTCAACCTTTTATGAACTTCTGTATAGTTT 3120
QY 3121 TGTGGAATTAATATTTGTAATGTAATTTTGTGTTCTAATATGATATGTAATTTCA 3180
DB 3121 TGTGGAATTAATATTTGTAATGTAATTTTGTGTTCTAATATGATATGTAATTTCA 3180
QY 3181 CGATTAAGAAAGACTTCTTTTATTTAATTTGAATTTAACTTTTGTGTTTGAATGACT 3240
DB 3181 CGATTAAGAAAGACTTCTTTTATTTAATTTGAATTTAAACCTTTTGTGTTTGAATGACT 3240
QY 3241 CATACACAGGTTAAGTTTATGATGTAATCCAAATTTAATAAATGTTTCAGAGTGCCTTC 3300
DB 3241 CATACACAGGTTAAGTTTATGATGTAATCCAAATTTAATAAATGTTTCAGAGTGCCTTC 3300
QY 3301 GAGTGTCTTACCAACATCGTACCAACTCGTATGAGTTTATATATAGGTTTTTCTTCTT 3360
DB 3301 GAGTGTCTTACCAACATCGTACCAACTCGTATGAGTTTATATATAGGTTTTTCTTCTT 3360
QY 3361 TTTCCATATGCTTTATATTTGAACCACTCTAATTTCTTTTAAATTAATAGTTAAGAT 3420
DB 3361 TTTCCATATGCTTTATATTTGAACCACTCTAATTTCTTTTAAATTAATAGTTAAGAT 3420
QY 3421 CTTGAATTTCTGTGATTTTAAACCAAGTTTTCATTTCTTTGACACAAAAAAAAA 3480
DB 3421 CTTGAATTTCTGTGATTTTAAACCAAGTTTTCATTTCTTTGACACAAAAAAAAA 3480
QY 3481 AAAAGTTTCAATTAATTAAGAAATCTAAATTTTGAAGTTCAAGATTTAATGATAGCT 3540
DB 3481 AAAAGTTTCAATTAATTAAGAAATCTAAATTTTGAAGTTCAAGATTTAATGATAGCT 3540
QY 3541 GAAAAATGATATGATGCAAGTTTGCAACAAATGCTGATGTAATCAAAAA 3600

Accession	Gene	Length (bp)
Db 3541	GAAAAGTATGAATGATGCAAGTTTGCAACGAAATGGTCGATGATGACATATCAAAA	3600
Qy 3601	CATGCATCAAAATATTAATTCGTGCTTAGACAAGAAAACGATTGAAATAAACAGAACAT	3660
Db 3601	CATGCATCAAAATATTAATTCGTGCTTAGACAAGAAAACGATTGAAATAAACAGAACAT	3660
Qy 3661	CGTTAACCACTTTAAAAATCTTAAGATAATTTTGTAGTATATTTCTGTAGAGAGAGG	3720
Db 3661	CGTTAACCACTTTAAAAATCTTAAGATAATTTTGTAGTATATTTCTGTAGAGAGAGG	3720
Qy 3721	TATCATATCTTACAAAAAAACCTCATTCGATTAATAATATGTTGCCATCGTTACCA	3780
Db 3721	TATCATATCTTACAAAAAAACCTCATTCGATTAATAATATGTTGCCATCGTTACCA	3780
Qy 3781	AGTATGTTTTGCTGTCATCAGTTGATTTGTAACTCGTCTCTTAAGCCATATAGTTCTAAG	3840
Db 3781	AGTATGTTTTGCTGTCATCAGTTGATTTGTAACTCGTCTCTTAAGCCATATAGTTCTAAG	3840
Qy 3841	TTTTTAATGTTTTCAAAAGACTTTTACAAAATAATTAATTAAGTGAATTTGTAGGG	3900
Db 3841	TTTTTAATGTTTTCAAAAGACTTTTACAAAATAATTAATTAAGTGAATTTGTAGGG	3900
Qy 3901	CTAAAGCGAAAAATTAATAATTAATAATTAAGAAACGCTCTTCTCAATAGAACAC	3960
Db 3901	CTAAAGCGAAAAATTAATAATTAATAATTAAGAAACGCTCTTCTCAATAGAACAC	3960
Qy 3961	AGATCCCAACGGATTCAAACAGCAAAATTTGTGCTTGTCTCTCTTATTAATATATC	4020
Db 3961	AGATCCCAACGGATTCAAACAGCAAAATTTGTGCTTGTCTCTCTTATTAATATATC	4020
Qy 4021	CTCTCAAAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTGTTCTCTACCGCA	4080
Db 4021	CTCTCAAAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTGTTCTCTACCGCA	4080
Qy 4081	CAAGGAAAAACCAAAAGTTTGAGAAAAATGCTGTGTGTTGTGTACCAATGATTGGGT	4140
Db 4081	CAAGGAAAAACCAAAAGTTTGAGAAAAATGCTGTGTGTTGTGTACCAATGATTGGGT	4140
Qy 4141	TTTGGCTTACTACTTCGAGAGATTATAGAAAGAAAGAGTGAAGTACATTATAGAAAGA	4200
Db 4141	TTTGGCTTACTACTTCGAGAGATTATAGAAAGAAAGAGTGAAGTACATTATAGAAAGA	4200
Qy 4201	AGAGAGCAGAAACCAAAAAAGAAACC 4228	
Db 4201	AGAGAGCAGAAACCAAAAAAGAAACC 4228	
RESULT 3		
ID AAA59221 standard, cDNA, 4227 BP.		
AC AAA59221;		
AC AAA59221;		
DT 07-NOV-2000 (first entry)		
DE Promoter sequence of the Arabidopsis aintegumenta (ANT) gene.		
DE Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility;		
KW asexual reproduction; plant; male sterile plant; female sterile plant;		
KW early flowering; promoter; ss.		
XX Arabidopsis sp.		
OS Arabidopsis sp.		
PN WO200040694-A2.		
PD 13-JUL-2000.		
PF 07-JAN-2000; 2000WO-US000465.		
PR 08-JAN-1999; 99US-00227421.		
PA (REGC) UNIV CALIFORNIA.		

[illegible]

Dh 661 TATGATATTCAGTTACGGATTGATATTACATTACGAGTAGTACATACATATATTTT 720
Qy 721 TGTTTTGTTTTACGATTAATAGAAATGTTGTGTTAAAAATTTGGTTTACTTA 780
Db 721 TGTTTTGTTTTACGATTAATAGAAATGTTGTGTTAAAAATTTGGTTTACTTA 780
Qy 781 AACTCGTTTTATGTTAACTATATATGCTTTCCGCAATGTAATTTGAAACAAACCTGTA 840
Db 781 AACTCGTTTTATGTTAACTATATATGCTTTCCGCAATGTAATTTGAAACAAACCTGTA 840
Qy 841 TACAAATTAATGTTAAGCCATTGCAATTAATAAATCCACGGGTAGTAATCCTCAGAAAT 900
Db 841 TACAAATTAATGTTAAGCCATTGCAATTAATAAATCCACGGGTAGTAATCCTCAGAAAT 900
Qy 901 TATGTTAAGCTACAAATTTTCTCTTATGATTAAGTTTGAACAAATTTATGTA 960
Db 901 TATGTTAAGCTACAAATTTTCTCTTATGATTAAGTTTGAACAAATTTATGTA 960
Qy 961 CTTTGACGGGGTATTAAGCTCACTGCATAGTCAAGTCAAGTCAAGAGTGTGTC 1020
Db 961 CTTTGACGGGGTATTAAGCTCACTGCATAGTCAAGTCAAGTCAAGAGTGTGTC 1020
Qy 1021 TCTGTCTTAAGAATATCTACAGCTGCTTCCCTGTGTAATAGAAAGAAATTTGATGTA 1080
Db 1021 TCTGTCTTAAGAATATCTACAGCTGCTTCCCTGTGTAATAGAAAGAAATTTGATGTA 1080
Qy 1081 GAATATCCCATCTAGCGTTTCACTGTTGCGTTCTCCGTGCACTTTGGCGGTTGTGACT 1140
Db 1081 GAATATCCCATCTAGCGTTTCACTGTTGCGTTCTCCGTGCACTTTGGCGGTTGTGACT 1140
Qy 1141 TTTTCTTATGTCGTGTTTGACTAATTTTCTCAGAGTAGAGTGTATCAAGAAACT 1200
Db 1141 TTTTCTTATGTCGTGTTTGACTAATTTTCTCAGAGTAGAGTGTATCAAGAAACT 1200
Qy 1201 AATATTCGAAAGAAAGAAAGAAAGCAAGAAACTATTTGCGAAAGACATTAATGAC 1260
Db 1201 AATATTCGAAAGAAAGAAAGAAAGCAAGAAACTATTTGCGAAAGACATTAATGAC 1260
Qy 1261 ACTTAAATTTGATTTAATAATGTAATATGTTTGTGTAATTTAATCATTAACAA 1320
Db 1261 ACTTAAATTTGATTTAATAATGTAATATGTTTGTGTAATTTAATCATTAACAA 1320
Qy 1321 AATCAAGAGAGAGAGAGGAGCCTCTGTCGTATGATTTCCCTCTTAAACAACCTGCT 1380
Db 1321 AATCAAGAGAGAGAGAGGAGCCTCTGTCGTATGATTTCCCTCTTAAACAACCTGCT 1380
Qy 1381 CCCACTATCTTTTACTTCAACAATAATCATTTCAACAGAGAAATCTGTCGTATGAC 1440
Db 1381 CCCACTATCTTTTACTTCAACAATAATCATTTCAACAGAGAAATCTGTCGTATGAC 1440
Qy 1441 ACTTTCAAGCAAAATTAACATAATTTTGGTATTTTGTCAAGTCTTGCTGTTTTAAG 1500
Db 1441 ACTTTCAAGCAAAATTAACATAATTTTGGTATTTTGTCAAGTCTTGCTGTTTTAAG 1500
Qy 1501 TCGATTAATTTGTAATATCTATATGTCGTATGTAATCAATCAAGCTTAATCAATTAATGAT 1560
Db 1501 TCGATTAATTTGTAATATCTATATGTCGTATGTAATCAATCAAGCTTAATCAATTAATGAT 1560
Qy 1561 CTCCTTCTGCTTATCAATAATTAACACATTAAGCTTAATCAAGCTTAATTAACCA 1620
Db 1561 CTCCTTCTGCTTATCAATAATTAACACATTAAGCTTAATCAAGCTTAATTAACCA 1620
Qy 1621 CATTTCTTATCAATTTTATGTAATTAATAAACAACGACTATAGGCTACAGAGTT 1680
Db 1621 CATTTCTTATCAATTTTATGTAATTAATAAACAACGACTATAGGCTACAGAGTT 1680
Qy 1681 GGTATTAAGGCAATTAATGCTTCTAGTCGAAGAAATTTTGTGTAATTAACATCTGTC 1740
Db 1681 GGTATTAAGGCAATTAATGCTTCTAGTCGAAGAAATTTTGTGTAATTAACATCTGTC 1740
Qy 1741 GGAATAAATTCAGCCTTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTTATCA 1800
Db 1741 GGAATAAATTCAGCCTTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTTATCA 1800

Qy 1801 TTAATAAATAAGGTTTTCCTTTTAAAGGTTACCAACGCTTAATTCATCATTAAGAAAT 1860
Db 1801 TTAATAAATAAGGTTTTCCTTTTAAAGGTTACCAACGCTTAATTCATCATTAAGAAAT 1860
Qy 1861 ATTAACTTTGATCGAAATTCGAAATCTTTTAAACATTAAGAAATTTTTCAGATTT 1920
Db 1861 ATTAACTTTGATCGAAATTCGAAATCTTTTAAACATTAAGAAATTTTTCAGATTT 1920
Qy 1921 TTAATAAAGGGTACATTTATGCGTTCAATTAATATGTTTCCACGTAAAGTTGAGGT 1980
Db 1921 TTAATAAAGGGTACATTTATGCGTTCAATTAATATGTTTCCACGTAAAGTTGAGGT 1980
Qy 1981 TTAACCCATGAAATGTTTTGATTTTAAATAACATTAATTTTCTATGTAATTAACAT 2040
Db 1981 TTAACCCATGAAATGTTTTGATTTTAAATAACATTAATTTTCTATGTAATTAACAT 2040
Qy 2041 TTTAACCGTCCATCCAGATTTGTAATAGTACAAATCTGAATAATTTTCTTCTG 2100
Db 2041 TTTAACCGTCCATCCAGATTTGTAATAGTACAAATCTGAATAATTTTCTTCTG 2100
Qy 2101 AATCTGTTTAAATCTCTGCTGCAATCTTGCAAGCAATTTGACCAACGACTATACATA 2160
Db 2101 AATCTGTTTAAATCTCTGCTGCAATCTTGCAAGCAATTTGACCAACGACTATACATA 2160
Qy 2161 TTGAAGCAAAATATCCACAGAGATGATGAGTTAGATCCCATTCATTAATCTTTGT 2220
Db 2161 TTGAAGCAAAATATCCACAGAGATGATGAGTTAGATCCCATTCATTAATCTTTGT 2220
Qy 2221 CTTTGTATTTAAGAAACAAATATTTATCAGAAACAAACGTTTCTCTAGAGGTA 2280
Db 2221 CTTTGTATTTAAGAAACAAATATTTATCAGAAACAAACGTTTCTCTAGAGGTA 2280
Qy 2281 TAAATATAGATTAATTAACAAATTTAATCTTATGTAATGTAATCTTCAACT 2340
Db 2281 TAAATATAGATTAATTAACAAATTTAATCTTATGTAATGTAATCTTCAACT 2340
Qy 2340 ACCATCTTCAACATTAATTTGATCAATTTTATTTTATTTTATCAATCTTCCACTA 2399
Db 2340 ACCATCTTCAACATTAATTTGATCAATTTTATTTTATTTTATCAATCTTCCACTA 2399
Qy 2401 AAAAAATGCAAAAGAGATATATATTAATTAAGCAAAATTAAGATGAGAGGAGAT 2460
Db 2401 AAAAAATGCAAAAGAGATATATATTAATTAAGCAAAATTAAGATGAGAGGAGAT 2460
Qy 2461 TCTTACGCAAAACGGGCGGTAGAGGTGCTTATCTCAATTAACACTGGGTGTGGCAG 2520
Db 2461 TCTTACGCAAAACGGGCGGTAGAGGTGCTTATCTCAATTAACACTGGGTGTGGCAG 2520
Qy 2521 ACATCATAGGGCTTACGTATATTTAGCTTTACTGTAACGTAAAGCTTTAATCATATCTAGT 2580
Db 2521 ACATCATAGGGCTTACGTATATTTAGCTTTACTGTAACGTAAAGCTTTAATCATATCTAGT 2580
Qy 2581 TAGTTCTCATCTGACAAACAAACAAATTCOAATTTGTAACATTAATTAACATTAACAT 2640
Db 2581 TAGTTCTCATCTGACAAACAAACAAATTCOAATTTGTAACATTAATTAACATTAACAT 2640
Qy 2641 GTACTAGATTAACGCTACGTATACATGCTTTTTCGAAATTTCTAATTAATCTATACAA 2700
Db 2641 GTACTAGATTAACGCTACGTATACATGCTTTTTCGAAATTTCTAATTAATCTATACAA 2700
Qy 2701 CAAACTGGAATGTTTGTGTAATTTATCTTAACCAAAAGTTTGAATTTGCAATGGG 2760
Db 2701 CAAACTGGAATGTTTGTGTAATTTATCTTAACCAAAAGTTTGAATTTGCAATGGG 2760
Qy 2761 AGCTACATCTAGTCCCTTTTTCGCAAAATTAATCTCTTAACATGACGAGGTTAAAGT 2820
Db 2761 AGCTACATCTAGTCCCTTTTTCGCAAAATTAATCTCTTAACATGACGAGGTTAAAGT 2820
Qy 2821 ATTAAACCAACAAATTTTAAATTTGTTGCTGAAGTACAAACATGTCATATATAGAGA 2880
Db 2821 ATTAAACCAACAAATTTTAAATTTGTTGCTGAAGTACAAACATGTCATATATAGAGA 2880

QY 2881 CAGCATGTTTATACAAATTAATGTCATGTTATTTGAAATCAATATTAATCAATTA 2940
 DB 2880 CAGCATGTTTATACAAATTAATGTCATGTTATTTGAAATCAATATTAATCAATTA 2939
 QY 2941 GCGACTCAGTTGTTTAAATGTTGGAAGTAATGAAATTAATAATGAAATTCAGAGATA 3000
 DB 2940 GCGACTCAGTTGTTTAAATGTTGGAAGTAATGAAATTAATAATGAAATTCAGAGATA 2999
 QY 3001 CAGAGCTAATATATGTCGGGTCAATTTAGACCCGACCAAAAGTTGTCGTATTTCTAC 3060
 DB 3000 CAGAGCTAATATATGTCGGGTCAATTTAGACCCGACCAAAAGTTGTCGTATTTCTAC 3059
 QY 3061 GGTGGCTCAATGAATTTTGGACCTTTCTCACCCCTTTTGAACCTCTGTATGTTT 3120
 DB 3060 GGTGGCTCAATGAATTTTGGACCTTTCTCACCCCTTTTGAACCTCTGTATGTTT 3119
 QY 3121 TGTGGATTAATATATTTGTAATTTGTAATTTTGTCTAATATGATACGTAAATTC 3180
 DB 3120 TGTGGATTAATATATTTGTAATTTTGTCTAATATGATACGTAAATTC 3179
 QY 3181 CCAATAAGAAAGACTCTTTTATTTATTTATTTGATTTTAAATCTTTGTTTGGAAATGACT 3240
 DB 3180 CCAATAAGAAAGACTCTTTTATTTATTTATTTGATTTTAAATCTTTGTTTGGAAATGACT 3239
 QY 3241 CATACACAAGTTAAAGTTGATGATCCAAATTTTCAAAAAATGTTTCAGAGATGCGTTC 3300
 DB 3240 CATACACAAGTTAAAGTTGATGATCCAAATTTTCAAAAAATGTTTCAGAGATGCGTTC 3299
 QY 3301 GAGTGTCTTACCAACATCGTACCACTCGTATGCGTTTATTTATTTAGGTTTCTTCTT 3360
 DB 3300 GAGTGTCTTACCAACATCGTACCACTCGTATGCGTTTATTTATTTAGGTTTCTTCTT 3359
 QY 3361 TTTCGAATGCTTTAATTAATGAACTCAATTTCTTTTAAATTTAGGTTAAGAAAT 3420
 DB 3360 TTTCGAATGCTTTAATTAATGAACTCAATTTCTTTTAAATTTAGGTTAAGAAAT 3419
 QY 3421 CTGGAATTTCTGTGATTTTAAACCAAGTTTCAATCTCTTGTAGCACAAAAAAATA 3480
 DB 3420 CTGGAATTTCTGTGATTTTAAACCAAGTTTCAATCTCTTGTAGCACAAAAAAATA 3479
 QY 3481 AAAAGTTTCAATTTAATAAGATCTAAATTTTGTGAGTTCAAGATTTAATGATAGCT 3540
 DB 3480 AAAAGTTTCAATTTAATAAGATCTAAATTTTGTGAGTTCAAGATTTAATGATAGCT 3539
 QY 3541 GAAAAATTATGATGATGTAAGTTTGCAACAGAAATGTCGATGATATATCAAAAA 3600
 DB 3540 GAAAAATTATGATGATGTAAGTTTGCAACAGAAATGTCGATGATATATCAAAAA 3599
 QY 3601 CAGCATCAAAATTAATATTCGTCTTAGCAAGAAACGATGAATAAACAACAAT 3660
 DB 3600 CAGCATCAAAATTAATATTCGTCTTAGCAAGAAACGATGAATAAACAACAAT 3659
 QY 3661 CGTTAACACTTAAATCTTGAATTAATTTGTAGATTAATTTCTGTAGAGAGAG 3720
 DB 3660 CGTTAACACTTAAATCTTGAATTAATTTGTAGATTAATTTCTGTAGAGAGAG 3719
 QY 3721 TATCATATCTTACAAAAAATACTCATTTGAGATTAATAATTTGTGCCAATGTTACCA 3780
 DB 3720 TATCATATCTTACAAAAAATACTCATTTGAGATTAATAATTTGTGCCAATGTTACCA 3779
 QY 3781 AGTATGTTTTTGTGTCATGATGTTATGTAATGCTGCTCTTAGCCATATAGTTCTAAG 3840
 DB 3780 AGTATGTTTTTGTGTCATGATGTTATGTAATGCTGCTCTTAGCCATATAGTTCTAAG 3839
 QY 3841 TTTTAAATGTTTTCAAGACTTTACAAAAATTAATATATAGGTGAATTTGTAGGG 3900
 DB 3840 TTTTAAATGTTTTCAAGACTTTACAAAAATTAATATATAGGTGAATTTGTAGGG 3899
 QY 3901 CTAAAAAGCGAAAAATTAATAATTAAGTAAGAAAGTCTTTCTCAATAGAACAC 3960
 DB 3900 CTAAAAAGCGAAAAATTAATAATTAAGTAAGAAAGTCTTTCTCAATAGAACAC 3959
 QY 3961 AGATCCCAAGGATTAAGCAAGCAAAATTTGTGCTTGTCTCTTATTAATATATC 4020

DB 3960 AGATCCCAAGGATTAAGCAAGCAAAATTTGTGCTTGTCTCTCTTATTAATATC 4019
 QY 4021 CTCTCAAAAACTCTCTCTATATCTCTCTTAAAGCCCCCTCTCTGTTTCTACCGCAA 4080
 DB 4020 CTCTCAAAAACTCTCTCTATATCTCTCTTAAAGCCCCCTCTCTGTTTCTACCGCAA 4079
 QY 4081 CAAAGAAAAACAAAGTTTGAAGAAAAATGTTGTTCTGTTGTACCAATGATGGGT 4140
 DB 4080 CAAAGAAAAACAAAGTTTGAAGAAAAATGTTGTTCTGTTGTACCAATGATGGGT 4139
 QY 4141 TTTAGCTTACTACTTCTGAGAGATTATTAAGAAAAAGTGAAGATACATTAATAGAAAG 4200
 DB 4140 TTTAGCTTACTACTTCTGAGAGATTATTAAGAAAAAGTGAAGATACATTAATAGAAAG 4199
 QY 4201 AGAAGACGAAACCAAAAAAGAAACC 4228
 DB 4200 AGAAGACGAAACCAAAAAAGAAACC 4227

RESULT 4
 ADG88432
 ID ADG88432 standard; DNA; 4228 BP.
 AC XX
 ADG88432;
 AC XX
 DT 11-MAR-2004 (first entry)
 XX
 XX Arabidopsis thaliana ainegumenta (ANT) promoter DNA.
 DE
 XX Plant; genetic engineering; cell proliferation; ainegumenta; ANT;
 KW transgenic; transgenic plant; organ mass alteration; fertility;
 KW asexual reproduction; de.
 OS
 OS Arabidopsis thaliana.
 PN US2003159180-A1.
 XX
 PD 21-AUG-2003.
 XX
 XX 28-JAN-2002; 2002US-00059911.
 PF
 XX 28-JAN-2002; 2002US-00059911.
 PR
 XX (REGC) UNIV CALIFORNIA OFFICE TECHNOLOGY.
 PA
 PI Fischer RL, Mizukami Y;
 XX
 DR WPI; 2003-787370/74.
 XX
 XX Increasing cell proliferation in a plant by introducing into the plant an
 PT expression cassette containing a plant promoter operably linked to a
 PT nucleic acid encoding a modified ANT polypeptide and selecting plants
 PT with increased mass.
 PS
 PS Disclosure; SEQ ID NO 3; 51pp; English.
 XX
 XX The present invention relates to plant genetic engineering. The invention
 CC particularly relates to a method of increasing cell proliferation in a
 CC plant. The method involves introducing into the plant an expression
 CC cassette containing a plant promoter operably linked to a nucleic acid
 CC encoding a modified ainegumenta (ANT) polypeptide comprising an ANT AP2
 CC domain and selecting plants the with increased size or mass. The
 CC invention is useful to generate transgenic plants. The method is useful
 CC for increasing cell proliferation in a plant for altering organ mass,
 CC controlling fertility or enhancing asexual reproduction. The present
 CC sequence is Arabidopsis thaliana ANT promoter DNA.
 XX
 SQ Sequence 4228 BP; 1488 A; 651 C; 643 G; 1446 T; 0 U; 0 Other;

Query Match 99.4%; Score 4203.4; DB 10; Length 4228;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4226; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

OY	1	GTGCACTTAGGCTCTCACTGCGCTTAATAAGACTCACTAATAGGAGCTCGAGAGCTCTTAA	60
Db	1	GTGCACTTAGGCTCTCACTGCGCTTAATAAGACTCACTAATAGGAGCTCGAGAGCTCTTAA	60
OY	61	GTTAATAAAAACTTTCTTTGTACGTGTGTGTGTGTAAAGTTCAATTATACTAGTC	120
Db	61	GTTAATAAAAACTTTCTTTGTACGTGTGTGTGTGTAAAGTTCAATTATACTAGTC	120
OY	121	ACATGTGATATCACAATATATATATGAAATGGAATTAATCATATTAATGAGTTAGAT	180
Db	121	ACATGTGATATCACAATATATATATGAAATGGAATTAATCATATTAATGAGTTAGAT	180
OY	181	TAAATATATAACGCTGACATTACCAACCAATGTTTGTCTTTATATGATAGTTCTATAT	240
Db	181	TAAATATATAACGCTGACATTACCAACCAATGTTTGTCTTTATATGATAGTTCTATAT	240
OY	241	GTTCGACTTGATTAATAGATCTATATAAACGTGGTTATTTAAATCCGATCCATAC	300
Db	241	GTTCGACTTGATTAATAGATCTATATAAACGTGGTTATTTAAATCCGATCCATAC	300
OY	301	AAAATGGACCAAAACGAGATCCAGATGTTGTGTATCTTTGTGTGTTAACCAATAT	360
Db	301	AAAATGGACCAAAACGAGATCCAGATGTTGTGTATCTTTGTGTGTTAACCAATAT	360
OY	361	ATGATATAGAAAGATTAAATCTTTACTAAATATATTAATTTGGAATAAACCAACTTA	420
Db	361	ATGATATAGAAAGATTAAATCTTTACTAAATATATTAATTTGGAATAAACCAACTTA	420
OY	421	ATATGTGAGTGTCTTCAGTGTCTACGTTCAGAAATAATCTGTATATCTTATGAA	480
Db	421	ATATGTGAGTGTCTTCAGTGTCTACGTTCAGAAATAATCTGTATATCTTATGAA	480
OY	481	CTAGAAGTGAATATCATTAACACGTGAATTTTAAAGACCGTACATPAACACATGAT	540
Db	481	CTAGAAGTGAATATCATTAACACGTGAATTTTAAAGACCGTACATPAACACATGAT	540
OY	541	CGATCAAAATACAAATTTATATGAGACTGAATCCAAAGATGAGATGACTTAGCAGATTA	600
Db	541	CGATCAAAATACAAATTTATATGAGACTGAATCCAAAGATGAGATGACTTAGCAGATTA	600
OY	601	TACACAGCTAAGAAATTTGTACACAGAGTCGAAAAATAGATCTTAATCATTTAAAAAGA	660
Db	601	TACACAGCTAAGAAATTTGTACACAGAGTCGAAAAATAGATCTTAATCATTTAAAAAGA	660
OY	661	TATGATTTCAAGTTACGAGATGATATTAACCATTAACGCAATGATACATACATAATTTT	720
Db	661	TATGATTTCAAGTTACGAGATGATATTAACCATTAACGCAATGATACATACATAATTTT	720
OY	721	TGTTTTGTTTTAACGATTAATGAATGAATGATGTTTAAAAATATGTGTTTTACTAA	780
Db	721	TGTTTTGTTTTAACGATTAATGAATGAATGATGTTTAAAAATATGTGTTTTACTAA	780
OY	781	AACTCGTTTTATGTTAACTATATATGTCTTCCGACTGTAATTTGAACAAACTGTAA	840
Db	781	AACTCGTTTTATGTTAACTATATATGTCTTCCGACTGTAATTTGAACAAACTGTAA	840
OY	841	TACAAATATGTTAAAGCAATTCGATTAATAAAATCAACGGGTAGTAAATCCTCAGAAAT	900
Db	841	TACAAATATGTTAAAGCAATTCGATTAATAAAATCAACGGGTAGTAAATCCTCAGAAAT	900
OY	901	TATGTTAGTCTACAAATTTTCTCTTTAGTTAGTAAGTTTGAGACAAATTTATGTATA	960
Db	901	TATGTTAGTCTACAAATTTTCTCTTTAGTTAGTAAGTTTGAGACAAATTTATGTATA	960
OY	961	CCTTGCAAGGGTATTAAGSTCACTGATCAAGCTCAGAGATGAAGCCAAGAGTGTCTC	1020
Db	961	CCTTGCAAGGGTATTAAGSTCACTGATCAAGCTCAGAGATGAAGCCAAGAGTGTCTC	1020
OY	1021	TCTGTCTTAAGATATCTACAGCTGTCTTCCCTGTGAATGAAGAAATTTGAATGATGA	1080
Db	1021	TCTGTCTTAAGATATCTACAGCTGTCTTCCCTGTGAATGAAGAAATTTGAATGATGA	1080

QY	1081	GAGATCCCATCTAGGGTTTCAAGTTTGGCTTCTCGGTGCAACTTTGGCGGTGTGTACT	1140
Db	1081	GAGATCCCATCTAGGGTTTCAAGTTTGGCTTCTCGGTGCAACTTTGGCGGTGTGTACT	1140
QY	1141	TTTTTCTTAATGCGTGTGTGACATAATTTCTGAGGTGAGGTAACTAAGAAACT	1200
Db	1141	TTTTTCTTAATGCGTGTGTGACATAATTTCTGAGGTGAGGTAACTAAGAAACT	1200
QY	1201	AATATTCGAAAAGAAAAGAAAAAGGCAAGAAAATCTATTCGAAAAGACATAAATGAC	1260
Db	1201	AATATTCGAAAAGAAAAGAAAAAGGCAAGAAAATCTATTCGAAAAGACATAAATGAC	1260
QY	1261	ACTAAATTTGATTTATTAATAATGGTAATATGTTTGGTGAATTTATATCATTTACCA	1320
Db	1261	ACTAAATTTGATTTATTAATAATGGTAATATGTTTGGTGAATTTATATCATTTACCA	1320
QY	1321	AATCAAAAGAAAGAGAGAGGAGCCCTCTGCGCTAATGATAATTCCTCCTTAACAACCTGCT	1380
Db	1321	AATCAAAAGAAAGAGAGAGGAGCCCTCTGCGCTAATGATAATTCCTCCTTAACAACCTGCT	1380
QY	1381	CCCATATCTCTTTTATCTTCCAAACAATCATTTCAACAGAAAATCTGCTCGTGATC	1440
Db	1381	CCCATATCTCTTTTATCTTCCAAACAATCATTTCAACAGAAAATCTGCTCGTGATC	1440
QY	1441	ACTTTCATGCAAAATTAACATAAATTTTGGTAATTTTGTCAAGTCTGCTGTTTTAAG	1500
Db	1441	ACTTTCATGCAAAATTAACATAAATTTTGGTAATTTTGTCAAGTCTGCTGTTTTAAG	1500
QY	1501	TGGAATATTTGGTAATCTATATATGTGTGATATACATCCAGCTAATCAATAATTCAT	1560
Db	1501	TGGAATATTTGGTAATCTATATATGTGTGATATACATCCAGCTAATCAATAATTCAT	1560
QY	1561	CTCCTTCGCTTATCAATTAATAATTACACACATTTAGCTAATCAAGCTAATAATTACCA	1620
Db	1561	CTCCTTCGCTTATCAATTAATAATTACACACATTTAGCTAATCAAGCTAATAATTACCA	1620
QY	1621	CATTCCTTATCAATTTTATATATGGTAATTAATAAACAACGACTATATAGGCTACAGATT	1680
Db	1621	CATTCCTTATCAATTTTATATATGGTAATTAATAAACAACGACTATATAGGCTACAGATT	1680
QY	1681	GGTATTAAGGCATTAATGCTTCTTAAGTCGAAAGAAATTTTGTATGATTAACACTCGTG	1740
Db	1681	GGTATTAAGGCATTAATGCTTCTTAAGTCGAAAGAAATTTTGTATGATTAACACTCGTG	1740
QY	1741	GGAATAAATCAGCGCTAATATAGCTCATTTAAAGATTAATGATTTAAAGCTTTAATCA	1800
Db	1741	GGAATAAATCAGCGCTAATATAGCTCATTTAAAGATTAATGATTTAATATCTTTAATCA	1800
QY	1801	TTAAATTAATAAGTTTTTGTCTTTTAAAGGTACACACGCTTAATTCATCTAGAGAAAT	1860
Db	1801	TTAAATTAATAAGTTTTTGTCTTTTAAAGGTACACACGCTTAATTCATCTAGAGAAAT	1860
QY	1861	ATTAACTTTGATTCGAAATTCGAAATAATCTTTTTPAACATATAGAAAATTTTCAGCAATT	1920
Db	1861	ATTAACTTTGATTCGAAATTCGAAATAATCTTTTTPAACATATAGAAAATTTTCAGCAATT	1920
QY	1921	TTAAATAAAGGTCATTTATTTGGGTCAATAAATATGTTTCCAGTAAAGTTTGGAGCT	1980
Db	1921	TTAAATAAAGGTCATTTATTTGGGTCAATAAATATGTTTCCAGTAAAGTTTGGAGCT	1980
QY	1981	TTAAACAATGAATGTTTTTGTGATTTAAATAAACAATATTTTCTAGTAATTCACATT	2040
Db	1981	TTAAACAATGAATGTTTTTGTGATTTAAATAAACAATATTTTCTAGTAATTCACATT	2040
QY	2041	TTTAAACGTCATCCAGATTGTAAATTAAGTGAACAATCTGAAAACATTTTTTTTTCTTG	2100
Db	2041	TTTAAACGTCATCCAGATTGTAAATTAAGTGAACAATCTGAAAACATTTTTTTTTCTTG	2100
QY	2101	AATCTGTGTTTAAATCTCTCTGCGCGCATATCTGGAAGCATTTTGACCAACATATACATA	2160
Db	2101	AATCTGTGTTTAAATCTCTCTGCGCGCATATCTGGAAGCATTTTGACCAACATATACATA	2160
QY	2161	TTGAAAGCAAAATATTCACACGAGATATATAGGTTAATCCACATTCATATCTTTTGT	2220

2161 TTGAAAGCAAAATATCCACGAGGATGATGGGTTAGATCCCATCTTCAATATCTTTGT 2220
2221 CTTTGTATTATTAAGAAAAACAATATTATTCAGAAAAAAAGCTTTCTCTAGTGGTA 2280
2222 CTTTGTATTATTAAGAAAAACAATATTATTCAGAAAAAAAGCTTTCTCTAGTGGTA 2280
2281 TAGGTATAGATATTAACAAATTTTATCTAGTTATAGTATTTTCTATCTTCAAACTT 2340
2282 TAGGTATAGATATTAACAAATTTTATCTAGTTATAGTATTTTCTATCTTCAAACTT 2340
2341 ACCATCTTCAACATTAATTTGATCAATTTTATTTTATTTTCTAACTCTTCCACTA 2400
2401 AAAAAATGCAAAAGAAAGATATATTTTAAAGTCAAAATTTTAAAGATGGGTGAT 2460
2402 AAAAAATGCAAAAGAAAGATATATTTTAAAGTCAAAATTTTAAAGATGGGTGAT 2460
2461 TCTTCAGCAAAAGGGGCGGTAGAGGCTTATCCACTTACAGCTGGGTTGTGGCAG 2520
2462 TCTTCAGCAAAAGGGGCGGTAGAGGCTTATCCACTTACAGCTGGGTTGTGGCAG 2520
2521 ACATCATAGGGCTTACGTATATTTGAGCTTTACTGTACGTAAAGCTTTTACATCTAGT 2580
2581 TAGTCTCACTGTACAAACAAACAAATCCAAATCCAAATCATATATACAAATCTACTA 2640
2582 TAGTCTCACTGTACAAACAAACAAATCCAAATCCAAATCATATATACAAATCTACTA 2640
2641 GTATCATATCTTACAAACAAACAAATCCAAATCCAAATCATATATACAAATCTACTA 2700
2642 GTATCATATCTTACAAACAAACAAATCCAAATCCAAATCATATATACAAATCTACTA 2700
2701 CAAACTGTGATGTTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTTGGG 2760
2702 CAAACTGTGATGTTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTTGGG 2760
2761 AGCTACACTGTAGTCCCTTTTCCCAAAATATCTCTTACATCGACCGGTTAAAGT 2820
2762 AGCTACACTGTAGTCCCTTTTCCCAAAATATCTCTTACATCGACCGGTTAAAGT 2820
2821 ATTAAACCAACAAATTTTATTTGCTGAAGGTACAAACATGTACATATATAGAGA 2880
2822 ATTAAACCAACAAATTTTATTTGCTGAAGGTACAAACATGTACATATATAGAGA 2880
2881 CAGCATCGTTTATACAAATATGTTGCAATGTTATGGAATCAAAATATTAATGCG-AGTA 2940
2882 CAGCATCGTTTATACAAATATGTTGCAATGTTATGGAATCAAAATATTAATGCG-AGTA 2940
2941 GCGACTACTGTTTATATGTTTGAAGATATGAATTAATAA-ATGAATTCAAAGAT 2999
2942 GCGACTACTGTTTATATGTTTGAAGATATGAATTAATAA-ATGAATTCAAAGAT 2999
2999 GCGACTACTGTTTATATGTTTGAAGATATGAATTAATAA-ATGAATTCAAAGAT 2999
3000 ACAGAGCTATATATGCGGCTCATTTAGACCGGACCAAAAGTTGCTGTATTTCTA 3059
3001 ACAGAGCTATATATGCGGCTCATTTAGACCGGACCAAAAGTTGCTGTATTTCTA 3059
3060 CCGTCCGCTATAAGAAATTTTGAATTTTCTCAACCTTTTATGAATCTGTATAGTTT 3119
3061 CCGTCCGCTATAAGAAATTTTGAATTTTCTCAACCTTTTATGAATCTGTATAGTTT 3119
3120 TTGTGCGATTAATATTTGATTCGATATATTTTGTCTAAATATGATAGTAAATTC 3179
3121 TTGTGCGATTAATATTTGATTCGATATATTTTGTCTAAATATGATAGTAAATTC 3179
3180 ACATTAAGAAAGCTTTTATTTATTTATTTGATTTAACTTTTGTGTTTGAAGATGAC 3239
3181 ACATTAAGAAAGCTTTTATTTATTTATTTGATTTAACTTTTGTGTTTGAAGATGAC 3239
3240 TCATTAACAAGTTAAAGTTGATGATCAATTTTCAAAATATGTTTGAAGATGCGTT 3299

3240 TCATTAACAAGTTAAAGTTGATGATCAATTTTCAAAATATGTTTGAAGATGCGTT 3299
3300 CGAGGTCTTACACCATGATACCAATGATGGGTTATATTAATGTTTCTTCT 3359
3301 CGAGGTCTTACACCATGATACCAATGATGGGTTATATTAATGTTTCTTCT 3359
3360 TTTTCCAAATGCTTTTATTAATGAACCACTTAAATTTCTTTTAAATTAAGTTAAGA 3419
3361 TTTTCCAAATGCTTTTATTAATGAACCACTTAAATTTCTTTTAAATTAAGTTAAGA 3419
3420 TTTTCCAAATGCTTTTATTAATGAACCACTTAAATTTCTTTTAAATTAAGTTAAGA 3479
3421 TTTTCCAAATGCTTTTATTAATGAACCACTTAAATTTCTTTTAAATTAAGTTAAGA 3479
3480 AAAAAAGTTTCAATTAATTAAGAAATTTTAAAGTAAATTTTAAAGTTTAAAGTAAAG 3539
3481 AAAAAAGTTTCAATTAATTAAGAAATTTTAAAGTAAATTTTAAAGTTTAAAGTAAAG 3539
3540 TGAAGATTAATGATTTGCAAGTTTGAAGAAAGTGTGATGATGATGATGATGATGATGAT 3599
3541 TGAAGATTAATGATTTGCAAGTTTGAAGAAAGTGTGATGATGATGATGATGATGATGAT 3599
3600 ACATGATCAAAATTAATTTGCTGTAGCAAGAAAGAAAGATGAAATTAACAGAAACA 3659
3601 ACATGATCAAAATTAATTTGCTGTAGCAAGAAAGAAAGATGAAATTAACAGAAACA 3659
3660 TCGTTAACCACTTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAAGTAAAG 3719
3661 TCGTTAACCACTTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAAGTAAAG 3719
3720 GTATCATATCTTACAAACAAACAAATCCAAATCCAAATCATATATACAAATCTACTA 3779
3721 GTATCATATCTTACAAACAAACAAATCCAAATCCAAATCATATATACAAATCTACTA 3779
3780 AAGTATGTTTGTGCTGTACAGTTGATTTGATCTGCTCTTACCATATATGTTCTAA 3839
3781 AAGTATGTTTGTGCTGTACAGTTGATTTGATCTGCTCTTACCATATATGTTCTAA 3839
3840 GTTTTAAATGTTTGAAGCTTTTACAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3899
3841 GTTTTAAATGTTTGAAGCTTTTACAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3899
3900 GCTTAAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
3901 GCTTAAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
3960 CAGATCCCAACGATTTCAACAGCAAAATTTGCTGCTTCTCTTATTAATATAT 4019
3961 CAGATCCCAACGATTTCAACAGCAAAATTTGCTGCTTCTCTTATTAATATATAT 4019
4020 CCTCTCAAAACCCCTCTCTATATCTCTTAAAGCCCTCTCTCTCTCTCTCTCTCTCTCT 4079
4021 CCTCTCAAAACCCCTCTCTATATCTCTTAAAGCCCTCTCTCTCTCTCTCTCTCTCTCT 4079
4080 ACAAGAAAAACCAAAAGTTTGAAGAAATGCTGTTGCTGTTGTTGTTGTTGTTGTTGTTG 4139
4081 ACAAGAAAAACCAAAAGTTTGAAGAAATGCTGTTGCTGTTGTTGTTGTTGTTGTTGTTG 4139
4140 TTTTACCTTACTTACTTGAAGATTTTAAAGAAAGAAAGATGATATATATATATATATAT 4199
4141 TTTTACCTTACTTACTTGAAGATTTTAAAGAAAGAAAGATGATATATATATATATATAT 4199
4200 AAGAGAAAGCAAAACCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 4228
4201 AAGAGAAAGCAAAACCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 4228

RESULT 5
AAAS9220
ID AAAS9220 standard; cDNA; 2148 BP.
XX
AC
XX AAAS9220;

07-NOV-2000 (first entry)
 cDNA encoding an Arabidopsis aintegumenta (ANT) polypeptide.
 Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility;
 asexual reproduction; plant; male sterile plant; female sterile plant;
 early flowering; ss.
 Arabidopsis sp.
 Location/Qualifiers
 Key CDS 269..1936
 /tag= a
 /product= "aintegumenta polypeptide"
 WO200040694-A2.
 13-JUL-2000.
 07-JAN-2000; 2000MO-US000465.
 08-JAN-1999; 99US-00227421.
 (REGC) UNIV CALIFORNIA.
 Fischer RL, Mizukami Y;
 WPI; 2000-465969/40.
 P-PSDB; AAB07724.
 Modulating growth and cell proliferation in a plant used to alter organ
 mass, control fertility and enhance asexual reproduction in plants
 comprises modulating ANT activity and selecting plants with altered cell
 number.
 Claim 9; Page 40-41; 54pp; English.
 The present sequence encodes an aintegumenta (ANT) polypeptide. The ANT
 gene is expressed and functions not only in developing ovules but also in
 various developing organs. Growth and cell proliferation in plant can be
 modulated by modulating ANT activity. Modulation of ANT activity is used
 to alter organ mass, control fertility and enhance asexual reproduction
 in plants. Increased ANT activity can be used to produce male or female
 sterile plants. Inhibition of ANT activity can be used to truncate
 vegetative growth, resulting in early flowering
 Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
 Query Match 6.3%; Score 268; DB 3; Length 2148;
 Best Local Similarity 100.0%; Pred. No. 3.1e-35;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 3961 AGATCCCAAGGATTCAAAAGCAAAATTTGCTTCTCTCTTAATTAATATC 4020
 1 AGATCCCAAGGATTCAAAAGCAAAATTTGCTTCTCTCTTAATTAATATC 60
 4021 CTCTCAAAACCCCTCTATATCTCTTAAGCCCCCTTCTCTTCTTAACGCAA 4080
 61 CTCTCAAAACCCCTCTATATCTCTTAAGCCCCCTTCTCTTCTTAACGCAA 120
 4081 CAAAGAAAAAAGTTGAGAAAAATGCTGCTTCTTGTATCAATGATTTGGGT 4140
 121 CAAAGAAAAAAGTTGAGAAAAATGCTGCTTGTATCAATGATTTGGGT 180
 4141 TTTAGCTTACTACTTTCGAGATTTTAAGAAAGAGTGAAGATCATTATGAAAGA 4200
 181 TTTAGCTTACTACTTTCGAGATTTTAAGAAAGAGTGAAGATCATTATGAAAGA 240
 4201 AGAAGACGAGAAACCAAAAAAGAAACC 4228
 241 AGAAGACGAGAAACCAAAAAAGAAACC 268

RESULT 6
 ABX13437
 ID ABX13437 standard; DNA; 2148 BP.
 AC ABX13437;
 XX 04-JUN-2003 (first entry)
 DE A. thaliana AINTEGUMENTA DNA corresponding to Genbank U40256.
 XX Expression cassette; transgenic; promoter; LOX5; plant; food production;
 XX animal feed; seed; stress resistance; disease resistance; starch content;
 XX lipid content; dormancy; fibre content; pharmaceutical production;
 XX fine chemical production; sterile plant; vitamin; flavouring; perfume;
 XX dye; cotyledon; embryonic tissue; stress factor; LOX; ds.
 Arabidopsis thaliana.
 DE10127882-A1.
 12-DEC-2002.
 11-JUN-2001; 2001DE-01027882.
 11-JUN-2001; 2001DE-01027882.
 (BAD1) BASF PLANT SCI GMBH.
 Bischoff F, Feussner I, Loyall LP;
 WPI; 2003-279966/28.
 Cassette for expressing transgene, useful e.g. in production of
 pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene
 of Arabidopsis, provides cotyledon-specific expression.
 Claim 5; Page; 28pp; German.
 This invention describes a novel cassette for the transgenic expression
 of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis
 thaliana or deletion variants of the LOX5 promoter which are functionally
 linked to the nucleic acid of the invention. The cassette is used to
 prepare transgenic organisms, especially plants, for production of foods,
 animal feeds, seeds (including those with increased resistance to stress
 and disease, altered starch/lipid contents or dormancy, or altered fibre
 content), pharmaceuticals (especially antibodies, vaccines, enzymes and
 pharmaceutical proteins) and fine chemicals (especially enzymes,
 vitamins, amino acids, sugars, (unsaturated fatty acids, flavourings,
 perfumes and dyes), also to produce sterile plants. The LOX5 promoter
 confers strong and specific expression in cotyledons and/or other early
 embryonic tissue, so can degrade, or protect against, stress factors to
 which these tissues are particularly sensitive. Since cotyledons are the
 main storage organs of seeds, expressing transgenes in them produces
 targeted increases/modifications in nutritional value. Expression in the
 cotyledons is homogeneous, there are no side effects on other plant
 organs (pollen) and the promoter is functional in a wide variety of
 plants (ornamentals or crops). This sequence represents a nucleic acid
 sequence associated with the Arabidopsis thaliana LOX gene described in
 the disclosure of the invention
 Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
 Query Match 6.3%; Score 268; DB 8; Length 2148;
 Best Local Similarity 100.0%; Pred. No. 3.1e-35;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 3961 AGATCCCAAGGATTCAAAAGCAAAATTTGCTTCTCTCTTAATTAATATC 4020
 1 AGATCCCAAGGATTCAAAAGCAAAATTTGCTTCTCTCTTAATTAATATC 60
 4021 CTCTCAAAACCCCTCTATATCTCTTAAGCCCCCTTCTCTTCTTAACGCAA 4080
 61 CTCTCAAAACCCCTCTATATCTCTTAAGCCCCCTTCTCTTCTTAACGCAA 120

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QY      4081 CAAAGAAAAACAAGTTTGAGAAAAATGGTGTGCTTGTGTACCAATGATTGGGT 4140
      |||
      121 CAAAGAAAAACAAGTTTGAGAAAAATGGTGTGCTTGTGTACCAATGATTGGGT 180
QY      4141 TTTAGCTTACTACTTGCAGAGATTATPAGAAAGAGTGAAGATPACATTATAGAAAGA 4200
      |||
      181 TTTAGCTTACTACTTGCAGAGATTATPAGAAAGAGTGAAGATPACATTATAGAAAGA 240
QY      4201 AGAGAAAGCAGAAACCAAAAAAGAAACC 4228
      |||
      241 AGAGAAAGCAGAAACCAAAAAAGAAACC 268
Db
RESULT 7
ADG25135
ID      ADG25135 standard; cDNA; 2148 BP.
AC      ADG25135;
XX
XX      26-FEB-2004 (first entry)
DT
XX      Thalecress cDNA encoding Aintegumenta, ANT.
XX
XX      Thalecress; ss; gene; Aintegumenta; ANT; AP2 domain; plant; seed mass;
XX      asexual reproduction; reduced fertility.
OS      Arabidopsis thaliana.
XX
XX      Key      Location/Qualifiers
XX      FT      CDS
XX      CDS      269..1936
XX      FT      /*tag= a
XX      FT      /product= "Aintegumenta, ANT"
XX
XX      US6639128-B1.
XX
XX      28-OCT-2003.
PD
XX      07-JAN-2000; 2000US-00479855.
PF
XX      08-JAN-1999; 99US-00227421.
PR
XX      (NASC-) NAT SCI FOUNDD.
XX      PA
XX      Fischer RL, Mizukami Y;
XX
XX      WPI; 2003-842795/78.
XX      DR      P-PSDB; ADG25136.
XX
XX      New nucleic acid, useful in conferring desired traits on plants, such as
XX      increased seed mass, asexual reproduction or reduced fertility.
XX
XX      Example 1; SEQ ID NO 1; 25pp; English.
XX
XX      The invention relates to an isolated nucleic acid comprising a
XX      polynucleotide encoding a polypeptide having at least 90% identity with a
XX      Cnola Aintegumenta, ANT, (appearing as ADG25139) as determined using a
XX      BLAST algorithm and comprising two AP2 domains. Also included are an
XX      expression cassette comprising a plant promoter operably linked to a
XX      heterologous polynucleotide encoding the polypeptide, a vector comprising
XX      the expression cassette, a plant comprising the plant promoter operably
XX      linked to the heterologous polynucleotide, a method of asexually
XX      reproducing a plant and a method of reducing fertility in a plant. The
XX      nucleic acid is useful in conferring desired traits on plants, such as
XX      increased seed mass, asexual reproduction or reduced fertility. The
XX      present sequence encodes Thalecress Aintegumenta, ANT.
XX
XX      Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
SO
Query Match      6.3%; Score 268; DB 10; Length 2148;
      Best Local Similarity 100.0%; Pred. No. 3.1e-35;
      Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3961 AGATCCCAACGATTCGAAACAGCAAAATTTGTGCTTCTCTCTATTATATATATC 4020
      |||
      1 AGATCCCAACGATTCGAAACAGCAAAATTTGTGCTTCTCTCTATTATATATATC 60
QY      4021 CTCTCAAAAACCTCTCTCTATATCTCTTAAGCCCCCTTCTCTTCTCTACCGCAA 4080
      |||
      61 CTCTCAAAAACCTCTCTCTATATCTCTTAAGCCCCCTTCTCTTCTCTACCGCAA 120
QY      4081 CAAAGAAAAACAAGTTTGAGAAAAATGGTGTGCTTGTGTACCAATGATTGGGT 4140
      |||
      121 CAAAGAAAAACAAGTTTGAGAAAAATGGTGTGCTTGTGTACCAATGATTGGGT 180
Db
QY      4141 TTTAGCTTACTACTTGCAGAGATTATPAGAAAGAGTGAAGATPACATTATAGAAAGA 4200
      |||
      181 TTTAGCTTACTACTTGCAGAGATTATPAGAAAGAGTGAAGATPACATTATAGAAAGA 240
QY      4201 AGAGAAAGCAGAAACCAAAAAAGAAACC 4228
      |||
      241 AGAGAAAGCAGAAACCAAAAAAGAAACC 268
Db
RESULT 8
ADG88430
ID      ADG88430 standard; cDNA; 2148 BP.
AC      ADG88430;
XX
XX      11-MAR-2004 (first entry)
DT
XX
XX      Arabidopsis thaliana aintegumenta (ANT) cDNA.
XX
XX      Plant; genetic engineering; cell proliferation; aintegumenta; ANT;
XX      transgenic; transgenic plant; organ mass alteration; fertility;
XX      asexual reproduction; gene; ss.
OS      Arabidopsis thaliana.
XX
XX      Key      Location/Qualifiers
XX      FT      CDS
XX      CDS      269..1936
XX      FT      /*tag= a
XX      FT      /product= "Arabidopsis thaliana ANT protein"
XX
XX      US2003159180-A1.
XX
XX      21-AUG-2003.
PD
XX      28-JAN-2002; 2002US-00059911.
PF
XX      28-JAN-2002; 2002US-00059911.
PR
XX      (REGC ) UNIV CALIFORNIA OFFICE TECHNOLOGY.
XX      PA
XX      Fischer RL, Mizukami Y;
XX
XX      WPI; 2003-787370/74.
XX      DR      P-PSDB; ADG88431.
XX
XX      Increasing cell proliferation in a plant by introducing into the plant an
XX      expression cassette containing a plant promoter operably linked to a
XX      nucleic acid encoding a modified ANT polypeptide and selecting plants
XX      with increased mass.
XX
XX      Example 1; SEQ ID NO 1; 51pp; English.
XX
XX      The present invention relates to plant genetic engineering. The invention
XX      particularly relates to a method of increasing cell proliferation in a
XX      plant. The method involves introducing into the plant an expression
XX      cassette containing a plant promoter operably linked to a nucleic acid
XX      encoding a modified aintegumenta (ANT) polypeptide comprising an ANT AP2
XX      domain and selecting plants the with increased size or mass. The
XX      invention is useful to generate transgenic plants. The method is useful
XX      for increasing cell proliferation in a plant for altering organ mass,
XX      controlling fertility or enhancing asexual reproduction. The present

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RESULT 11
 ABZ10246
 ID ABZ10246 standard; DNA; 8056 BP.
 XX
 XX ABZ10246;
 AC
 XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Haematopoietic cell proliferation disorder related DNA sequence #386.
 XX
 XX Human; haematopoietic cell proliferation disorder; cytostatic;
 KM Gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KM cytosine methylation state; gene; de.
 XX
 OS Homo sapiens.
 XX
 PN MO20027272-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 26-MAR-2002; 2002MO-EP003401.
 XX
 PR 26-MAR-2001; 2001US-0278333P.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Berlin K, Braun A, Dietler J, Guettig D, Howe A, Mueller J,
 PI Olek A, Plegendroek C, Adorjan P, Grabs G, Lesche R, Leu E,
 PI Lewin A, Lipscher E, Meier S, Model F, Mueller V, Otto T, Pelet C,
 PI Schwobe I, Ziebarth H;
 XX
 DR WPI; 2003-018942/01.
 PT
 PT Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 XX
 PS Claim 28; SEQ ID NO 386; 117bp; English.
 XX
 XX The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 XX Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
 SQ
 Query Match 2.5%; Score 107.8; DB 8; Length 8056;
 Best Local Similarity 43.4%; Pred. No. 1.4e-08;
 Matches 1170; Conservative 0; Mismatches 1477; Indels 46; Gaps 13;
 QY 1505 TTATTGGTAATCTATATGCTGATATACACATCCAGCTATCAATATGATCTCC 1564
 DB 1868 TAATTAATATTTTATTTTATTTATTAATAAATAAATTTATTAATAAATAAATAA 1927

QY 1565 TTCTGCTATCAATTAATTACACCATTAGCTAATCAAGCTAATAATTACACCATTT 1624
 DB 1928 TTAATTTAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATT 1987
 QY 1625 CTCTTATCAATTTTATATGATATTAATAACACCGATATAGGCTACAGATTGTA 1684
 DB 1988 TTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2044
 QY 1685 TTAAGCATTAATGCTTCAGTCGAAAGAAATTTTGTATGATTAACATCGTGGAA 1744
 DB 2045 ATTTTATTTTATTTTAAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTA 2104
 QY 1745 AAAATCCAGCCATATATGCTCATTTTAAAGATTAATGATTTAAATGCTTTAATCA 1804
 DB 2105 AATTAATTAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2162
 QY 1805 AATAAAGGTTTTGCTTTTAAAGTTACACCGCTTAATTCATCTAGAGAAATTTA 1864
 DB 2163 AAAAAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2222
 QY 1865 ACTTGATGAAATTCGAAATTAATCTTTTAAACATTAAGAAATTTTCAGATTTTAA 1924
 DB 2223 AATTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2282
 QY 1925 ATAAAGGTAATTTATGCGTTCATTAATAATATGTTCCAGCTAAAGTTTGAGTTTAA 1984
 DB 2283 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2342
 QY 1985 CCACATGAATGTTTGTGATTTTAAATAACATTAATTTTCTAGTAAATTAACATTTTA 2044
 DB 2343 TTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2402
 QY 2045 ACCGTCATCCAGATTTGTAATTAAGCAAAATCTGAAACATTTTCTGTAATC 2104
 DB 2403 GAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATT 2462
 QY 2105 T--TGTTTAAATTTCTCTGCTGCATCTGACGAGCATTTGACCAAGCTATACATAT 2161
 DB 2463 TATATTTTATTTATTTATTTGTTTAAATTAATAATTAATTAATTAATTAATTAAT 2522
 QY 2162 TGAAGCAAAATATTCACACGAGGATATAGGTTAGATCCACATTCATATCTTTGTC 2221
 DB 2523 ATAAATTAATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2582
 QY 2222 TTTGTTATTTATGAAATAAATAAATAATTTATCAGGAAATAAAGCTTCTCTAGTGTAT 2281
 DB 2583 TAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2639
 QY 2282 AAGTATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2341
 DB 2640 AAAAAAATGTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 2699
 QY 2342 CCAATCTGACATTAATAATGATCAATTTTATTTTAACTAACTAATCTTCACTAA 2401
 DB 2700 TTAATTTTATTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2755
 QY 2402 AAAAATGCAAAAGAAAGATATATTTAAGTCAAAAGTATTAAGATGATGGTGAT 2461
 DB 2756 AAAAAATTTTAAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2815
 QY 2462 CTTCAGCAAAAGCGCCGATAGAGTGTCTATCTACATTAACAGCTGGGTGTGGCAGA 2521
 DB 2816 ATTAATTAATAATGATATTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATA 2875
 QY 2522 CATCATAGGCGCTACGATATTTGAGCT--TTACTGATCGTAAAGCTTTAATATCTAGT 2580
 DB 2876 AATTTTGTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2935
 QY 2581 TAGTCTCACTGTACAAACAAATTCGAATTTGTAACATATATACAAATCTACTA 2640
 DB 2936 AATGTAATAATTTTAAAGATTTATTTGTTTAAATAAATAAATAAATAAATAAATAAATT 2995
 QY 2641 GTACTAGATTAAGCTACGATATACATGCTTTTTCGAAATTTCTAAATCTATACAA 2700

[illegible]

Db	4049	ATTATTTTAAATTGCGTTTAAATGTTTTTTTAAATTTTGTGATATGTAATTTTTTTTAA	4108
Qy	3779	CAAGATGTTTTTTCGTGTCATCAGTGTGATTTGTAATCGTCTTACCCATATAGTTCTA	3838
Db	4109	ATTTTTTTTTTTTTATTTGTTTTTGTTTTTTATTTTAAATATATTTTTTGTTTAAATTTTTT	4168
Qy	3839	AGTTTTAAATGTTTTCAAAGACTTTACAAAATATAATTAATTAAGGTGAATTTGTAG	3898
Db	4169	TTATTTAATTTTTTTTTTTTTTTTTTTTGTGATTTAAATATGATTAATTAATGTAATTTTAA	4228
Qy	3899	GGCTTAAAGCAGAAAATTTAAATTTAAATTTAAAGTAAAGAAACGCTTTCTCAATAGAAC	3958
Db	4229	TATTTTTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTTTTGTATT	4288
Qy	3959	ACAGATCCCAACGGATTCAAACAGCAATTTGTGCTTGTCTCTATATATATA	4018
Db	4289	TAAATTTGAAATTAATTAATTAATTTTAAATTTT - TTTTATGATATTTTTTTGAAATTTATT	4347
Qy	4019	TCCTCTCAAAAACCCCTCTCCTATATCTCTCAAAAGCCGCCCTTGTCTCTACCGC	4078
Db	4348	TATTAATAATAATATATATATTTTAAATATGTTTAAATTTTTTTTGTATTTTTTTGT	4407
Qy	4079	AACAAAGAAAAACAAAGTTTGAGAAAATGCTGTGTTGTTGTATACCAATGATTGG	4138
Db	4408	ATTTTGAATGTGAAAAATTTTGGAAATGATTTGTATTAATAATTAATTAATTAAGAA	4467
Qy	4139	GTTTTAGCTTCTACTTCGAGAGATTTTAAAGAAAGAAAGTGAAGTACATT	4191
Db	4468	AAATTTGTTTAAATTTTTTTTAAATTAATGATTTAATAAAATTAATGAATATATTTT	4520
RESULT 12			
ABZ10100/C			
ID	ABZ10100	standard; DNA; 8056 BP.	
XX	AC	ABZ10100;	
XX	DT	16-JAN-2003 (first entry)	
XX	DE	Haematopoietic cell proliferation disorder related DNA sequence #240.	
XX	KX	Human; haematopoietic cell proliferation disorder; cytostatic;	
KM		gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;	
KM		Cytosine methylation state; gene; ds.	
XX	OS	Homo sapiens.	
OS	XX		
XX	PN	WO20027272-A2.	
XX	PD	03-OCT-2002.	
XX	PF	26-MAR-2002; 2002WO-EP003401.	
XX	PR	26-MAR-2001; 2001US-0278333P.	
XX	PA	(EPIC-) EPIGENOMICS AG.	
XX	PI	Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J,	
PI		Olek A, Pienbrock C, Adorjan P, Grabs G, Lesche R, Leu B,	
PI		Lewin A, Lipscher B, Maier S, Model F, Mueller V, Otto T, Pelet C;	
PI		Schwöpe I, Ziebarth H;	
XX	DR	WPI; 2003-018942/01.	
XX	PT	Detecting and differentiating between hematopoietic cell proliferative	
PT		disorders, comprises contacting a target nucleic acid with a reagent that	
XX	CC	distinguishes between methylated and non-methylated CpG dinucleotides.	
CC		Claim 28; SEQ ID NO 240; 117pp; English.	
CC		The present invention describes a method for detecting and	
CC		differentiating between haematopoietic cell proliferative disorders	
CC		associated with at least 1 gene and/or their regulatory regions in a	

CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. AB209861 to AB211118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients

XX Sequence 8056 BP; 371 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

Query Match 2.5%; Score 106.8; DB 8; Length 8056;

Best Local Similarity 41.8%; Pred. No. 2.1e-08;

Matches 1210; Conservative 0; Mismatches 1652; Indels 32; Gaps 8;

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QY 1140 TTTTCTTATGTCGTTGTTGCTAATTTTCTCGAGAGAGGTATCAAGAAAC 1199
DB 2890 TTTTCGAGAAATTTTTCGTAAATTAATTCGAAATTTTAATTTTAAATAA 2831
QY 1200 TAATATCGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1259
DB 2830 TCGTTTATTTATTAATAAGATTTTAATTAAGAAATTCGTTAAATTTAATA 2771
QY 1260 CACTAAATGATTAATAAAATGTAATATGTTGTAATTAATCAATTAACA 1319
DB 2770 CGATTAATTTTATTTTATTTAATTAATTTAATTAATTAATTTTATTA 2711
QY 1320 AATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379
DB 2710 AAAAAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2652
QY 1380 TCCACATCTCTTTTACTTCCAAACAAATCAATCAAGAGAAATCTGCTGAT 1439
DB 2651 TAAAGTTTTTTTATTTTATTTTAAATTAATTAATTAATTTTATTTTCTG 2592
QY 1440 CACTTCAGCAAAATTAATTAATTTTGTATTTTGTCAAGTTCTGCTGTTAA 1499
DB 2591 TATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2532
QY 1500 GTGATTAATTTGTATTAATCTATATGCTGATTAATCAATCAAGTAATTA 1559
DB 2531 TTAATTTATTTTATTTTATTTTGTATTAATTTTAAATTTTAAATTTTAA 2472
QY 1560 TCTCTTCTCTATCAATTAATTAATCAATTAATCAATTAATTAATTAATCA 1619
DB 2471 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2412
QY 1620 ACATCTCTTATCAATTTTATTAATGTAATTAATTAATTAATTAATTAAT 1679
DB 2411 TTAATTTGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2352
QY 1680 TGTATTAAGGATTAATGCTTCTAGTCGAGAGAAATTTTGTATTAATCA 1739
DB 2351 AAAAAATTAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTA 2292
QY 1740 GGGAGAAAAATCCAGCTTAATGCTCAATTAAGATTAATTAATTAATTA 1799
DB 2291 AATTAATTAATTAATTTTATTAATTTATTTAATTAATTAATTAATTAAT 2238
QY 1800 AATTAATTAATTAATTTTGTCTTTTAAAGTTACCAAGCTTAATTAATTA 1859
DB 2237 AATTAATTAATTAATTTTATTTTATTTTATTTTGTCTTTTAAATTTTAA 2178
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QY 1860 TATTAATCTTGAATCGAAATTCGAAATTAATTAATTAATTAATTAATTA 1919
DB 2177 AATTAATTAATTTTATTTTATTTTATTTTATTTTATTAATTAATTAATTA 2118
QY 1920 TTTAAATTAAGGATCAATTAATTTGGTTCGATTAATTAATTTTCCAGTAA 1979
DB 2117 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2058
QY 1980 TTTAACCAGATGAAGTTTATTTGATTAATAAAACATTAATTTCTAGTAAT 2039
DB 2057 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1998
QY 2040 TTTTAAACGTCATCCAGATTTGTAATTAAGTGAATTAATTAATTAATTAAT 2099
DB 1997 TTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1938
QY 2100 GAATCTTGTAAATTTCTCTGCTGCAATCTTGACGCAATTTGACCAATTA 2159
DB 1937 TATTAATTAATTAATTTTATTTTATTAATTAATTAATTAATTAATTAAT 1878
QY 2160 ATTGAAGAGAAATATCCACAGGATGAATAGGCTAGATCCAGATTAATCTTT 2219
DB 1877 TAATTAATTAATTAATTTTATTTTATTTTATTTTATTAATTAATTAATTA 1818
QY 2220 TCTTGTATTAATTAAGAAACAA-----ATATTTATCGAGAAAGAAAGCT 2265
DB 1817 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1758
QY 2266 TCTTCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2322
DB 1757 TTTATTTATTTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 1698
QY 2323 TTTACTATCTCAAACTTAATCAATCTTCAATTAATTAATTAATTAATTTT 2382
DB 1697 TTTATTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1638
QY 2383 ACTTAATCACTTCCACTAATAAAATGCAAAAGAGATTAATTAATTAATTAAT 2442
DB 1637 TACGATTCGTTTATTTTCAATTTTAAATTAATTAATTAATTAATTAATTA 1579
QY 2443 TAAAGATGATGGGATTTCTTCAAGCAAAAGCGCGTAGAGTCTTATCTCAT 2502
DB 1578 TAAATTAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTTTAA 1519
QY 2503 AAGCTGGGTTGGGAGATCATATAGGCTTAATTAATTAATTAATTAATTA 2562
DB 1518 ATATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1459
QY 2563 AGCTTAACATTAATCTAGTATGTTCTCACTGTACAAACAAATCCAAATCGTA 2622
DB 1458 AAAAAATTAATTTTATTTTATTTTATTTTAA-----AAAAAATTAATTA 1403
QY 2623 TATTAATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2682
DB 1402 TCGATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1343
QY 2683 CTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2742
DB 1342 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1283
QY 2743 TTTGAATTTGCAATTTGGAGCTTACACTTAATGCTTATTTTCCCAAAATTA 2802
DB 1282 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1225
QY 2803 ACATCGACCGTTTAAAGTATTTTAAACCAAAATTTTATTTGCTGAGGTACAA 2862
DB 1224 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1165
QY 2863 ATGTCATATTAATTAAGACAGATGTTTATTAATTAATTAATTAATTAATTA 2922
DB 1164 AATTAATTAATTTTATTTTCAATTCGAAATTAATTAATTAATTAATTAATTA 1106
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QY 2923 AATATATATACGAATTAGGACCTCAGTGGTTTATATAGTTGGAGATATAGAAATATA 2982
 DB 1105 TTTTAAACGTTAAAAAAGCAATTAACGAAATTTTATTTTACGTAATTTAA 1046
 QY 2983 AATGATTCAGAAAGATACAGCTATATATGCGGTCATTTAGACCGTGACCAAG 3042
 DB 1045 TTTCGAAATTAATAATTAATAATAATTTTAAATAATTTTAAATAATTTAA 986
 QY 3043 TTTCGTCGTAATTTCTACGCGTCATTAAGAAATTTTGACCTTTCTCACCTTTAT 3102
 DB 985 TATATATTTTATTCGTTTAAATTAATAATAATAATAATAATAATAATAATA 926
 QY 3103 GAATCTGTATGTTTGTTCGATATATATTTGATTCGTAATTTTGTTCGTA 3162
 DB 925 GAAACACAGAAATTAATTAATAATTAATAATTAATAATTAATAATTAATAATTA 866
 QY 3163 TAATGATACGTAATTTACGATTAAGAAAGCTCTTTTATTTTATTTGATTTAACTT 3222
 DB 865 AAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 806
 QY 3223 TTGTTTGGAAATGACTCATACCAAGTTAAAGTTGATGTCATTCATTAATAA 3282
 DB 805 ATTTTAAATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAA 746
 QY 3283 TGTTCGAGAGTCGCTCGAGTCCTACCACTCGTACCACTCGTATGGCTTATTA 3342
 DB 745 TTTTAAATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAAT 686
 QY 3343 TTAGTTTTTTTCTTTTCCAAATGCTTTATATTTGAACACACTGAAATTTCTTTT 3402
 DB 685 TTATATATTTTATTTTATTTTAAATTAATTAATTAATAATAATAATAATAATTT 626
 QY 3403 TTAATTTAGGTTAAGATCTGAATTTCTGTTGATTTTAAACCAAGTTTCAATCTT 3462
 DB 625 AATATTAATTAATTTTATTAATAATAATAATAATAATAATAATAATAATAATA 566
 QY 3463 CTTAGCACAAAAAAGGTTTCAATTTTAAAGATTTAAATTTTGAAGTTC 3522
 DB 565 CGTTTAAATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAAT 506
 QY 3523 AAGAGTTAATGATGAGCAAAAGTTTGAATGATTCAGATTTGCAACGAATGTCGA 3582
 DB 505 TATTAATTTTATTTTATTTTAAATTAATTTTATTTTAAATTTTATTTTAAATTT 446
 QY 3583 TGTAGTACATATCAAAAAATGATCAATAATTAATTTGCTTACCAAGAACAT 3642
 DB 445 TTATTTTAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 386
 QY 3643 TGAATTAACAGAACATCGTTAACCTTAATAATCTTAAGATTAATTTGTAGTATA 3702
 DB 385 AATATATTTTATTTGTTTTTTTTTTTAAATTAATTTTATTTTATTTTATTTTAA 326
 QY 3703 TTTTCGTAGAGAGAGGTATCAATCTTAATAATAATAATAATAATAATAATAAT 3762
 DB 325 ATATATTTTAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 266
 QY 3763 GTTGTCATCGTTACCAAGATGTTTTCGTGTCATCAGTGTATTTGAATCTGTCCT 3822
 DB 265 TAAAAATTTTAAATTTTAAATTTTAAATAATTTTAAATAATTTTAAATAATTAAT 206
 QY 3823 TAGCATATAGTTCTAAGTTTAAATGTTTCAAGACTTTACAAAAATTAATAATTAAT 3882
 DB 205 AATATATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 146
 QY 3883 AAGGTGAATTTGTAGGCTTAAGCAAAATTAATAATAATAATAATAATAAGTAAGAACGT 3942
 DB 145 ATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 86
 QY 3943 CTTTTCATATAGAACACAGATCCCAAGATTCAAACAGCAATTTGTGCTTGTCTT 4002
 DB 85 AAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 26
 QY 4003 CTCTCTTATTAATA 4016

DB 25 TTTATTTTATTTTAA 12
 RESULT 13
 ABZ10100
 ID ABZ10100 standard; DNA; 8056 BP.
 XX
 AC ABZ10100;
 XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Haematopoietic cell proliferation disorder related DNA sequence #240.
 XX
 KM Human; haematopoietic cell proliferation disorder; cytostatic;
 KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KM cytosine methylation state; gene; de.
 XX
 OS Homo sapiens.
 XX
 PN W0200277272-A2.
 PD 03-OCT-2002.
 XX
 PF 26-MAR-2002; 2002MO-EP003401.
 XX
 PR 26-MAR-2001; 2001US-0278333P.
 XX
 PA (EPig-) EPIGENOMICS AG.
 PI Berlin K, Braun A, Dietler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepndrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 PI Lewin A, Lipscher B, Mater S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwope I, Ziebarth H;
 XX
 DR WPI; 2003-018942/01.
 XX
 PT Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 XX
 PS Claim 28; SEQ ID NO 240; 117bp; English.
 XX
 CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 SQ Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;
 Query Match 2.4%; Score 99.4; DB 8; Length 8056;
 Best Local Similarity 42.6%; Pred. No. 3.5e-07;
 Matches 1195; Conservative 0; Mismatches 1566; Indels 46; Gaps 11;
 QY 1138 ACTTTTTCATATGTCGTTGTTGACTAATTTTCTCAGAGTGAGAGTGTAAATCAAGAA 1197

D	b	408	AATATATTATTAATTAATTTATTTTAAATAATATAAAAAATTAATTTAAAA	467
Q	y	1198	ACTAATATTCGAAAGAAGAAAAAGGCAGAAACATTAATGCGAAAAAGCATAAAT	1257
D	b	468	AATATTAATTAATTTAAATTAATAAAAAATTAATAATTTAATATTAATTAATTA	527
Q	y	1258	GACACTAATAATGGATTAATTAATAATGGTATATATATGTTGGTGAATTTATATCATTAAC	1317
D	b	528	TATATTTAAAAATTTAAATTTTATATATAATTAATTAACGTTTTATTAATAATTAATAT	587
Q	y	1318	CAAAATCAAGGAAGAGAGGAGACCTCTTCGCTATGATTTCCCTCCTAAACAAC	1377
D	b	588	TAAATATATATTAATTAATAAAAAATTAATATAAAATTTTAAAAATTTTAAAAATTAATTT	647
Q	y	1378	GCTCCCACTATCCTTTTAACTTCCAACAAAATCATTTACAAGAAAAATCTGCTCGT	1437
D	b	648	TAAATATATTAATTTTAAAAAATAAAAAATTAATAATTAATAAAAAATTTTATAT	707
Q	y	1438	ATCATTTCATGCAAAATTAACATAAATTTGGTATTTTGTGCAAGTCTGCTGTTTT	1497
D	b	708	TTAAATTTTAATTAATAATTAATTAATTAATTAATTAATTTTAAATTTTAAATTTTA	765
Q	y	1498	AAGTCGATTAATTTGGTAACTATATATGTTGGATATATACATCCAACTATCATTAAT	1557
D	b	766	ATTAATAATTAATAATTAATTAATTAATTAATTAATTAATAATTTTAAACGTTATTT	825
Q	y	1558	GATCCTCCTGCTTATCAATTAATTAACAACATATGCTAATCAGCTAATTAATTAACA	1617
D	b	826	AAATATATTTTATTAATAAAAAATCGTTTTTTTATTTTATTCGATATAAAAAATTTG	885
Q	y	1618	CCACATTCCTATCAATTTTATATATGATTAATAATAAACACGCACTATAGCTACAGA	1677
D	b	886	AATATTTAAATTAATTAATTTAAATTAATTTGTCGTTTTGCTAATAATTTTAAAAA	945
Q	y	1678	GTTGGTATTAAGGCAATTAATGCTTCATAGTGAAAGAAATTTTGTATGATTAACCTC	1737
D	b	946	ATTAATTTTATTTTATTTTAAACGATTAATAATATATTAATTAATTTTAAAAATA	1005
Q	y	1738	GTTGGAAAAAATACAGCTTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTAA	1797
D	b	1006	ATTAATTTTAAATAATTTTATTAATTTTATTTTAAATTTTAAATTAATTAATTAATA	1065
Q	y	1798	TCATTAATAATAAAGTTTGTCTTTTAAAGTTTACACGCTTAATTCATCATTAAGAG	1857
D	b	1066	AAATTTGTTTAAATCGTTTTTTTTTTTAAAGTTTAAACGTTATATATTCGTTTTTA	1125
Q	y	1858	AATATTAACCTTGATCGAAATTCGAAATATCTTTTAAACATTAAGAAATTTTCAGCA	1917
D	b	1126	A-----TATTTTTTCGATATCCGAAATTTAAATTAATTAATTTTCGATTAATTAATA	1180
Q	y	1918	TTTTTAATAATAAGGTCATTTATTTGGGTCAATTAATATGTTCCACGTAAATTTGGA	1977
D	b	1181	TTTAATTTTAAATTTTAAATTAATTAATTAATTTTATTAATTAATAATAATTTTTC	1240
Q	y	1978	GGTT-----TAACCATGATGATGTTTTTGAATTTAAAAAAACATAAATTTTCTAGTAA	2031
D	b	1241	GAAATTAATAAAAAAGTTACGTAAATTAATTAATTAATTAATAAAGCTAATTTTAAATA	1300
Q	y	2032	TTACACATTTTAAACGTCATCCAGATGTAATAGTGACAAATCTGAATAACATTTTTT	2091
D	b	1301	TTAATTAATTAATAAAAAATTTATTAATTAATTTTAAATAAAAAATTAATTTTAAT	1360
Q	y	2092	TTTTTCTGAATCTGTTTAAATCTCTGCTGCGATTAATTCGACGCAATTTGACCAACA	2151
D	b	1361	TTTAATTAATAAATTTATTTTATTAATAAATAATTAATTCGATTTTTTTTATTTTTT	1420
Q	y	2152	CTATACATTAAT---GAAGAATAATATTCACACGAGATGATAGGTTAGATCCACATTC	2208
D	b	1421	ATTTTATTTTATTAATAAAAAATTAATAATTTTATTAATAAATTAATTAATAATA	1480
Q	y	2209	AATATCTTTGTCCTTGTATTTATGAAAACAATAATTAATCAGAAAAAAACGTTTCT	2268

D	b		1461	AATTAATTATAATTAAATTATTTATATTAATATTAATAATATAATACGTTAAAAAATTTTTT	1540
O	y		2269	TCTCAGTGGRATPAAGTATPAGATATATACAAAATTTAACTACTAGTAAATGAATTTACT	2328
D	b		1541	AATAAAAATTAATTTTTTAAAAAATATATATTTAAATTTAATTTAATTTATATTTGTAA	1600
O	y		2329	ATCTCAAACTTACCACCTCTTCAAACATTAATATGATTCAAATTTTTATTTTTTTTACTBAA	2388
D	b		1601	TTTTATATTTTTYAAAAAAATCGAAATPMAAGAAATCGTAAAAATTTAAAAAAATTTTTAAT	1660
O	y		2389	CTACTCCACGTAAAAAAATGCAAAAGAAGATATATTTTTTAAGTCAGAAATTAAGA	2448
D	b		1661	TAATACGATAAAATTTTATTTTATTTAAATATATAAAAATTAAATTTATATTAATATATA	1720
O	y		2449	TGGATGGGTGATCTCTCACGAAACGGCGCGTAGAGTGCTTATCTACATTACACT	2508
D	b		1721	TATTTATATTTTAAATTATTTAATTAATAAATAAAAAATTTTTTAAATTAATAAATTT	1780
O	y		2509	GGGTTTGGCAGACATCATAGGGCCTACGTATATTGACCTTTACTGTACG--TAAAGC	2565
D	b		1781	AAAAATTATTTACGTTATTTATTTTAAATTTATATAATAAATMAAATTCGTTTTAAAAA	1840
O	y		2566	TTTACATATCTAGTATGTTCTCACGCTACAAACAACAAACAAATCCAATCGTACATAT	2625
D	b		1841	AAAAAAAAAAAAAAAAAAAAAAAAATTAATTTATTAATTTATTTTATTTTTTATATBAAA	1900
O	y		2626	ATACAAATCTACTAGTACTAGATTACGCTAGCTATACATCGCTTTTCGCAAAATTTCTA	2685
D	b		1901	ATPAABAAATTTTATAAAAAABAAAATPATTAATNTNA-----ATRTAATBAAAAAAA	1953
O	y		2686	AACATATCTATACAAACAACCTGAATGTTTGTGTTGAATTAATCTTAAACCAAGTTT	2745
D	b		1954	TATATTTTTTTAAAAATAAAAATPATTAATTAATTTTATTAATAAATTTAATAAATTTTA	2013
O	y		2746	GAAATGCCATTGGAGCTACCTCAGTACCCCTTTTCCCAGAAATATATCCTTACA	2805
D	b		2014	AATATATTTTAAAAATAAAAATATATTTTAAATATTTTATTTTAAABAAAATTTATBAA	2073
O	y		2806	TCGACCGGTTAAAGTATTTTAAACAACAATTTTAAATTTGTGCTAGAGCTACAAACATG	2865
D	b		2074	AATATTTTAAATATTAATAATATATTAATTAATTAATTAATTAATTAATTAATTAATTTT	2132
O	y		2866	TCACATATATAGAGACAGCATCGTTTATACAAATAATGTTCGATGTTATTTGAAAT---	2921
D	b		2133	TTAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAATTTTATTTAAAAAATTTTAA	2192
O	y		2922	-----CAANATTAATATPCGAATTAGCAGCTCCTGTTTATAGTTTGAAGAAAT	2974
D	b		2193	AAAAACGAAAAAATAAATAAATAAATAAATAAATAAATTTAATTTTAAATAAATAATTTT	2252
O	y		2975	GAATATTAATAATGAATTCAGAGATACAGAGCTATATATGTCCGGTCATTTAGCCGTG	3034
D	b		2253	AATATTTTAAATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT	2312
O	y		3035	ACCAAAAGTTTCGTGTAATTTCTACGCTCGGTCATPAGAATTTTGGACTTTTCTTAC	3094
D	b		2313	TATTAATTTTTCGTATTTAAATAAATTTATTTAATTTTAAATAATATTTTATTTTAA	2372
O	y		3095	CCTTTTATGAACCTCTGTATAGTTTTTGTCGATTAATATTTGTATTCGTATATTTTTT	3154
D	b		2373	TAAATTAATTTTAAATATTTTATTTTATTTTCGAAAAATTAATAAATAAATAATTTAAT	2432
O	y		3155	GTTCCTAATTAATGATACGTAAATTCACGATTAAGAAAGACTTCCTTTTATTTAAATTTGAT	3214
D	b		2433	TTTAAAAATTTAATTTTTTTTATTTTTTATTT--TATTAATTTTTTATTTATTTTCGTTTTAAA	2490
O	y		3215	TAAAACTTTTGTTTTTGGAAATGACTCATACACAAGTTTAAAGTTTGAATGTATCCAAAT	3274
D	b		2491	ATTAATTTAAATTTTAAACGAAAAATBAAAAAATAAATTTAATTAATAAATAATTAATAA	2550
O	y		3275	TACAAAAATGTTTTCGAGAGTGGCTTCGAGTGTCTACACCACTGTATCAACTGTATGG	3334
D	b		2551	AATTTAAAAATTTAATATATAATTTTTTAAAAAATTTAAAAAATTTAAACGAAAAAATAATATA	2610

QY 3335 GTTATATATAGGTTTCTTCTTTCATGCTTATATGACACCTTAAT 3394
 DB 2611 AATATTAATATATATATATATATATATATATATATATATATAT 2670
 QY 3395 TTTCTTTTAAATAGGTTTGAATGTTTCTGTTGATTTTAAACCAAGTTT 3454
 DB 2671 TAAATTAATTTTAAATTTTATATATATATATATATATATATAT 2730
 QY 3455 CAATCTCTTACGACAAATATATATATATATATATATATATATAT 3509
 DB 2731 TAAATTAATTTTAAATATATATATATATATATATATATATAT 2790
 QY 3510 ATTTTGAAGTTCAAGGTTTATGATGCTGAAAGTTATGATGCTGCA 3569
 DB 2791 ACGAATTTCTTTATATATATATATATATATATATATATATAT 2850
 QY 3570 ACGAATGCTGATGATGATGATGATGATGATGATGATGATGAT 3629
 DB 2851 AATATTCGAATTTTATGACAAATATATATATATATATATATAT 2910
 QY 3630 CAGAGAAACGATGAAATTAACAGAAATGCTTAACTTAAATCTTAA 3689
 DB 2911 AAAAAAAGCTTAAATTTTACGAAATGTTAAAGATTTATATGCTTAA 2970
 QY 3690 TTTGATGATATTTTCTGATGAGAGAGATGATGATGATGATGAT 3749
 DB 2971 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3030
 QY 3750 CAGATTAATTAATGTTTGTCAATGCTTAACTTAACTTAACTTAA 3808
 DB 3031 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3090
 QY 3809 TGTAACTGCTCTTACGATGATGATGATGATGATGATGATGAT 3868
 DB 3091 TTTTACGCGTAAATTTATATATATATATATATATATATATAT 3150
 QY 3869 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3915
 DB 3151 AATCGTTTATATATATATATATATATATATATATATATATAT 3197

 RESULT 14
 ADZ71091
 ID ADZ71091 standard; DNA; 2482 BP.
 AC ADZ71091;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE Human chromosome 2 contig DNA SBO ID NO 215.
 KM de; matrix attachment region; MAR; protein production.
 XX Homo sapiens.
 OS
 XX
 PN MO2005040377-A2.
 XX
 PD 06-MAY-2005.
 XX
 PF 22-OCT-2004; 2004MO-BP011974.
 XX
 PR 24-OCT-2003; 2003US-0513574P.
 XX
 PR 06-FEB-2004; 2004BP-00002722.
 XX
 PA (SELEX-) SELEXIS SA.
 PI Mermod N, Girod PA, Bucher P, Nguyen D, Calabrese D, Saugy D;
 PI Puttini S;
 XX WPI; 2005-333507/34.
 DR
 XX New purified and isolated DNA sequence having protein production

PT increasing activity comprises a bent DNA element and a binding site for a
 PT DNA binding protein, useful for increasing protein production activity in
 PT eukaryotic host cell.
 PS Disclosure; SEQ ID NO 215; 282bp; English.
 XX
 CC The invention relates to a purified and isolated DNA sequence having
 CC protein production increasing activity comprising at least one bent DNA
 CC element, and at least one binding site for a DNA binding protein. The
 CC purified and isolated DNA sequence comprising a first and a second
 CC isolated matrix attachment region (MAR) nucleotide sequence, which is a
 CC MAR nucleotide sequence selected from a purified and isolated DNA
 CC sequence above, a purified and isolated MAR DNA above, a purified and
 CC isolated clysmar element and/or fragment, a synthetic MAR sequence, a
 CC sequence complementary to it, its molecular chimera, or its combinations
 CC and variants, is useful for increasing protein production activity in a
 CC eukaryotic host cell. The present sequence represents a human chromosome
 CC 2 contig DNA.
 CC
 SQ Sequence 2482 BP; 1110 A; 27 C; 44 G; 1301 T; 0 U; 0 Other;

 Query Match 2.3%; Score 96.6; DB 14; Length 2482;
 Best Local Similarity 42.5%; Pred. No. 9.4e-07;
 Matches 949; Conservative 0; Mismatches 1249; Indels 33; Gaps 7;

 QY 1765 TCATTTAAGATTAATGATTTAATGCTTATATCATTAATTAATTAAGCTTTTCTTTT 1824
 DB 206 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 265
 QY 1825 AAGGTTACACCGCTTAATTCATCATTAGAGAAATTAATTAATTAATTAATTAAT 1884
 DB 266 TATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 325
 QY 1885 ATACTTTTAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1944
 DB 326 AATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 385
 QY 1945 GTTCATTAATTAATGTTTCCAGTAAAGTTGAGGTTTAAACATGATGATTTTGGAT 2004
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QY 2653 GCTACGATATACGCTTTTCCGCAATTTCTTAACCTATCTATACAAACAACTGATG 2712
DB 1106 TATCAT 1165
QY 2713 TTTGTTTGTATATATCTTAAACCAAGTTTGAATGTGCATGGAGCTACACTCTA 2772
DB 1166 TATATCTACAT 1225
QY 2773 GTCCCTTTTTCGCCAAATATCTCTTACATCGACCGGTAAAGTATTTAAACCAAC 2832
DB 1226 TATACAT 1285
QY 2833 AATTTTAAATTTGTCTGAGAGGTACAAACATGTACATATATATAGACAGCATCGT-- 2890
DB 1286 TATATATATATATCTTTTATATATATATATATATATATATATATATATATATAT 1345
QY 2891 -TATACAAATATATGTCATGTTATTTGAAATCAAAATATATATATATATATATAT 2949
DB 1346 ATATATAATGTAAT 1405
QY 2950 TTGGTTTAAATAGTTGGAAAGATATAGAAATATATATATATATATATATATATAT 3008
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DB 1586 AT 1645
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DB 2126 TGTAT 2185
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DB 2186 AAT 2245
QY 3773 CGTTACCAAGTATGTTTGTCTGTATATATATATATATATATATATATATATATAT 3832
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QY 3893 TTGTAGGCTAAAGCGAAAAATATATATATATATATATATATATATATATATATATAT 3952
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QY 3953 AAGACACACA 3963
DB 2425 TAT 2435

RESULT 15
ABN80291
ID ABN80291 standard; DNA; 7306 BP.
XX
AC ABN80291;
XX
DT 15-JUL-2002 (first entry)
XX
XX
DE Human chemically modified disease associated gene SEQ ID NO 308.
XX
KW Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
KW heart disease; epilepsy; histone deacetylation; muscular dystrophy;
KW dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
KW antidiabetic; cyclostatic; anticonvulsant; ds.
XX
OS Homo sapiens.
OS Synthetic.
PN MO200200927-A2.
XX
XX
PD 03-JAN-2002.
XX
PD 02-JUL-2001; 2001WO-EP007536.
XX
PF 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-130908/17.
XX
XX Novel nucleic acid useful for diagnosis and therapy of diseases
XX associated with development genes such as diabetes, comprises a sequence
XX of a segment of chemically pretreated DNA of genes associated with
XX development.
XX Claim 1; SEQ ID NO 308; 27bp; English.
XX
XX The invention relates to a nucleic acid (I) comprising a sequence at

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 09:02:01 ; Search time 20772 Seconds
(Without alignments)

11570.100 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtgcactctgcgcctcacg.....agaacccaacaaagaacc 4228

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5083141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Genembl:.*
1: gb_ba:.*
2: gb_in:.*
3: gb_env:.*
4: gb_cm:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pr:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sy:.*
12: gb_un:.*
13: gb_vl:.*
14: gb_hcg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4228	100.0	4228	6	BD274517 Methods f
2	4228	100.0	4228	6	AR316368 Sequence
3	4228	100.0	4228	6	AR427902 Sequence
4	4072.2	96.3	110766	15	ATT28119 Arabidops
5	4072.2	96.3	198493	15	ATCR1988 Arabidops
6	366.4	8.7	371	15	ATHS30550 Arabidops
7	366.4	8.7	371	15	ATHS31085 Arabidops
8	268	6.3	2148	6	BD274516 Methods f
9	268	6.3	2148	6	AR316367 Sequence
10	268	6.3	2148	6	AR427901 Sequence
11	268	6.3	2148	15	ATU60256 Arabidops
12	155	3.7	2056	15	AY080706 Arabidops
13	147	3.5	8056	6	AX599046 Sequence
14	120.6	2.9	349751	2	PFMAL4P3 Plasmodi
15	114	2.7	178670	8	AC104073 Homo sapi
16	107.8	2.5	8056	6	AX599046 Sequence
17	107.8	2.5	313050	2	PF929352 Plasmodi
18	106.8	2.5	8056	6	AX598900 Sequence

19	105.2	2.5	86826	2	PFMAL3P5	AL034556 Plasmodi
20	105	2.5	104992	14	AC005504	AC005504 Plasmodi
21	105	2.5	169546	14	AC004157	AC004157 Plasmodi
22	105	2.5	250421	2	AE014849	AE014849 Plasmodi
23	105	2.5	349751	2	PFMAL4P3	AL035476 Plasmodi
24	104.6	2.5	205130	14	AC105425	AC105425 Homo sapi
25	104	2.5	4601	2	DMU11584	U1584 Drosophila
26	104	2.5	19517	2	DMU37541	U37541 Drosophila
27	103.8	2.5	25757	2	AE014837	AE014837 Plasmodi
28	102.8	2.4	313050	2	PF929352	AL929352 Plasmodi
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44	92.6	2.2	7306	6	AX344883	AX344883 Sequence
45	92.4	2.2	67970	2	PFMAL1P3	AL031746 Plasmodi

ALIGNMENTS

RESULT 1	BD274517	4228 bp	DNA	linear	PAT 17-JUN-2003
LOCUS	BD274517				
DEFINITION	Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant.				
ACCESSION	BD274517				
VERSION	BD274517.1	GI:33084285			
KEYWORDS	JP 2002534078-A/2				
SOURCE	Arabidopsis thaliana				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Fischer, R.L. and Mizukami, Y.				
AUTHORS					
TITLE	Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant				
JOURNAL	Patent: JP 2002534078-A 2 15-OCT-2002;				
COMMENT	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA				
	OS Arabidopsis thaliana (thale cress)				
	PN JP 2002534078-A/2				
	PD 15-OCT-2002	JP 2000592392			
	PF 07-JAN-2000	US 09/227421			
	PI 08-JAN-1999	US 09/227421			
	PC ROBERT L FISCHER, YUKIKO MIZUKAMI				
	AC A01H1/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00	CC ANT			
FEATURES	source	Location/Qualifiers			
	FT promoter	Location/Qualifiers			
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		/organism="Arabidopsis thaliana"			
		/mol_type="genomic DNA"			
		/db_xref="taxon:3702"			
ORIGIN					
Query Match	100.0%;	Score 4228;	DB 6;	Length 4228;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 4228;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
1	GTGACTTGAAGCCTACCTGCTCTAATGACGACTGATGAGGAGCTCGAGATCCTTTA	60			

|||||
Db 1 GTCGACCTAGGCGCTCACTGGCGCTAAATACGACTCACTATGAGGAGCTCGAGATCTCTTA 60
QY 61 GTTAGAAAAAATCTTTCTTTGTAAGTGTGTGTGTGTTTAAGTCAATTAATACAGTAC 120
Db 61 GTTAGAAAAAATCTTTCTTTGTAAGTGTGTGTGTGTTTAAGTCAATTAATACAGTAC 120
QY 121 ACATGATATACCAATATATATATATGAAATGGAATATATCATTTAATGATGATGACAT 180
Db 121 ACATGATATACCAATATATATATATGAAATGGAATATATCATTTAATGATGATGACAT 180
QY 181 TAATATATATACGCTGACATTAACCAACCAATGTCTGCTTTATGATGATGATGAT 240
Db 181 TAATATATATACGCTGACATTAACCAACCAATGTCTGCTTTATGATGATGATGAT 240
QY 241 GTTGCACTTGATTAATGATATCTATATATTAATCTGGTTTATTTAAATCCGTCATAC 300
Db 241 GTTGCACTTGATTAATGATATCTATATTAATCTGGTTTATTTAAATCCGTCATAC 300
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Db 361 ATGATTATGGAAGATTAAATCTTTACTTAATTTAATAATTAATTTGAAAAACAACTTAA 420
QY 421 ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGAAATATCTGCTGTATCTCACTTGA 480
Db 421 ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGAAATATCTGCTGTATCTCACTTGA 480
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Db 901 TATGTTAAGTCTACAAATTTTCTCTTTAGATTAAGTGTGAGACAAATTTATGTATA 960
QY 961 CCTTGAGAGGGGTATTAAGGCTCACTGATGTCAAGTCACTCAAGTCAAGGAGAGTGTG 1020
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Db 1081 GAGATCCCATCTAGCGTTTCAAGTGTGCGTCTCCGTCCAACTTTGGCGTGTGACT 1140

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Db 1201 AATATTCGAAAAAGAAAAAGGCAAGAAAACTATGTGCAAAAGACATTAATGAC 1260
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QY 1381 CCCACTATCTTTTACTTCCACAAAAATCAATTCACAGAAAAATCTGCTCGATAC 1440
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Db 1441 ACTTTCATGCAAAATTTAACTAAATTTTGTGTAATTTTGTCAAGTCTTGCTTTAAG 1500
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Db 1501 TCGATTAATTTGATATATCTATATGTTGATATACATCCAGCTAATCAATTAATGAT 1560
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Db 2041 TTTAACCGTCAATCCAGATTTGAATTAAGGACAAATCTGAAACATTTTCTG 2100
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AR316368
LOCUS AR316368 4228 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6559357.
ACCESSION AR316368
VERSION AR316368.1 GI:31711159
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4228)
AUTHORS Fischer, R.L. and Mizukami, Y.
TITLE Methode for altering mass and fertility in plants
JOURNAL Patent: US 6559357-A 3 06-MAY-2003;
The Regents of the University of California; Oakland, CA
FEATURES
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 ACATGTGATATCAAT 180
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QY 1621 CATTCCTTATCAATTTTAT 1680
Db 1621 CATTCCTTATCAATTTTAT 1680
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Dp	1921	TTAAATTAAGGGGTACATTATTTGGGTCAATAAATATGTTCACGTAAGGTTGGAGT	1980
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Dp	1981	TTAAACCAATGATATGTTTTTGTATTTAAAAACATATAATTTTCTAGTAATACACAT	2040
Qy	2041	TTTAAACCGTCCATCCAGATGTGTAATAGTGCAAATCTGAAAACAATTTTTTTTTCTGG	2100
Dp	2041	TTTAAACCGTCCATCCAGATGTGTAATAGTGCAAATCTGAAAACAATTTTTTTTTCTGG	2100
Qy	2101	AATCGTGTAAATCTCTGCTGCGCATCTTGACGGATTTGACCAACGATACATA	2160
Dp	2101	AATCGTGTAAATCTCTGCTGCGCATCTTGACGGATTTGACCAACGATACATA	2160
Qy	2161	TTGAAAGCAAAATATTCACACAGGATGATAGGTTAGATCCCACTCAATCTTTTGT	2220
Dp	2161	TTGAAAGCAAAATATTCACACAGGATGATAGGTTAGATCCCACTCAATCTTTTGT	2220
Qy	2221	CTTGTGTATTTATGAAAAACAATATTTTATCAGGAAAAAAAGTTTCTTCTAGTGTA	2280
Dp	2221	CTTGTGTATTTATGAAAAACAATATTTTATCAGGAAAAAAAGTTTCTTCTAGTGTA	2280
Qy	2281	TAAAGTAATAGTAATTAACAAATTTTAATCTAGTAATGTAATTTACTTCTCAACT	2340
Dp	2281	TAAAGTAATAGTAATTAACAAATTTTAATCTAGTAATGTAATTTACTTCTCAACT	2340
Qy	2341	ACCATCTTCAACATTAAATATGATCAATTTTTTATTTTTTACTAACTACCTCCACTA	2400
Dp	2341	ACCATCTTCAACATTAAATATGATCAATTTTTTATTTTTTACTAACTACCTCCACTA	2400
Qy	2401	AAAAAATGCAAAAGAGATATATATTTAAGTCAAAGTAATTTAAGAATGATGGTGAT	2460
Dp	2401	AAAAAATGCAAAAGAGATATATATTTAAGTCAAAGTAATTTAAGAATGATGGTGAT	2460
Qy	2461	TCTTCAGCAAAACGGCCGCTAGAGGTGTCTTATCTTACATTACAGCTGGGTGTGGAG	2520
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Dp	2581	TAGTCTCTCACTGTACAAACAAATTCGTAATATATCAATACTACTA	2640
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Dp	2641	GTACTAGATTACGCTACGTATACATCGCTTTTTCGCAAAATTTCTAACTATATCAAA	2700
Qy	2701	CAAACTGAAATGTTGTTTGTATTTATCTTAAACCAAAAGTTTGAATGTGCAATGGG	2760
Dp	2701	CAAACTGAAATGTTGTTTGTATTTATCTTAAACCAAAAGTTTGAATGTGCAATGGG	2760
Qy	2761	AGTACACACTAGTCCCTTTTTCCTCCCAAAATATCTCTTACATCGACCGGTTAAAGT	2820
Dp	2761	AGTACACACTAGTCCCTTTTTCCTCCCAAAATATCTCTTACATCGACCGGTTAAAGT	2820
Qy	2821	ATTTTAAACCAAAATTTTAAATTTGTGCTGAGAGTCAAAATGTCCATATATAGAGA	2880
Dp	2821	ATTTTAAACCAAAATTTTAAATTTGTGCTGAGAGTCAAAATGTCCATATATAGAGA	2880
Qy	2881	CAGACATGTTATACAAATATNGTTCGATGTTATGGAATCAAAATATAATTAAGAAATTA	2940
Dp	2881	CAGACATGTTATACAAATATNGTTCGATGTTATGGAATCAAAATATAATTAAGAAATTA	2940
Qy	2941	GCGACTCACTTGTTTAAATAGTTTGGAGATATGAAATTAATAATGAAATCAAGATA	3000
Dp	2941	GCGACTCACTTGTTTAAATAGTTTGGAGATATGAAATTAATAATGAAATCAAGATA	3000
Qy	3001	CAGAGCTATATATGTCCGGTCAATTTAGACCGGTGACAAAAAGTTTCGTGTAATTTCTAC	3060

Db	3001	CAGAGCTATATATGTGGGTCAATTAGAGCCGTGACAAAGTTTCGTGTAAATTTCTAC	3060
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QY	3121	TGTCGGATTATATTTGTATTCGTATATTTTGTTCCTATATATGATACGTAAATTC	3180
Db	3121	TGTCGGATTATATTTGTATTCGTATATTTTGTTCCTATATATGATACGTAAATTC	3180
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Db	4081	CAAAAGAAAAACAAAGTTTGAAGAAAAATGTTGTCTTGTGTATACCAATGATTTGGT	4140

Qy	4141	TTTAGCTTACTACTCTTCGAGACATTTATAGAAAGAAAGAGTGAATCACTTATAGAAAGA	4200
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LOCUS	AR427902	4228 bp	DNA
DEFINITION	Sequence 3 from patent US 6639128.		linear
ACCESSION	AR427902		
VERSION	AR427902.1	GI:40186931	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 4228)		
TITLE	Flecher, R.L. and Mizukami, Y.		
JOURNAL	Methods for altering organ mass, controlling fertility and enhancing asexual reproduction in plants		
FEATURES	Patent: US 6639128-A 3 28-OCT-2003;		
source	National Science Foundation; Arlington, VA		
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Db	61	GTTAGAAAAAAGCTTTCTTTGTAACGTGTGTGTGTGTTTAAGTTCAATTAACTAGTC	120
Qy	121	ACATGTGATATCAACAATATATATATATGAAATTGGAATTAATCATATTAAGTTAGCAT	180
Db	121	ACATGTGATATCAACAATATATATATATGGAATTAATCATATTAAGTTAGCAT	180
Qy	181	TAAATATATATACGCTGACATTAACCAACCAATGTTCTGCTTTATAGATAGTTCTATAT	240
Db	181	TAAATATATATACGCTGACATTAACCAACCAATGTTCTGCTTTATAGATAGTTCTATAT	240
Qy	241	GTTGCACTGATATATAGTACTATATTAACCTGGGTTTATTTAAATCCGATCCATTAAC	300
Db	241	GTTGCACTGATATATAGTACTATATTAACCTGGGTTTATTTAAATCCGATCCATTAAC	300
Qy	301	AAAAGTGACAAAAAAGAGATCCATAGTGTGTTTACTTTGTTGTTACAGAGATAT	360
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Qy	361	ATGATTTATGAGAGATTAAATCTTTATCTAAATTAATTAATTTGAAAAAACAACCTTAA	420
Db	361	ATGATTTATGAGAGATTAAATCTTTATCTAAATTAATTAATTTGAAAAAACAACCTTAA	420
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Db	421	ATAATGTAAGGTCTTCAGTGTCTCACTGTTCAAGAAATATCTCGTATCTTCTTGA	480
Qy	481	CTAAGAGTTGATATACATAAACAAGTGAATTTTAAACGACCGTACATAACAATGAT	540
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Qy	541	CGATCAAAATACAAATTAATATATAGATCTAGAAATCCAGATGAGATGACTTAGAGATA	600

Db	541	CGATCGAATACAAATTTATTATGACATAGAAATCCAAAGTAGAGATGACTCTAGACGAAATG	600
Qy	601	TACACAGCTAAGAAATTTGTACAGAGAGTCGAAAAATAGATTCATATCATTTAAAAAGA	660
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Qy	1021	TCGTGCTTAAGATATCTACAGCTGCTTCGCTGTGAATAGAGAAATTTGAATGATGA	1080
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Qy	1081	GAGATCCCATGTACGGTTTCAAGTTTCCGTCGCGCAACTTGTGGCGTGTGTGACT	1140
Db	1081	GAGATCCCATGTACGGTTTCAAGTTTCCGTCGCGCAACTTGTGGCGTGTGTGACT	1140
Qy	1141	TTTTTCTTATATGTCGTTGTGACTAAATTTTCTCAGAGTAGAGTGTATCAAGAAAAC	1200
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Qy	1201	AATATTCGAAAAGAAAGAAAAAGCAGAGAAAATATTTGTGCAAAAAGACATTAATGAC	1260
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Qy	1261	ACTAATAATGTGATTAATTAATAATGTATATATGTTGTGGTGAATTTATATCAATTAACAA	1320
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Qy	1381	CCGACTATCCTTTTATCCTTCGCAACAAATCATTTCAACGAGAAAATCTGTCGTGATC	1440
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Qy	1441	ACTTTTCATGCAAAATTAACCTAAATTTTGTGATTTTGTGCAATTTCTTGCTGTTTTAAG	1500
Db	1441	ACTTTTCATGCAAAATTAACCTAAATTTTGTGATTTTGTGCAATTTCTTGCTGTTTTAAG	1500
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Qy	1621	CATTCTGTATCAATTTTATATGTATTAATTAACACCGACTATATAGGTACAGAGTT	1680
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Bevan, M., Robben, J., Grymoperez, B., Volckaert, G., Bancroft, I.,
Mewes, H. W., Lemcke, K. and Mayer, K. F. X.
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 110766)
EU Arabidopsis sequencing project.
REFERENCE Direct Submission
AUTHORS Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer
JOURNAL Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mpi.biochem.mpg.de, mayer@mpi.biochem.mpg.de Project
COORDINATOR: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@brc.ac.uk
COMMENT Information on performance of analysis and a more detailed
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 JOURNAL Unpublished
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 JOURNAL Unpublished
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 EU Arabidopsis sequencing project.
 AUTHORS Direct Submission
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 lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
 Laboratory, John Innes Centre, Colney Lane, NR4 7JY Norwich, UK,
 E-mail: michael.bevan@bbsrc.ac.uk
 COMMENT Information on performance of analysis and a more detailed
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 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>
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Db 39844 TAGAGAAATTTAATCTTGAATGCAAAATTCGAAATCTTTTAAACATTAAGAAATTT 39903
Qy 1912 TCAGATTTTAAATTAAGGGTACATTTATGAGTCAATTAATTAATGTTTCCAGTAAAG 1971
Db 39904 TCAGATTTTAAATTAAGGGTACATTTATGAGTCAATTAATTAATGTTTCCAGTAAAG 39963
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Db 39964 TTTGAGGTTTAAACACATGAATGTTTGTATTTAAATTAATTAATTTTC-TAGTA 40023
Qy 2031 ATTAACATTTTAAACGCTCAATCCAGATTTGTAATTAAGTGAACAAATCTGAAAAATTTT 2090
Db 40024 ATTAACATTTTAAACGCTCAATCCAGATTTGTAATTAAGTGAACAAATCTGAAAAATTTT 40083
Qy 2091 TTTTCTGTAATCTGTTTAAATTTCTCTGCTGCACTACTGCAAGCATTTGCAAGCAAG 2150
Db 40084 TTTTCTGTAATCTGTTTAAATTTCTCTGCTGCACTACTGCAAGCATTTGCAAGCAAG 40143
Qy 2151 ACTATACATTTGAAGCAAAATATCCACAGGAGTATAGGGTTAGATCCACATTCAA 2210
Db 40144 ACTATACATTTGAAGCAAAATATCCACAGGAGTATAGGGTTAGATCCACATTCAA 40203
Qy 2211 TATCTTTGTCTTGTATTTATGAAAAACAATTTTATCAGGAAAAAAAGCTTTCTTC 2270
Db 40204 TATCTTTGTCTTGTATTTATGAAAAACAATTTTATCAGGAAAAAAAGCTTTCTTC 40263
Qy 2271 TCTAGGCTATTAAGTATTAAGTATTAACAATTTTATCTAGTAAATGATTTACTAT 2330
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 DB 41036 GTAATTTCTACGGTCCGTCAATAAGAAATTTTGAACCTTTCTTCAACCCTTTATGAACCTTC 41095
 QY 3110 TGTATAGTTTGTGCGATTAATATATTTGATTCGTATATTTTGTCTTAATAATGAT 3169
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 QY 3770 AATCGTTACCAATATGTTTGTCTGATCATGTTGATTTGTAACCTGCTCTTACCAT 3829
 DB 41756 AATCGTTACCAATATGTTTGTCTGATCATGTTGATTTGTAACCTGCTCTTACCAT 41815
 QY 3830 ATATGTTCTAAGTTTAAATGTTTCAAGACCTTTACAAATAATTAATATATAGTGG 3889
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 QY 3890 AATTTGTAGGGCTTAAAGGCAAAATTAATAATTAAGTAAAGAAAGCTTCTCTC 3949
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 DB 41996 ATTTATATATCTCTCAAAAAACCTCTCTCTATATCTCTTAATAGCCCTCTCTGTTT 42055
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 DB 42116 AATGATGGGTTTATGCTTACTACTTCAAGATTTTAAGAAAGATGTAAGATACA 42175
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 DB 42176 TTATAGAAAGAGAGAGCAAAACCAAAAAAGAAACC 42214

RESULT 6
 ATHS30550 371 bp DNA linear PLN 29-MAR-2003
 LOCUS
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 21206.
 ACCESSION AJ530550
 VERSION AJ530550.1 GI:26798810
 KEYWORDS left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1
 REFERENCE
 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.

TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

PUBMED 12446565

REFERENCE 2 (bases 1 to 371)

AUTHORS Balzerque, S.

TITLE Direct Submission

JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobio.gen.fr>).

FEATURES

Source

1. .371

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="212A06"

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/ecotype="Wassilewskija"

1. .371

/note="T-DNA flanking sequence

left border"

ORIGIN

Query Match 8.7%; Score 366.4; DB 15; Length 371;

Best Local Similarity 99.7%; Pred. No. 2.5e-39;

Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2457 TGAATTCGCAAAACGGCGCGGTAGAGTGTCTTATCTTACATTAACAGCTGGGTGTG 2516

DB 4 TCAATCTTCGCAAAACGGCGCGGTAGAGTGTCTTATCTTACATTAACAGCTGGGTGTG 63

QY 2517 GCAGACATCATAGGGCGCTACGTATATTGAGCTTTAGCTGTAACGTTTAACATATC 2576

DB 64 GCAGACATCATAGGGCGCTACGTATATTGAGCTTTAGCTGTAACGTTTAACATATC 123

QY 2577 TAGTATGTTCTCACTGTAACAAACAAATCAATTCGTAACATATATACAAATATCT 2636

DB 124 TAGTATGTTCTCACTGTAACAAACAAATCAATTCGTAACATATATACAAATATCT 183

QY 2637 ACTAGTACTAGTATAGGCTACGTATACATCGCTTTTTCGCAAAATTTCTAAATCTAT 2696

DB 184 ACTAGTACTAGTATAGGCTACGTATACATCGCTTTTTCGCAAAATTTCTAAATCTAT 243

QY 2697 ACAACAACTGTAATGTTGTTTGTATTTATCTTAACCAAGTTTGAATTTGTCAT 2756

DB 244 ACAACAACTGTAATGTTGTTTGTATTTATCTTAACCAAGTTTGAATTTGTCAT 303

QY 2757 TGGAGCTACACTGATGTCCTTTTTCGCCAAATAATCTCTTACATGACCGGTTA 2816

DB 304 TGGAGCTACACTGATGTCCTTTTTCGCCAAATAATCTCTTACATGACCGGTTA 363

QY 2817 AAGTATTT 2824

DB 364 AAGTATTT 371

RESULT 7

ATHS31085 371 bp DNA linear PLN 29-MAR-2003

LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone

DEFINITION 225808.

ACCESSION AJ531085

VERSION AJ531085.1 GI:26799345

KEYWORDS left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1

AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Denose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.

TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

PUBMED 12446565

REFERENCE 2 (bases 1 to 371)

AUTHORS Balzerque, S.

TITLE Direct Submission

JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

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FEATURES

Source

1. .371

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="225808"

/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Wassilewskija"

1. .371

/note="T-DNA flanking sequence

left border"

ORIGIN

Query Match 8.7%; Score 366.4; DB 15; Length 371;

Best Local Similarity 99.7%; Pred. No. 2.5e-39;

Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2457 TGAATTCGCAAAACGGCGCGGTAGAGTGTCTTATCTTACATTAACAGCTGGGTGTG 2516

DB 4 TCAATCTTCGCAAAACGGCGCGGTAGAGTGTCTTATCTTACATTAACAGCTGGGTGTG 63

QY 2517 GCAGACATCATAGGGCGCTACGTATATTGAGCTTTAGCTGTAACGTTTAACATATC 2576

DB 64 GCAGACATCATAGGGCGCTACGTATATTGAGCTTTAGCTGTAACGTTTAACATATC 123

QY 2577 TAGTATGTTCTCACTGTAACAAACAAATCAATTCGTAACATATATACAAATATCT 2636

DB 124 TAGTATGTTCTCACTGTAACAAACAAATCAATTCGTAACATATATACAAATATCT 183

QY 2637 ACTAGTACTAGTATAGGCTACGTATACATCGCTTTTTCGCAAAATTTCTAAATCTAT 2696

DB 184 ACTAGTACTAGTATAGGCTACGTATACATCGCTTTTTCGCAAAATTTCTAAATCTAT 243

QY 2697 ACAACAACTGTAATGTTGTTTGTATTTATCTTAACCAAGTTTGAATTTGTCAT 2756

DB 244 ACAACAACTGTAATGTTGTTTGTATTTATCTTAACCAAGTTTGAATTTGTCAT 303

QY 2757 TGGAGCTACACTGATGTCCTTTTTCGCCAAATAATCTCTTACATGACCGGTTA 2816

DB 304 TGGAGCTACACTGATGTCCTTTTTCGCCAAATAATCTCTTACATGACCGGTTA 363

QY 2817 AAGTATTT 2824

DB 364 AAGTATTT 371

Db 364 AAGTATT 371

RESULT 8
LOCUS BD274516

DEFINITION BD274516 2148 bp DNA linear PAT 17-JUL-2003
enhancing asexual reproduction in plant.

ACCESSION BD274516

VERSION BD274516.1 GI:33084284

KEYWORDS JP 2002534078-A/1.
Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 2148)
Fischer, R.L. and Mizukami, Y.
Methods for modifying weight of organ, controlling fertility and
enhancing asexual reproduction in plant
Patent: JP 2002534078-A 1 15-OCT-2002;

AUTHORS THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

JOURNAL OS Arabidopsis thaliana (thale cress)

COMMENT PN JP 2002534078-A/1
PD 15-OCT-2002
PF 07-JAN-2000 JP 2000592392
PR 08-JAN-1999 US 09/227421
PI ROBERT L FISCHER, YUKIKO MIZUKAMI
PC A01H1/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC
A1NTEGUMENTA (ANT)

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/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4021 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTCTCTTGTCTTACCGCA 4080
61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTCTCTTGTCTTACCGCA 120

Db 4081 CAAAGAAAAACAAAGTTGAGAAAAATGTGTCTTCTGTACCAATATGGGT 4140
121 CAAAGAAAAACAAAGTTGAGAAAAATGTGTCTTCTGTACCAATATGGGT 180

QY 4141 TTATGCTTACTACTTGAGAGATTATAGAAAAGAGAGATACATTATAGAAAG 4200
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Db 4201 AGAGAGACAGAAACCAAAAAGAAACC 4228

QY 241 AGAGAGACAGAAACCAAAAAGAAACC 268

RESULT 9
LOCUS AR316367

AR316367 2148 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 1 from patent US 6559357.
ACCESSION AR316367
VERSION AR316367.1 GI:31711158

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2148)
Fischer, R.L. and Mizukami, Y.
Methods for altering mass and fertility in plants
Patent: US 6559357-A 1 06-MAY-2003;
The Regents of the University of California; Oakland, CA

AUTHORS

JOURNAL

FEATURES
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 6.3%; Score 268; DB 6; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3961 AGATCCCAACGATTCACCAAGCAAAATTTGTGCTTCTCTCTTATTAATATC 4020
1 AGATCCCAACGATTCACCAAGCAAAATTTGTGCTTCTCTCTTATTAATATC 60

QY 4021 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTCTCTTGTCTTACCGCA 4080
61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTCTCTTGTCTTACCGCA 120

Db 4081 CAAAGAAAAACAAAGTTGAGAAAAATGTGTCTTCTGTACCAATATGGGT 4140
121 CAAAGAAAAACAAAGTTGAGAAAAATGTGTCTTCTGTACCAATATGGGT 180

QY 4141 TTATGCTTACTACTTGAGAGATTATAGAAAAGAGATACATTATAGAAAG 4200
181 TTATGCTTACTACTTGAGAGATTATAGAAAAGAGATACATTATAGAAAG 240

Db 4201 AGAGAGACAGAAACCAAAAAGAAACC 4228

QY 241 AGAGAGACAGAAACCAAAAAGAAACC 268

RESULT 10
LOCUS AR427901

DEFINITION AR427901 2148 bp DNA linear PAT 18-DEC-2003
Sequence 1 from patent US 6639128.

ACCESSION AR427901

VERSION AR427901.1 GI:40186930

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2148)
Fischer, R.L. and Mizukami, Y.
Methods for altering organ mass, controlling fertility and
enhancing asexual reproduction in plants
Patent: US 6639128-A 1 28-OCT-2003;
National Science Foundation; Arlington, VA

AUTHORS

JOURNAL

FEATURES
source 1..2148
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/mol_type="genomic DNA"

ORIGIN

Query Match 6.3%; Score 268; DB 6; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3961 AGATCCCAACGATTCACCAAGCAAAATTTGTGCTTCTCTCTTATTAATATC 4020
1 AGATCCCAACGATTCACCAAGCAAAATTTGTGCTTCTCTCTTATTAATATC 60

QY 4021 CTCTCAAAAAACCTCTCTATATCTCTCTAAAGCCCTTCTTGTCTCTACCGCA 4080
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 QY 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTAAACCAATGATGGGT 4140
 DB 121 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTAAACCAATGATGGGT 180
 QY 4141 TTTTACTTACTCTCGAGAGATTATAGAAAAAGAGTGAAGATCATTTATGAAAGA 4200
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 DB 241 AGAAGACGAGAAACCAAAAAAGAAACC 268
 RESULT 11
 ATU40256 2148 bp mRNA linear PLN 10-JAN-2005
 LOCUS Arabidopsis thaliana ovule development protein (AINTEGUMENTA) mRNA,
 complete cds.
 ACCESSION U40256
 VERSION U40256.1 GI:1209098
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2148)
 REFERENCE Klucher K.M., Chow H., Reiser L. and Fischer R.L.
 TITLE The AINTEGUMENTA gene of Arabidopsis required for ovule and female
 gametophyte development is related to the floral homeotic gene
 APETALA2
 JOURNAL Plant Cell 8 8 (2), 137-153 (1996)
 PUBMED 8742706
 REFERENCE 2 (bases 1 to 2148)
 AUTHORS Klucher K.
 TITLE Direct Submission
 JOURNAL Submitted (07-NOV-1995) L. Reiser, Plant Biology, UC Berkeley, 111
 Koshland Hall, Berkeley, CA 94720, USA
 FEATURES
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 269..1936
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 /note="Ap2 domain containing protein"
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 /protein_id="AA01040.1"
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 ORIGIN
 Query Match 6.3%; Score 268; DB 15; Length 2148;
 Best Local Similarity 100.0%; Pred. No. 1.6e-26;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3961 AGATCCCAAGGATTCGAAGCAAAATTTGCTTGTCTCTCTATATATATATC 4020
 DB 1 AGATCCCAAGGATTCGAAGCAAAATTTGCTTGTCTCTCTCTATATATATC 60
 QY 4021 CTCTCAAAAAACCTCTCTATATCTCTCTAAAGCCCTTCTTGTCTCTACCGCA 4080
 DB 61 CTCTCAAAAAACCTCTCTATATCTCTCTAAAGCCCTTCTTGTCTCTACCGCA 120
 QY 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTAAACCAATGATGGGT 4140
 DB 121 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTCTGTGTAAACCAATGATGGGT 180
 QY 4141 TTTTACTTACTCTCGAGAGATTATAGAAAAAGAGTGAAGATCATTTATGAAAGA 4200
 DB 181 TTTTACTTACTCTCGAGAGATTATAGAAAAAGAGTGAAGATCATTTATGAAAGA 240
 QY 4201 AGAAGACGAGAAACCAAAAAAGAAACC 4228
 DB 241 AGAAGACGAGAAACCAAAAAAGAAACC 268
 RESULT 12
 AY080706 2056 bp mRNA linear PLN 18-SEP-2002
 LOCUS Arabidopsis thaliana putative ovule development protein
 Aintegumenta (At4g37750) mRNA, complete cds.
 ACCESSION AY080706
 VERSION AY080706.1 GI:19310586
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2056)
 REFERENCE Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bower L.,
 Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B.,
 Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T.,
 Satou M., Seki M., Shim P., Southwick A., Shinozaki K.,
 Davis R.W., Ecker J.R. and Theologis A.
 TITLE Arabidopsis Full Length cDNA Clones
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2056)
 AUTHORS Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 Dang J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 Tang C.C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bower L.,
 Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B.,
 Lin J., Meyer M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 Sakurai T., Satou M., Seki M., Shim P., Southwick A.,
 Shinozaki K., Davis R.W., Ecker J.R. and Theologis A.
 TITLE Direct Submission
 JOURNAL Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN
 Arabidopsis Full-length cDNA') : Seki M., Narusaka M., Ishida J.,
 Satou M., Kamiya A., Sakurai T., Carninci P., Kawai J.,
 Hayashizaki Y. and Shinozaki K.
 The Salk, Stanford, PGSC (SSP) Consortium members carried out the
 sequencing and annotation of the RAPL cDNAs: Yamada K., Banh J.,
 Chan M.M., Chang C.H., Chang E., Dale J.M., Dang J.M.,
 Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C.C.,
 Toriumi M., Wu H.C., Yamamura Y., Yu G., Bower L., Chen H.,
 Cheuk R., Jones T., Karlin-Neumann G., Kim C., Lam B., Lin J.,
 Meyer M.C., Miranda M., Nguyen M., Palm C.J., Shim P.,
 Southwick A., Davis R.W., Ecker J.R. and Theologis A.
 Yamada K. (SSP/PGSC) and Seki M. (RIKEN GSC) contributed equally to
 this work. Shinozaki K. (RIKEN GSC) and Theologis A. (SSP/PGSC)

Qy	891	CTCGAAGACTATGTAGTAGTCACAAATTTTCTCTTGATGTATGTAAGAGTTTGAGACAA	950
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Db	1649	TTTTTTTAAATTTTACATTTATTTATTTTCAATTTTTTAAATTAATTAATAATTAATTA	1590
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D	68448	TATATTTTATTTAATTAATTTATTTATTAATTAATTAATTAATTAATTAATTAATTA	68389
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QY	3339	ATTATTAAGTTTCTTCTTTTCCAAATGCTTTTAAATTTGAACACTCTAAATTTCT	3398
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DEFINITION Homo sapiens BAC clone RP11-328P23 from 7, complete sequence.
ACCESSION AC104073 AC060805
VERSION AC104073.3 GI:19310339
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE 1 (bases 1 to 178670)
AUTHORS Sulston, J.E. and Wilson, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 9847074
REFERENCE 2 (bases 1 to 178670)
AUTHORS Cotton, M., Dignan, G. and Kyung, K.
TITLE The sequence of Homo sapiens BAC clone RP11-328P23
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 178670)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE 4 (bases 1 to 178670)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 5 (bases 1 to 178670)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (29-APR-2003) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 6 (bases 1 to 178670)
AUTHORS Wilson, R.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-2003) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
            On Mar 9, 2002 this sequence version replaced gi:18042409.
COMMENT ----- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu
            Contact: sapiens@watson.wustl.edu
            ----- Summary Statistics
            Center project name: H_NH0328P23
            Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NIGRI Chromosome 7 Mapping
Project (Eric D. Green, Director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/CTB/CHR7, send
mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu

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SOURCE INFORMATION:
The RPCT-11 human BAC library was made from the blood of one male
donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Cataneese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACe3.6.
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Best Local Similarity 43.0%; Pred. No. 9.6e-07;
Matches 1134; Conservative 0; Mismatches 1480; Indels 22; Gaps 11;

QY 1142 TTTTCTTATGTCGTTGTTGACTAATTTCTCAGAGTGAGAGTGAATCAGAAAACTA 1201
DB 91351 TATATATCATATATATATATATATATATATATATATATATATATATATATATATAT 91292
QY 1202 ATATTGGAAGAAAAAGAAAAAGCAAAAGCAATTTGCGAAGAAAGCATTAATGACA 1261
DB 91291 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 91232
QY 1262 CTAAATTTGATTTATTAATATGATATATATGTTGGGAAATTTAAATCATTAAC--CA 1319
DB 91231 TATTAATATATATATATATATATATATATATATATATATATATATATATATATAT 91172
QY 1320 AATCAAGAGAGAGAGAGAGCTTCCTGTCGCTTAATGATTTCCCTCTAAACAATGCG 1379
DB 91171 TATATATATTTATCATATATATATATATATATATATATATATATATATATATATAT 91112
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QY 1380 TCCCACTATCTTTTCTTCTCCAACAAAATCATTCACAGAGAAATCTG--TCTGCTGA 1438
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QY 1439 TCACCTTCATGCAAAATTAACATAATTTGGTATTTTGGCAAGTCTTCTGCTTTTA 1498
DB 91051 TTTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 90992
QY 1499 AGTCGATTTATTTGGTAATCTATATGTCGATATATACATCCAGCTAATCAATTAATG 1558
DB 90991 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 90932
QY 1559 ATCTCCTTCCTTCATATTAATTAACACAGATTAAGTAAATCAAGCTAATTAATTAAC 1618
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QY 1679 TTGATATTAAGCATTAATGCTTCATGCGAAGAAATTTTGTATATATACACTCG 1738
DB 90811 TAAATATATATATATATATATATATATATATATATATATATATATATATATATAT 90752
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DB 90751 ATTTATTAATATATATATATATATATATATATATATATATATATATATATATATAT 90692
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DB 90691 AATTATATATATATATATATATATATATATATATATATATATATATATATATATAT 90632
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DB 90631 TTATTAACATATATTTATATATATATATATATATATATATATATATATATATATAT 90572
QY 1919 TTTTAAATTAAGGATCATTTTATGGGTTCAATTAATATGTTTCCAGTAAAGTTGGAG 1978
DB 90571 AAGTATATATATATATATATATATATATATATATATATATATATATATATATATAT 90512
QY 1979 GTTTAAACAATGAATGTTTTTGAATTTAAAAAACATTAATTTTCTATATATTAACA 2038
DB 90511 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 90452
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DB 90214 TATATATGTTATATGATATATATATATATATATATATATATATATATATATATAT 90155
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DB 90154 TATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 90095
QY 2399 TAAAAAATGCAAAAAGAGATATATATTTTAAGTCAAGTATTTAAAGATGAGTGGG 2458
DB 90094 AATATTAATGATATATATATATATATATATATATATATATATATATATATATATAT 90035
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Oy	2459	ATTCTTCAGCAAAACGGGCGGTAGAGTGTCTATTCCTACATTAACGCTGGTTGTGC	2518
Dd	90034	TACATTATATATATATATATATATATA-----CTTATATATATATATATATATATAT	89980
Oy	2519	AGACATCATAGGGCCCTAGTATATTTTAGCTTTACTGTACGTAAAGCTTTAACAATCTCA	2578
Dd	89979	AATTGTAT	89920
Oy	2579	GTTAGTTCTCCTGTACAAAACAAAACAAATCCAATTCGTACATATATACAAATCTAC	2638
Dd	89919	ATTAAT	89860
Oy	2639	TAGACATAGATAGCTACGTACGTATACAGCTTTTTGCCAAATTCCTAACCTA-ATCTATA	2697
Dd	89859	ATATATATGTA	89800
Oy	2698	CACAAACTTGAAATGTTGTTTGTGAATTTATCTTAAACCAGAGTTTGATTTGCATT	2757
Dd	89799	TATTTAT	89740
Oy	2758	GGAGACTACACTAGTCCCCTTTTTTCCCCAAATATCTCCTTACATCGACCGTTAA	2817
Dd	89739	ATATATATATGTATATATATATATATATATCAATATTTATATATATATATATATATATAT	89680
Oy	2818	AGTATTTTAAACCAACAATTTTATTTGTGTGCGAAGGTACAACTGTCAATATATG	2877
Dd	89679	AATTTAT	89621
Oy	2878	AGACAGCATGCTTATACAAATATGTGATGCTTATGTGAATTCAAATATATATACGA	2937
Dd	89620	ATACATTTA	89561
Oy	2938	TTAGCGACTCACTGTTTATATAGTTTGGAGAAGATATGAATTTAAAAATGAAATTCAGG	2997
Dd	89560	ATATATATGTATACATATATACAAATAT--AATATATATAGTTACATATATACAAATATA	89503
Oy	2998	ATACAGAGCTATATATGTGGGTCATTTAGACCGGTACCAAAGTTTGTGCTGAATTC	3057
Dd	89502	ATATATATATATATATAGTACGAATATATATATATATATATATATATATATATATATAT	89443
Oy	3058	TAGCGTGGCTATAGAAATTTTGGACTTTTCTTCAACCTTTATATGACTCTGTATAGT	3117
Dd	89442	ATA	89383
Oy	3118	TTTTGTGCGAT-TATATATTTGTATTCGTATATTTTTTGTCTTAAATATGATAGCTAAA	3176
Dd	89382	TACA	89323
Oy	3177	TTCCAGATTAAGAAAGCTCTCTTTTATTTAATTTGATTTAAAATTGTTTGGAAAT	3236
Dd	89322	TATATATATATATATATATATATATATATTTTATATATATATATATATATATATATAT	89263
Oy	3237	GATCATACACAAGGTAAAGTTGANGATATCCATTTACAAAATGTTTGAGAGTGC	3296
Dd	89262	AATAG	89203
Oy	3297	GTTGAGAGTGTCTTACCAACATCGACCACTCGTATGGGTTTATTTAGTTTTTTTCT	3356
Dd	89202	AAATACATATATACATACA	89144
Oy	3357	TCTTTTTCATATGTCCTTATATATGGAACAACCTGAATTTCTTTTATATATAGGTAA	3416
Dd	89143	TAGAAATATATACAAATATGATTTTATGTTATATATATATATATATATATATATATAT	89084
Oy	3417	GAACTTGAATTTTCTGTGATTTTAAACCAAGTTTCAATCTTCTTAGCACAAAAA	3476
Dd	89083	ATATATATATTTGTTAT	89024
Oy	3477	AAAAAAAAGTTTCAATTTATTTAAAGATCTAAATTTTTTGTGCTCAAGATTTATATGAT	3536
Dd	89023	ATACA	88964
Oy	3537	AGCTGAAAAGTTATGAATGATGCAAGTTTGCAACGAATGTCATGTATACATATCA	3596

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